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From: Marvich, Maria
Sent: Wednesday, April 06, 2005 10:28 AM
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*Please search SEQ ID NO:s nucleotides 1-1524 of 120 , 121 (508 amino acids),
nucleotides 2007-3668 of 104 and 105 (553 amino acid)*

:Thank you

Maria Bonovich Marvich, PhD
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 09:56:57 ; Search time 6626.48 Seconds
(without alignment)
11144.035 Million cell updates/sec

Title: US-10-087-167-120_COPY_1_1524
Perfect score: 1524
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.hcg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	100.0	1767	6	AX555368 Sequence
2	1414.2	92.8	1782	6	AX555372 Sequence
3	1332	87.4	1848	6	AX555382 Sequence
4	1332	87.4	1863	6	AX555384 Sequence
5	1332	87.4	3972	6	AX555352 Sequence
6	1328.8	87.2	1767	6	AX555370 Sequence
7	1311.2	86.0	1776	6	AX555366 Sequence
8	1222.2	80.2	1800	6	AX555374 Sequence
9	1209	79.3	1428	6	AX555376 Sequence
10	1208.2	79.3	1809	6	AX555390 Sequence
11	1073	70.4	1800	6	AX555395 Sequence
12	955.6	62.7	1500	6	AX555315 Sequence
13	848.8	55.7	1515	6	AX555323 Sequence
14	836	54.9	2126	6	BD224646 Novel ecd
15	836	54.9	2126	6	AX274109 Sequence
16	763.6	50.1	1518	6	AX555341 Sequence
17	763.6	50.1	2840	3	MSU19812 Manduca sex
18	763.6	50.1	2840	6	AX555249 Sequence
19	760.4	49.9	1500	6	AX555317 Sequence

20	742.8	48.7	1509	6	AX555313	AX555313 Sequence
21	719.4	47.2	763	6	AX555253	AX555253 Sequence
22	698	45.8	1017	3	PCO251809	AJ251809 Precis co
23	693.8	44.9	6083	3	AY489269	AY489269 Plodia in
24	683.6	43.5	2036	3	AB067811	AB067811 Chilo sup
25	663.6	43.5	2501	3	AB067812	AB067812 Chilo sup
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27	638.6	41.9	838	6	AX555255	AX555255 Sequence
28	636	41.7	1524	6	AX555325	AX555325 Sequence
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32	628	41.2	1288	6	AX256353	AX256353 Sequence
33	628	41.2	1542	6	AX256401	AX256401 Sequence
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36	626.4	41.1	1290	6	AX407011	AX407011 Sequence
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45	621.6	40.8	1934	6	AR207904	AR207904 Sequence

ALIGNMENTS

RESULT 1	AX555368	Sequence 120 from Patent WO02061102.	1767 bp	DNA	linear	PAT 27-NOV-2002
LOCUS	AX555368	AX555368				
DEFINITION	AX555368	AX555368				
ACCESSION	AX555368	AX555368				
VERSION	AX555368.1	GI:25898887				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.					
TITLE	Control of gene expression in plants					
JOURNAL	Patent: WO 02061102-A 120 08-AUG-2002;					
FEATUERS	Syngenta Participations AG (CH)					
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	/transl_table=11					
	/protein_id="CAD58255.1"					
	/db_xref="GI:25898888"					
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ORIGIN						
Query Match	100.0%	Score 1524;	DB 6;	Length 1767;		

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCAGCAGCTATGTGATATTTTATAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60
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Qy	61	TACTGTTCTTTTGTTCGATGCTCACCCCTGTTGTTTGGTGTACTTCTCGAGGATCGCC	120
Db	61	TACTGTTCTTTTGTTCGATGCTCACCCCTGTTGTTTGGTGTACTTCTCGAGGATCGCC	120
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Db	121	ACCATGAAGCTACTGCTCTTCATCGAACCAAGCATCGATATTTGCGGACTTTAAAGAGCTC	180
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Db	241	TACTCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGACATCTGACAGAGTGAATCA	300
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Db	421	GATTAATGTGAATAAAGATGCGGTCA CAGATAGATTGGCTTCAGTGGAGACTCATATGCT	480
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Qy	601	ACGTGCAAGAAACAAAGAGAGAAAGAGACACAGAGAGAAAAGACAACTGCCAGTTC	660
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Qy	661	AGTAGCAGCAGTGGACGATCATATGCTTGCCTATATGCAATGTGACCTCGCCGCCCA	720
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Db	1021	TCAAAGATCTCAAACTGACAGATCAATTATTAAAGGCATGCTCAAGCGAAGTGATG	1080
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RESULT 2			
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LOCUS			linear
DEFINITION	Sequence 124 from Patent WO02061102.		PAT 27-NOV-2002
ACCESSION	AX555372		
VERSION	AX555372.1	GI:25898891	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1		
	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 124 08-AUG-2002;		
	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
source	1..1782		

[illegible]

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Db	121	ACCATGAAGCTACTGCTTCTTATCGAAACAAGATCGGATATTTGCGGATCTAAAGATC	180
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Db	181	AAGTCTCCAAAGAAAACCGAAGTGCCTGCTGCTGAGCAAACTGCGGAGTGTGCG	240
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Qy	421	GATATGTGAATAAAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCT	480
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Qy	481	CTAACATTGAGCAGCATAGATAAAGTGCATCATCATCATCATCATCATCATCATCAT	540
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RESULT 3

AX555382

LOCUS

Sequence 134 from Patent WO02061102.

DEFINITION

AX555382

ACCESSION

AX555382.1

VERSION

GI:25898901

KEYWORDS

synthetic construct

SOURCE

other sequences; artificial sequences.

ORGANISM

REFERENCE

1

AUTHORS

Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.

TITLE

Control of gene expression in plants

JOURNAL

Patent: WO 02061102-A 134 08-AUG-2002;

Syngeta Participations AG (CH)

FEATURES

Location/Qualifiers

1..1848

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1..1848

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ORIGIN		Query Match	87.4%; Score 1332; DB 6; Length 1848;
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Qy	121	ACCATGAAGCTACTGCTTCTTATCAACCAAGCATCGGATATTTGCGGACTTTAAAAAGCTC	180
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Qy	181	AAGTGTCTCAAGAAAAACCGAAGTGCAGGCTGCTGTAAGAACAACTGGGAGTGTGCG	240
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Qy	241	TACTCTCCAAAACCAAGGCTCTCCGCTGACTAGGCGACATCTGACAGAGTGGATCA	300
Db	241	TACTCTCCAAAACCAAGGCTCTCCGCTGACTAGGCGACATCTGACAGAGTGGATCA	300
Qy	301	AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTTCTCGAGAGAGCTTTGACATG	360
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Qy	361	ATTTTGAAGATGGATTTCTTTACAGATATAAAGCATTTGTAACAGGATTTATTTGTACAA	420
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Qy	481	CTAACATTTGACAGCAGCATAGATTAAGTGCAGACATCATCGAAGAGAGTAGTAACAAA	540
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Qy	541	GGTCAAGACAGTTGACTGTTATCGACGGTATGAGCCCGAGTGGTCCGAGAGTCC	600
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Qy	601	ACGTGCAAGAACAAAAGAGAGAAAAGGAGCAGAGAGAAAAGACAACTGCCAGTC	660
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Db	661	AGTACGACGACAGTGGAGCTATATGCTTCCCATATGCAATGTGACCCCTCCGCCCCCA	720
Qy	721	GAGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTTAATGGAGAG	780
Db	721	GAGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTTAATGGAGAG	780
Qy	781	AACAGACTGAAGATGTGACCCGCTGTCGCGAACCCAGAGTCCCTGATCGCGAGGCTC	840
Db	781	AACAGACTGAAGATGTGACCCGCTGTCGCGAACCCAGAGTCCCTGATCGCGAGGCTC	840
Qy	841	GTGTGGTACCCAGGAGCGGATACGACGAGCGCTCGGAGGAGATCTCAAGAGAGTTTACACAG	900
Db	841	GTGTGGTACCCAGGAGCGGATACGACGAGCGCTCGGAGGAGATCTCAAGAGAGTTTACACAG	900
Qy	901	ACTTGGCAATCAGAGATGAAGAGAGAGAGCTCAGACATGCCATTCGCGCAGATCACA	960
Db	901	ACTTGGCAATCAGAGATGAAGAGAGAGAGCTCAGACATGCCATTCGCGCAGATCACA	960

Db	901	ACATGGCAGTTTGAAGAAGAAGAGAGAGAAATGACATGCTCCCTTCGTCAGATCACA	960
Qy	961	GAAATGACCATCTTCACAGTACAGCTAATAGTCAGATTTGCCAAAGGCTTACCTGCTTTT	1020
Db	961	GAGATGACCATCTTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAGGGAATACCGGATTC	1020
Qy	1021	TCAAAGATCTCACAACTGACCCAGATCATATTATTAAGGCTGCTCAAGCGAAGTGTATG	1080
Db	1021	TCCAAGATATCTAGTCCGATCAAAATTTACATTTATTAAGGCTGCTCATCAGCGAAGTGTATG	1080
Qy	1081	ATGCTGCGAGTACGAGGCGGTACGACGCGGTGTCGATAGCGTTCGTGTTCCGCAACAAC	1140
Db	1081	ATGCTGCGAGTGGCGGACGCTACGACGCGCGACGACAGCGTGTCTGTTCCGCAACAAC	1140
Qy	1141	CAGCGCTACACTCGCGAACACTACCGCAAGCGCGGCTAGGCTACGTCATCGAAGACCTG	1200
Db	1141	CAGCGCTACACGCGCACTACCGCAAGCGCGGCTAGGCTACGTCATCGAAGACCTG	1200
Qy	1201	CTGCACATCTGCGCTGCATGTACTCGATGTCGATGACACGTCGATTAACGCGCTCTC	1260
Db	1201	CTGCACATCTGCGCTGCATGTACTCGATGTCGATGACACGTCGATTAACGCGCTCTC	1260
Qy	1261	ACTGCCATCGTTATTTCTCGGATCGCGCGGCTAGAGCAGCCACAGTAGTAGAAGAG	1320
Db	1261	ACGCCATCGTTATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTATGTCGAGGAA	1320
Qy	1321	ATCCAGCGGTATTTACCTGAAACAGCTCGGCTGTCATCATGAACACGACGCGCTCG	1380
Db	1321	ATCCAGAGATTAATTTGAAAGCGCTCGGCTTTTACATTTTAAATCAGCAGCGCGCTCG	1380
Qy	1381	CCGCGTTGCGCGCTCATCTACGCAAGATTTCTGCGGTGCTTACCGAGTTTCGCGACGCTG	1440
Db	1381	CCTCGCTGCGCGCTGCTGTTCCGCAAGATCCTCGCGTGTGTCGCGAAGTTCGCGACGCTC	1440
Qy	1441	GGCATGCAAGATTCGAACATGTGATCTCGCTGAAGCTCAAGAACAGAAAGCTCCGCGC	1500
Db	1441	GGCAGCAGAACTCCAACTGTCATCTCGCTGAAGCTGAAGAACAGAAAGTTCGCGCA	1500
Qy	1501	TTCTCGAGGAGATCTGGGACGTG 1524	
Db	1501	TTCTCGAGGAGATCTGGGACGTG 1524	

RESULT 4		AX555384	1863 bp	DNA	linear	PAT 27-NOV-2002
LOCUS		Sequence 136 from Patent WO02061102.				
DEFINITION		AX555384				
ACCESSION		AX555384.1				
VERSION		GI:25898903				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE		1				
AUTHORS		Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.				
TITLE		Control of gene expression in plants				
JOURNAL		Patent; WO 02061102-A 136 08-AUG-2002;				
FEATURES		Syngenta Participations AG (CH)				
source		Location/Qualifiers				
		1..1863				
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		/db_xref="taxon:32630"				
CDS		1..1863				
		/notes="unnamed protein product; Ecdysone receptor chimera G(M)D"				
		/codon_start=1				
		/transl_table=11				
		/protein_id="CAD58261.1"				
		/db_xref="GI:25898904"				
		/translation="MOQLVDFPSPAFIRYLFPAWYFFRCRSPCCLLVLLQGSATMKL LSSIEQACDICRLKUKCKSKPKCAKCLKNWECRYSPKTRKSPLTRAHLTVEESRL				

ORIGIN
Query Match 87.4%; Score 1332; DB 6; Length 1863;
Best Local Similarity 92.1%; Pred. No. 0; Mismatches 120; Indels 0; Gaps 0;
Matches 1404; Conservative 0;
1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
Db 1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
61 TACTGTTCTTTTGTGCGATGCTACCCCTGTTGTTGTTGTTACTTCTGCGAGGATCCGCC 120
Db 61 TACTGTTCTTTTGTGCGATGCTACCCCTGTTGTTGTTGTTACTTCTGCGAGGATCCGCC 120
121 ACCATGAGCTACTGTTCTTATCGAACAAGCATGCTATTTGCGACTTAAAAAGCTC 180
Db 121 ACCATGAGCTACTGTTCTTATCGAACAAGCATGCTATTTGCGACTTAAAAAGCTC 180
181 AAGTGTCTCAAGAAAGAAACCGAAGTGCCTGCTGCTGAAGAAACAACTGGAGTGTGCG 240
Db 181 AAGTGTCTCAAGAAAGAAACCGAAGTGCCTGCTGCTGAAGAAACAACTGGAGTGTGCG 240
241 TACTCTCCAAACCAAAAGGCTCTCGCTGACTAGGGACATCTGACAGAACTGGAATCA 300
Db 241 TACTCTCCAAACCAAAAGGCTCTCGCTGACTAGGGACATCTGACAGAACTGGAATCA 300
301 AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG 360
Db 301 AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG 360
361 ATTTTGAAGATGATTTTCAAGGATATAAAGCAATTTGTTAAAGGATTTATTTGACAA 420
Db 361 ATTTTGAAGATGATTTTCAAGGATATAAAGCAATTTGTTAAAGGATTTATTTGACAA 420
421 GATAATGTGAATAAAGATGCGCTCAAGATGAGTTCAGTGGAGATGATATGCTT 480
Db 421 GATAATGTGAATAAAGATGCGCTCAAGATGAGTTCAGTGGAGATGATATGCTT 480
481 CTAACTTGAAGACATGAGTAAGTGGACATCATCTCGAAGAGAGATGATACAAA 540
Db 481 CTAACTTGAAGACATGAGTAAGTGGACATCATCTCGAAGAGAGATGATACAAA 540
541 GGTCAAGACAGTTGACTGTATCGAGCGGTATGAGGCCGAGTGCCTGCTCCAGAGTCC 600
Db 541 GGTCAAGACAGTTGACTGTATCGAGCGGTATGAGGCCGAGTGCCTGCTCCAGAGTCC 600
601 ACCTGCAAGAACCAAAAG 660
Db 601 ACCTGCAAGAACCAAAAG 660
661 AGTACGACGAGTGGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 AGTACGACGAGTGGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721 GAGCGCGAAGGATTTCAAGAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAG 780
Db 721 GAGCGCGAAGGATTTCAAGAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAG 780
781 AACAGACTGAAGATGTGAGCCGCTGTGCGCGAAGCAGAGAGTCCCTGATCGCGAGCTC 840
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841 GTGTGTTACCGAGGAGATACGAGCCCTTCCGAGAGAGATCTCAAAAGGTTGACGCGAG 900

Db 841 GTGTGTTACCGAGGAGGTTACGAGCCCTCGGAGAGAGATCTCAAGAGAGTTACACAG 900
Qy 901 ACTTGGCAATCAGCAGATGAAGAGAGAGAGATCTCAGACATGCTCCGCGCAGATCACA 960
Db 901 ACATGGCAGTTAG 960
Qy 961 GAAATGACCATCTCTCAGCAGTACAGCTAATAGTCAAGTTTGGCAAGGCTACCTGTTT 1020
Db 961 GAGATGACGATCTTAAACAGTGCAGCTTATTTAGTAATTCGCAAGGAGACTACCGGATTC 1020
Qy 1021 TCAAGATCTCACAACCTGACCATCACAATTTAAAGGCATGCTCAAGCGAAGTGAATG 1080
Db 1021 TCCAAGATATCTCAGTCCGATCAAAATTAACAATTTAAAGGCGTCATCAAGCGAAGTGAATG 1080
Qy 1081 ATGCTGCGAGTAGGAGCGGTACGACGCGGTGTCGATAGCTGCTTCTGTCGCAACAC 1140
Db 1081 ATGCTGCGAGTGGCGGACGCTACGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 CAGCGTACACTCGCGCAACTACCGCAAGCGGCGATGGCTTACGTCATCGAAGACCTG 1200
Db 1141 CAGCGTACACTCGCGCAACTACCGCAAGCGGCGATGGCTTACGTCATCGAAGACCTG 1200
Qy 1201 CTGCACTTCTGCGTGTATGCTTCTTCCATGAGCATGGAATGTCATCTGCGCTGCTC 1260
Db 1201 CTGCACTTCTGCGTGTATGCTTCTTCCATGAGCATGGAATGTCATCTGCGCTGCTC 1260
Qy 1261 ACTGCACTGTTATTTCTCGATCGCGCGGCTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 ACCGCGATCTGTTATTTCTCAGACGCGGCGCTCGAGCAACCCCTTTTAGTGGAGAA 1320
Qy 1321 ATCCAGCGGATTTACTCTGAACAACGCTGCGGCTGTTACATCATGAAACAGCAGCGCTG 1380
Db 1321 ATCCAGAGATACTACTTGAAGACGCTGCGGCTTACATTTTAAATCAGCAGCGCTG 1380
Qy 1381 CCGGCTTGGCGCTCATCTACCGAGATTTCTGCGTGTCTTACCGAGTTGCGGAGCTG 1440
Db 1381 CCGGCTTGGCGCTCATCTACCGAGATTTCTGCGTGTCTTACCGAGTTGCGGAGCTG 1440
Qy 1441 GGCATGCAAGATTCGAAACATGTCATCTGCTGAAAGCTCAAGAGAGAGAGAGAGAGAG 1500
Db 1441 GGCATGCAAGATTCGAAACATGTCATCTGCTGAAAGCTCAAGAGAGAGAGAGAGAG 1500
Qy 1501 TTCTCTGAGGAGATCTGCGACCTG 1524
Db 1501 TTCTCTGAGGAGATCTGCGACCTG 1524

RESULT 5
AX555352
LOCUS AX555352 3972 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 104 from Patent WO02061102.
ACCESSION AX555352
VERSION AX555352.1 GI:25898871
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Pascal,B.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 104 08-AUG-2002;
Syngenta Participations AG (CH)
FEATURES
source 1..3972
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
misc_feature 1..3972
/note="GAL4-Manduca Ecr-VP16 fragment in pGSG202"
CDS 2007..3668
/notes="unnamed protein product; GAL4-Manduca Ecr-VP16 chimera"

Query Match	87.4%	Score 1332	DB 6	Length 3972
Best Local Similarity	92.1%	Prod. No. 0	Mismatches 120	Indels 0
Matches 1404	Conservative	0		
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1884	ATCGAGCAGCTATATGTGGATTTTTTTTATAGCCCTCGCTTCATACGCTATTTATTTGTCTGG 1943			
61	TACTGTTTCTTTTGTGATGCTCTCAACCTGTGTTGTTGTTACTTCTGACGGGATCGCC 120			
1944	TACTGTTTCTTTTGTGATGCTCACCTGTGTTGTTGTTACTTCTGACGGGATCGCC 2003			
121	ACCATGAAGCTACTGTCTTCTATCGAAACAGCATCGCATATTTGCCGACTTAAAAAGCTC 180			
2004	ACCATGAAGCTACTGTCTTCTATCGAAACAGCATCGCATATTTGCCGACTTAAAAAGCTC 2063			
181	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAACAACTGGAGGTGTGCG 240			
2064	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAACAACTGGAGGTGTGCG 2123			
241	TACTCTCCAAAACCAAAGGTCTCGCTGACTGAGGCACATCTGACAGAAGTGGAAATCA 300			
2124	TACTCTCCAAAACCAAAGGTCTCGCTGACTGAGGCACATCTGACAGAAGTGGAAATCA 2183			
301	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAAGAGACTTGTGACATG 360			
2184	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAAGAGACTTGTGACATG 2243			
361	ATTTTGAANAATGGATCTTTTACAGATATAAAGCAATGTTTAAAGGATTTATTTGTACAA 420			
2244	ATTTTGAANAATGGATCTTTTACAGGATATAAAGCAATGTTTAAAGGATTTATTTGTACAA 2303			
421	GATTAATGTGAATAAAGATCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCT 480			
2304	GATTAATGTGAATAAAGATCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCT 2363			
481	CTAACATTGGACAGCAATAGAATAAGTGGCAATCATATCGGAAGAGAGTAGTAAACAA 540			
2364	CTAACATTGGACAGCATAAGATAAGTGGCAATCATATCGGAAGAGAGTAGTAAACAA 2423			
541	GGTCAAGAAGCAGTTGACTGTATCGACCGTATGAGCCCGAGTGGTGGTCCCGAGAGTCC 600			
2424	GGTCAAGAAGCAGTTGACTGTATCGACCGTATGAGCCCGAGTGGTGGTCCCGAGAGTCC 2483			
601	ACGTGCAAGAACAAAAGAGAAAAGGAAGCAACAGAGAGAAAAGACAAAATGCGCAGTC 660			
2484	ACGTGCAAGAACAAAAGAGAAAAGGAAGCAACAGAGAGAAAAGACAAAATGCGCAGTC 2543			
661	AGTACGACGACAGTGGACGATCATATGCTTGCATTAATGCAATGTGAACCTTCGCCCCCA 720			
2544	AGTACGACGACAGTGGACGATCATATGCTTGCATTAATGCAATGTGAACCTTCGCCCCCA 2603			
721	GAGCGGCAAGGATTCACGAAGTGGTCCCGAGGTCTCTAACGGAGAAAGCTAATGAGCAG 780			
2604	GAGCGGCAAGGATTCACGAAGTGGTCCCGAGGTCTCTAACGGAGAAAGCTAATGAGCAG 2663			
781	AACGACTTGAAGAATGTGACGCCGCTGTGCGCGAACACAGAGTCTCTGATTCGAGGCTC 840			

source	1..1776	/organism="synthetic construct"	
		/mol_type="unassigned DNA"	
CDS	1..1776	/db_xref="taxon:32630"	
	note="unnamed protein product; Ecdysone receptor chimera G(M)BV"		
	/codon_start=1		
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	/protein_id="CAD58254.1"		
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	/translation="MOQLYVDFPSPAFIRYLFAWYCFRCSPCLVLLQSGATMKL LSSLEQACDILRLKWKSKKPKCAKLNKWEKRYSPKTKRSPLEAHLTEVESPL ERLEQLFLILFPREDLMDLKWDSQDILKLLGLFVQDNVKNKDAVDRLASVETDNP LTLQHRISATSSSESNKQRLTVSTRNPECVPEKSEKKNRREKAQREKOKL PVSTTVDDHMPAIMQCDPPPEARIEHVVPRLTEKJMEQNRKLVTPLSANQKSL IARLVYQEGVEQSEEDLKVOTWQSDDEBESDMPFRQITEMTILITVQLIVEFAK GLPFAKLSQSDILTLKACSEVMVLRVARYDAATDSVLFANNOAVSRDNYRKAGM SYVEDLHLFRCHMYMMNDVHYHALLTAIVIFSDRPLGLEPILLAVEIORVYLNTLV YILNQNSASPRCPVVFALIKILGLTLRLTGLMGNMCLSLKLNKRLPPFLEEINDVE SRGLAPPTDVLGDELGDVEDVAMAHADALDDFDLMDLGDGDSPGPGFTPHDSAFY GALDWDAPFEFEQMTDALIDIEYGG"		
ORIGIN	86.0%; Score 1311.2; DB 6; Length 1776;		
	Query Match 91.7%; Pred. No. 5.8e-309; Mismatches 123; Indels 3; Gaps 1;		
	Matches 1398; Conservative 0;		
QY	1	ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60
DB	1	ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60
QY	61	TACTGTTCTTTTGTGATGCTACCCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC	120
DB	61	TACTGTTCTTTTGTGATGCTACCCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC	120
QY	121	ACCATGAAGCTACTGTTCTTATCGAACAGCATCGATATTTGCGGACTTAAAAAGCTC	180
DB	121	ACCATGAAGCTACTGTTCTTATCGAACAGCATCGATATTTGCGGACTTAAAAAGCTC	180
QY	181	AAGTGTCTCCAAAGAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAACTGGAGTGTGCG	240
DB	181	AAGTGTCTCCAAAGAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAACTGGAGTGTGCG	240
QY	241	TACTCTCCAAACCAAAGGTCTCGCTGACTAGGGACATCTGCAGAGTGAATCA	300
DB	241	TACTCTCCAAACCAAAGGTCTCGCTGACTAGGGACATCTGCAGAGTGAATCA	300
QY	301	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAACCTTGACATG	360
DB	301	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAACCTTGACATG	360
QY	361	ATTTTGAATAATGATTTCTTTACAGATATAAAGCAATTTGTTAACAGGATTTTGTACAA	420
DB	361	ATTTTGAATAATGATTTCTTTACAGATATAAAGCAATTTGTTAACAGGATTTTGTACAA	420
QY	421	GATAATGTGAATAAGATCCGTCACAGATAGATTTGCTTCTAGTGGAGACTGATATGCT	480
DB	421	GATAATGTGAATAAGATCCGTCACAGATAGATTTGCTTCTAGTGGAGACTGATATGCT	480
QY	481	CTAACATTGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAA	540
DB	481	CTAACATTGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAA	540
QY	541	GGTCAAAGACAGTTGATGTATCGACGCTATAGAGCCGAGTGCCTCCAGAGTCC	600
DB	541	GGTCAAAGACAGTTGATGTATCGACGCTATAGAGCCGAGTGCCTCCAGAGTCC	600
QY	601	ACGTGCAAGAACAAAAGAGAGAAAAGGACACAGACAGAGAAAAAGACAACTGCCAGTTC	660
DB	601	ACGTGCAAGAACAAAAGAGAGAAAAGGACACAGACAGAGAAAAAGACAACTGCCAGTTC	660
QY	661	AGTACGACGACAGTGGAGACGATCATATATGCTGCGCATATGCAATGTGACCCCTCGCCCCCA	720

DB	661	AGTACGACGACAGTGGACGATCATATGCTGCCATATGCAATGTGACCTCGCCCCCA	720
QY	721	GAGCGCGCAAGGATTCACGAAGTGTCCGAGGTTCCTAACCGGAGAGCTAATGGAGCAG	780
DB	721	GAGCGCGCAAGGATTCACGAAGTGTCCGAGGTTCCTAACCGGAGAGCTAATGGAGCAG	780
QY	781	AACAGACTGAAGAATGTGACGCGCTGTGCGGCAACACAGAACTCCCTGATCGGAGGCTC	840
DB	781	AACAGACTGAAGAATGTGACGCGCTGTGCGGCAACACAGAACTCCCTGATCGGAGGCTC	840
QY	841	GTGTGGTACCAGACCGATACGAGCAGCTTTCGGAAGAGATCTTAAAAGGTGAGCGCAG	900
DB	841	GTGTGGTACCAGACCGATACGAGCAGCTTTCGGAAGAGATCTTAAAAGGTGAGCGCAG	900
QY	901	ACTTGGCAATCAGACATGAAAGACGAGACTCAGACATGCCATTTCGCGCAGATACACA	960
DB	901	ACTTGGCAATCAGACATGAAAGACGAGACTCAGACATGCCATTTCGCGCAGATACACA	960
QY	957	ACCTGGCAGT---CGGACGAGGATGAAGAGAGTCAAGATATGCCGTTCCGCAAGATCAC	957
QY	961	GAATGACCATCTCTCAGTACAGTAAATAGTCAAGTTCGCAAAAGCCCTTACCTGTTTT	1020
DB	958	GAGTACAGATCTTGACAGTCAACTCATCGTAGAATTCGCAAAAGCCCTGCCAGGCTTC	1017
QY	1021	TCAAAGATCTCAACAACCTGACAGATCAATTAATTAAGSCATGCTCAAGCGAAGTGATG	1080
DB	1018	GCCAAGATCTCGCAGTCGGATCAATCAACGTTACTAAAGCGGTGTTCAAGTGAAGTGATG	1077
QY	1081	ATGCTCGCAGTACGAGCGGTACGAGCGGTGTCGATAGCGTTCCTGTTTCGCAACAAC	1140
DB	1078	ATGCTCGCAGTACGAGCGGTACGAGCGGTGTCGATAGCGTTCCTGTTTCGCAACAAC	1137
QY	1141	CAGCGGTACACTCGCGCAAACTACCGAAGCGCGGATGCGCTACGTCATCGAAGACTG	1200
DB	1138	CAGCGGTACTCCGCGGACAACTACCGAAGCGAGCATGCTTACGTCATCGAGGATCTC	1197
QY	1201	CTGCACTTCTGCGCTGCATGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG	1260
DB	1198	TTGCACCTTCTGCGTGCATGCTTCCATGATGATGATGATGATGATGATGATGATGATG	1257
QY	1261	ACTGCCATCGTTATTTCTCGGATCGGCGCGGCTAGAGCAGGCCACAGCTAGTAGAAGAG	1320
DB	1258	ACGCCATTTGCTATTTCTCAGACCGGCTGGGCTCGAGCAACCTTTATTGGTGGAAAGAA	1317
QY	1321	ATCCAGCGGATTTACCTGAAACAGCTCGGGGTGTATCATATGACACGACAGCGGCTCG	1380
DB	1318	ATCCAGCGGATTTACCTGAAACAGCTCGGGGTGTATCATATGACACCAAAACAGTGCCTG	1377
QY	1381	CCGCGTTGCGCGCTCATCTAGCGGAAGATTTCTGCGTGTCTTACCGAGTTGCGGACGCTG	1440
DB	1378	CCGCGCTGCGCGCTGATGCTTCCGCAAGATCTGCGGGAATTTGACGGAGCTGCGGACCTC	1437
QY	1441	GGCATGCAAGATTCGAACATGTGATCTCGCTGAAGCTCAAGAACAGAGAGCTGCGCGCG	1500
DB	1438	GGCATGCAAGATTCGAACATGTGATCTCGTTGAAGCTGAAGATAGAGAGCTGCGCGCG	1497
QY	1501	TTCTCGAGGAGATCTGGGACGCTG 1524	
DB	1498	TTCTCGAGGAGATCTGGGACGCTG 1521	

RESULT 8	AX555374	1800 bp	DNA	linear	PAT 27-NOV-2002
LOCUS	Sequence 126 from Patent WO02061102.				
DEFINITION	AX555374				
ACCESSION	AX555374				
VERSION	AX555374.1 GI:25898893				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.				

RESULT	9
AX55376	
LOCUS	AX555376
.DEFINITION	Sequence 128 from Patent WO02061102.
ACCESSION	AX555376
VERSION	AX555376.1 GI:25898895
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
	linear DNA 1428 bp PAT 27-NOV-2002

REFERENCE AUTHORS	other sequences; artificial sequences.		1		Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		541		ACGACGACAGTGGACGATCATATGCTGCCATAATGTAATGTGACCTCCGCCCCCCAGAG		600	
	Control of gene expression in plants		2		Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		724		GGGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTAATGAGCAGAAC		783	
TITLE JOURNAL	Patent: WO 02061102-A 128 08-AUG-2002;		3		Syngenta Participations AG (CH)		601		GGGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTAATGAGCAGAAC		660	
	Location/Qualifiers		4		1..1428		784		AGACTCAAGAATGTGACGCGCTGTCCGGCAACCAAGAGTCCCTGATCCGAGGCTCGTG		843	
FEATURES	source		5		/organism="synthetic construct"		661		AGACTCAAGAATGTGACGCGCTGTCCGGCAACCAAGAGTCCCTGATCCGAGGCTCGTG		720	
	CDS		6		/db_xref="caxon:32630"		844		TGGTACCAGGACGATACGAGAGCTTCCGAGAGGATCTCAAAAGGCTGACGAGACT		903	
CDS	1..1428		7		/note="unnamed protein product; G(M)M (GAL4 DNA Binding Domain) fused to the Manduca Ecr Hinge and Ligand Binding Domain"		721		TGGTACCAGGAGGGTACGAGAGCTTCCGAGAGGATCTCAAGAGAGTTACACAGACA		780	
	/codon_start=1		8		/protein_id="CAD58259.1"		904		TGCAATCAGCAGATCAAGAAGACGAGAGCTCAGACATGCCATTCGCCAGAGTACACAGAA		963	
ORIGIN	/translation="MKLSSIEQACDICRLKJGKSKKPKCAKCLKNNECRVSPKT		9		/db_xref="gi:25898896"		781		TGGCAGTTTGAAGAAGAAGAGGAGGAAACTGACATGCCCTTCCTGATCAGATCAGAG		840	
	KSDPUTRAHLEVESRLRLQLFLIPREDLMDLMDLSODIKALLTGLFVODNV		10		/transl_table=11		964		ATGACCATCTCAAGTACAGTAAATAGTTCGAGTTTTCGCAAGGCTTACTCTGTTTTC		1023	
Query Match	79.3%; Score 1209; DB 6; Length 1428;		11		/db_xref="gi:25898896"		841		ATGACCATCTTAACAGTTCGAGCTTATTGTAGAAATTCGAAAGGACTACCGGGATTCTCC		900	
	Best Local Similarity 91.4%; Pred. No. 5.1e-284;		12		Matches 1281; Conservative 0; Mismatches 120; Indels 0; Gaps 0;		1024		AAGATCTCAACCTGACACGATCAATATTAAAGGCTGCTCAAGCGAGTGTGATG		1083	
124	ATGAGCTACTGCTTCTATCGAACCAAGCATCGGATATTTCGCGACTTAAAGAGCTCAAG		13		1083		901		AAGATATCTCAGTCCGATCAATATTACATTTATTAAAGGCGTCATCAAGCGAGTGTGATG		960	
	124		14		1083		1084		CTCGAGTACGAGGCGGTACGACGCGTGTCCGATAGCGTTCTGTTGCGCAACCAACAG		1143	
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TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 147 08-AUG-2002;		
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VERSION AX555315.1 GI:25898834
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ORGANISM other sequences; artificial sequences.
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AUTHORS Pascal,B.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and
Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 67 08-AUG-2002;
Syngenta Participations AG (CH)
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QY 1343 CGCTCGCGGTGTACATCATGAACCAACAGCAGCGCGTCCGCGTTCGCGCGTCACTACG 1402
DB 1076 CGCTCGCGGTGTACATCATGAACCAACAGCAGCGCGTTCGCGCGTCACTACG 1135
QY 1403 CGAAGATTCTGTCGCTGCTTACCGAGTTGCGGACGCTGGGATCGAGAAATTCGAACATGT 1462
DB 1136 CGAAGATTCTGTCGCTGCTTACCGAGTTGCGGACGCTGGGATCGAGAAATTCGAACATGT 1195
QY 1463 GCATCTCGCTGAAGCTCAAGAACAGAGTTCGCCCGCTTCCTCGAGGAGATCTGGGAGC 1522
DB 1196 GCATCTCGCTGAAGCTCAAGAACAGAGTTCGCCCGCTTCCTCGAGGAGATCTGGGAGC 1255
QY 1523 TG 1524
DB 1256 TG 1257
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RESULT 13
AX555323
LOCUS AX555323 1515 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 75 from Patent WO02061102.
ACCESSION AX555323
VERSION AX555323.1 GI:25898842
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pascal,B.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and
Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 75 08-AUG-2002;
Syngenta Participations AG (CH)
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ORIGIN

Query Match	55.7%	Score 848.8	DB 6	Length 1515
Best Local Similarity	90.9%	Pred. No. 4.6e-196		
Matches 920	Conservative 0	Mismatches 77	Indels 15	Gaps 1
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Db	261	GAATGTCAAGATGCGGTT	GAAAGTAGTTTAGCGGTGGGATCGAGCCCGAGTGCCT	320
Qy	588	CGTCCCAGAGTCCACGTG	CAAGAACAAAAGAGAAAGAGACGACAGAGAGAAAAGA	647
Db	321	GGTGCCAGAAACGCGAGT	TCGCGAAAAGAAAGAGAAAGAGACGACAGAGAGAAAAGA	380
Qy	648	CAAACTCCAGTCAGTAGC	ACGACAGTGGACGATCATATGCTCGTCCCATATATGCAATGTGA	707
Db	381	CNAACTACCACTGAGCA	CAACGACAGTAGACGATCATATGCTCGTCCCATATATGCAATGTGA	440
Qy	708	CCCTCCCGCCCGCAGAG	CGGCAAGATT-----CACGAAGTGTGCCGAG	752
Db	441	TCCACCACCCCGGAGG	CGAGGATTCTGGAATGTTTCGACATGAAGTGTGCCGCG	500
Qy	753	GTTCTTAACGGAGAGCT	TAATGGAGCAGAAACAGACTGCAAGAAATGTACGCCGCTGTCCGC	812
Db	501	GTTCTCTCGAGAAAGCT	GATGGAGCAGAAATCGCTGGAAGAAATATACCCCTCTACCCGC	560
Qy	813	GAACCAAGTCCCTGAT	CGCGAGCTCGTGTGTACCGAGCGGATACGAGCAGAGCTTC	872
Db	561	CAACACAGATTCTCTG	ATCGCGAGCTGTGTGTACCGAGCGGATACGAGCAGAGCTTC	620
Qy	873	GGAAAGAGATCTCAAA	AGGTGACGACAGCTTGGCAATCAGCAGATGAAGAGACGAGAA	932
Db	621	GGAAAGAGATCTCAAA	AGGGTGACGACAGCTTGGCAATCAGCAGATGAAGAGACGAGAA	680
Qy	933	CTCAGACATGCCATTCC	GCCAGATCACAGAAATGACCATCTCACAGTACAGACTAATAGT	992
Db	681	CTCAGACATGCCATTCC	GCCAGATCACAGAAATGACCATCTCACAGTACAGACTAATAGT	740
Qy	993	CGAGTTTGCCAAAGGCT	TACTGTGTTTTCAAGATCTCAACCTGACAGATCAATT	1052
Db	741	CGAGTTTGCCAAAGGCT	TACTGTGTTTTCAAGATCTCAACCTGACAGATCAATT	800
Qy	1053	ATTTAAAGGCATGCTCA	AGCGAAGTATGATGCTCGGAGTACGAGGCGGTACGACGCGT	1112
Db	801	ATTTAAAGGCATGCTCA	AGCGAAGTATGATGCTCGGAGTACGAGGCGGTACGACGCGT	860
Qy	1113	GTCGGATAGCGTTCTGT	TCGCCAACAAACACGAGCGGTACACTCGCGACAACCTACGCAAGGC	1172
Db	861	GTCGGATAGCGTTCTGT	TCGCCAACAAACACGAGCGGTACACTCGCGACAACCTACGCAAGGC	920
Qy	1173	GGCGATGCGCTACGTCA	TCGGAAGACCTGCTGCACTTCTGCCGCTGCATGTACTCGATGTC	1232
Db	921	GGCGATGCGCTACGTCA	TCGGAAGACCTGCTGCACTTCTGCCGCTGCATGTACTCGATGTC	980
Qy	1233	GATGGACAACGTGCATT	ACGCGCTCCTCACGTGCCATGTTATATTTCTCGGATCGGCGCGG	1292
Db	981	GATGGACAACGTGCATT	ACGCGCTCCTCACGTGCCATGTTATATTTCTCGGATCGGCGCGG	1040
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Qy	1353	GTACATCATGAACGAC	GACGCGGTGCGCGCTGCGCGCTCATCTACGCGGAAGATTCT	1412
Db	1101	GTACATCATGAACGAC	GACGCGGTGCGCGCTGCGCGCTCATCTACGCGGAAGATTCT	1160
Qy	1413	GTCCGTGCTTACCGAGT	TGCGGACGCTGGGATCGAAGTTTCGAAACATGTGCATCTCGCT	1472

Db	1161	GTCCGGTCTTACCGAGTTCGGACGCTGGCGATGCAGAAATCGAAATGTGCAATCTCGCT	1222
Qy	1473	GAAGCTCAAGAACAGAGAACTGCCCGCGTCTCTGGAGGAGATCTGGGAGTG	1524
Db	1221	GAAGCTCAAGAACAGAGAACTGCCCGCGTCTCTGGAGGAGATCTGGGAGCG	1272

RESULT 14

BD224646	2126 bp	DNA	linear	PAT 17-JUL-2003
LOCUS				
DEFINITION	Novel ecdysone receptors and methods for their use.			
ACCESSION	BD224646			
VERSION	BD224646.1 GI:33034416			
KEYWORDS	JP 2002525053-A/1.			
SOURCE	Ostrinia nubilalis (European corn borer)			
ORGANISM	Ostrinia nubilalis			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea; Pyralidae; Pyraustinae; Ostrinia.			
AUTHORS	1. (bases 1 to 2126)			
TITLE	Albertsen,M.C., Brooke,C.D., Garnaat,C.W. and Roth,B.A.			
JOURNAL	Novel ecdysone receptors and methods for their use			
COMMENT	Patent: JP 2002525053-A 1 13-AUG-2002; PIONEER HI BRED INTERNATIONAL INC OS Ostrinia nubilalis PN JP 2002525053-A/1 PD 13-AUG-2002 PF 10-SEP-1999 JP 2000570318 PR 10-SEP-1998 US 60/099793 PI MARC C ALBERTSEN,CATHERINE D BROOKE,CARL W GARNAAT,BRADLEY PI ALLEN ROTH PC C12N15/09,A01H5/00,C07K14/705,C12N5/10,C12P21/02//C07K19/00, PC C12N15/00, PC C12N5/00 CC Nucleotide sequence and deduced amino acid sequence of CC Ecdysone receptor FH Key Location/Qualifiers FT CDS Location/Qualifiers 1. .2126 /organism="Ostrinia nubilalis" /mol_type="genomic DNA" /db_xref="taxon:29057"			
FEATURES	source			

ORIGIN

Query Match	54.9%;	Score 836;	DB 6;	Length 2126;
Best Local Similarity	90.1%;	Pred. No. 6.4e-193;		
Matches 912;	Conservative 0;	Mismatches 85;	Indels 15;	Gaps 1;
QY	528	GAGTAGTAAACAAGGTC	CAAGACAGTGTGACTGATCGACGCGTATCGAGGCGCCGAGTGCCT	587
DB	940	GAATGTC	CAAGAAATGCCGGTTGAAGAAAGTGTTAGCGGTGGGCATGAGGCCCGAGTGCCT	999
QY	588	CGTCCCAGAGTCCACG	TGCACGCAAGAAACAAAAGACAGAGAAAAGGAAGACACAGAGAGAAAAGA	647
DB	1000	GGTGCCAGAAACCG	CAGTGTGCGCAAAAANAGAAAGACAGAAAGACACAGAGAGAAAAGA	1059
QY	648	CAAACTGCCAGT	CAGTACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGA	707
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QY	708	CCCTCCGCCCCC	CAGAGCGGCAAGGATT-----CAGAAATGTCGCCGAG	752
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QY	753	GTTCTTAA	CGGAGAAGCTAATGGAGCAGAACAGACTGAAGAANTGACGCGGCTGTCCG	812
DB	1180	GTTCTCTCGAGAAG	CTGATGGAGCAGAAATCGTTGAAGAAACATACCCGCCCTCACCG	1239
QY	813	GAACAGAAAGTCCCT	GTATCGGAGGCTCGTGTGTTACCGAGCGGATACGAGCAGCGCTTC	872
DB	1240	CAACACAGAGTTCCT	GTATCGGAGGCTGTGTGTGTACCGAGCGGATACGAGCAGCGCTTC	1299

QY	873	GAAGAGGATCTCAAAAGGGTGCACGACAGCTTGGCAATCAGCAGATGAAGAAACGAAAGA	932
DB	1300	GAAGAGGATCTCAAAAGGGTGCACGACAGCTTGGCAATCAGCAGATGAAGAAACGAAAGA	1359
QY	933	CTCAGACATGCCATTCGGCCAGATCACAGAAATGACCAATCTCTCAAGTACAGTAAATAGT	992
DB	1360	CTCAGACATGCCATTCGGCCAGATCACAGAAATGACCAATCTCTCAAGTACAGTAAATAGT	1419
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DEFINITION	Sequence 1 from patent US 6504082.		
ACCESSION	AR274109		
VERSION	AR274109.1 GI:29706084		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2126)		
AUTHORS	Albertsen, M.C., Brooke, C.D., Garnaat, C.W. and Roth, B.A.		
TITLE	Ecdysone receptors and methods for their use		
JOURNAL	Patent: US 6504082-A 1 07-JAN-2003;		
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Best Local Similarity	90.1%;	Pred. No. 6.4e-193;	
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QY	528	GAGTAGTAAACAAAGTCAACAGACAGATTCGACTGTATCGACCGGTATGAGCCCGAGTCGCT	587
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QY	588	CGTCCAGAGTCCACGTCGCAAGAACAAAGAGAGAGAAAGAGAGACAGAGAGAAAAGA	647
DB	1000	GGTCCAGAAACGCGAGTGTGCGCAAAAGAGAGAGAAAGAGACAGAGAGAAAAAGA	1059
QY	648	CAAACTGCCAGTCACTAGCAGACAGTGGAGAGATCATATGCTGCCATAATGCCAATGTA	707
DB	1060	CAAACTGCCAGTCACTAGCAGACAGTGGAGAGATCATATGCTGCCCAATCATGCGAGTGA	1119
QY	708	CCCTCCGCCCCCAGAGGGCGCAAGATT-----CACGAAGTGGTCCCGAG	752
DB	1120	TCCGCCACCCCGAGAGGAGGAGGATCTCGAATGTTTGCAGCATGAAGTGGTCCCGCG	1179
QY	753	GTTCTTAAACGAGAAAGCTTAATGGAGAGAAACAGACTGAAAGATGAGCGCGCTGTCCGC	812
DB	1180	GTTCTTCTCGGAGAGCTGATGGAGAGAAATCGGTTGAAGAACATACCCCTCCCTCACCGC	1239
QY	813	GAAACAGAAAGTCCCTGATCGGAGGCTGTGTGTACCCAGGACGATACGAGCAGCTTC	872
DB	1240	CAACAGCAGTTCCTGATCGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1299
QY	873	GGAGAGGATCTCAAAAGGGTGACGACACTTGGCAATCAGCAGATGAAGAGAGAGAAAGA	932
DB	1300	GGAGAGGATCTCAAAAGGGTGACGACACTTGGCAATCAGCAGATGAAGAGAGAGAAAGA	1359
QY	933	CTCAGACATGCCATTCGCCAGATCACAGAAATGACCAATCTCTCAAGTACAGTAAATAGT	992
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QY	1053	ATTAAAGGATGCTCAAGCGAAGTGAATGATGCTGCGAGTAGCGGCGGTACGACCGGT	1112
DB	1480	ATTAAAGGATGCTCAAGCGAAGTGAATGATGCTGCGAGTAGCGGCGGTACGACCGGT	1539
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QY	1233	GATGACAAAGTGCATTCAGCGCTCTCACTGCGATCTGTTATATCTCGGATCGCGCGG	1292
DB	1660	GATGACAAAGTGCATTCAGCGCTCTCACTGCGATCTGTTATATCTCGGATCGCGCGG	1719
QY	1293	CCTAGAGCCACACAGTGTAGAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGT	1352
DB	1720	CCTAGAGCCACACAGTGTAGAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGT	1779
QY	1353	GTACATCATGAACACGAGTGTAGAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGT	1412
DB	1780	GTACATCATGAACACGAGTGTAGAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGT	1839
QY	1413	GTCGGTGTACCGGATTCGCGACGCTGGGCGATGAGAAATTCGAAATGCTGCTCGGT	1472
DB	1840	GTCGGTGTACCGGATTCGCGACGCTGGGCGATGAGAAATTCGAAATGCTGCTCGGT	1899
QY	1473	GAAGCTCAAGAACAGGAAGCTGCCCGGTTCTCGGAGGAGATCTGGGACGTG	1524
DB	1900	GAAGCTCAAGAACAGGAAGCTGCCCGGTTCTCGGAGGAGATCTGGGACGTG	1951

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002as:
7: Geneseqn2002bs:
8: Geneseqn2003as:
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11: Geneseqn2003ds:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1524	100.0	1767	6	ABT07367 Chimeric
2	1524	100.0	1767	10	ADF49192 Ecdysone
3	1414.2	92.8	1782	6	ABT07369 Chimeric
4	1414.2	92.8	1782	10	ADF49196 Ecdysone
5	1332	87.4	1848	6	ABT07376 Chimeric
6	1332	87.4	1848	10	ADF49206 Ecdysone
7	1332	87.4	1863	6	ABT07377 Chimeric
8	1332	87.4	1863	10	ADF49208 Ecdysone
9	1332	87.4	3972	6	ABT07353 Ecdysone
10	1332	87.4	3972	10	ADF49176 Ecdysone
11	1328.8	87.2	1767	6	ABT07368 Chimeric
12	1328.8	87.2	1767	10	ADF49194 Ecdysone
13	1311.2	86.0	1776	6	ABT07366 Chimeric
14	1311.2	86.0	1776	10	ADF49190 Ecdysone
15	1222.2	80.2	1800	6	ABT07370 Chimeric
16	1222.2	80.2	1800	10	ADF49198 Ecdysone
17	1209	79.3	1428	6	ABT07371 Chimeric
18	1209	79.3	1428	10	ADF49200 Ecdysone
19	1208.2	79.3	1809	6	ABT07382 Chimeric
20	1208.2	79.3	1809	10	ADF49214 Ecdysone

21	1073	70.4	1800	6	ABT07386 Chimeric
22	1073	70.4	1800	10	ADF49219 Ecdysone
23	955.6	62.7	1500	6	ABT07331 Chimeric
24	955.6	62.7	1500	10	ADF49139 Ecdysone
25	848.8	55.7	1515	6	ABT07335 Chimeric
26	848.8	55.7	1515	10	ADF49147 Ecdysone
27	836	54.9	2126	3	AAAL0312 European
28	763.6	50.1	1518	6	ABT07344 Chimeric
29	763.6	50.1	1518	10	ADF49165 Ecdysone
30	763.6	50.1	2840	6	ABT07274 Manduca s
31	763.6	50.1	2840	10	ADF49073 Manduca s
32	763.6	50.1	2840	12	ADI33132 Tobacco h
33	760.4	49.9	1500	6	ABT07332 Chimeric
34	760.4	49.9	1500	10	ADF49141 Ecdysone
35	742.8	48.7	1509	6	ABT07330 Chimeric
36	742.8	48.7	1509	10	ADF49137 Ecdysone
37	719.4	47.2	763	6	ABT07276 Ostrinia
38	719.4	47.2	763	10	ADF49077 Fall army
39	656.8	43.1	1533	6	ABT07337 Chimeric
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41	638.6	41.9	838	6	ABT07277 Spodopter
42	638.6	41.9	838	10	ADF49079 Fall army
43	638	41.9	3054	13	ADR48569 DNA seque
44	636	41.7	1524	6	ABT07336 Chimeric
45	636	41.7	1524	10	ADF49149 Ecdysone

ALIGNMENTS

RESULT 1
ID ABT07367 standard; DNA; 1767 BP.
XX AC ABT07367;
XX 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 120.
XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.
XX Manduca sexta.
OS Ostrinia nubilalis.
OS Chimeric.
XX WO200261102-A2.
XX 08-AUG-2002.
XX 24-OCT-2001; 2001WO-US051417.
XX 24-OCT-2000; 2000US-0242969P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
WPI; 2002-619259/66.
P-PSDB; ABJ05373.
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
regulating expression of target polypeptides in plants in the presence of
appropriate ligands that may be used in controlling plant fertility.
XX Claim 13; Page 270-272; 319pp; English.
XX The present invention relates to a receptor cassette encoding a chimeric
receptor polypeptide comprising at least one DNA binding domain, a hinge
domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
domain of an insect Ecr, where the ligand binding domain is heterologous

CC with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a coding sequence described in the exemplification of the invention. (Updated on 29-AUG-2003 to standardise OS field)	
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Query Match 100.0%; Score 1524; DB 6; Length 1767;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
Db	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
Qy	61 TACTGTTCTTTTGTGATGCTCACCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120
Db	61 TACTGTTCTTTTGTGATGCTCACCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120
Qy	121 ACCATGAGCTACTGCTCTTATCGAACAAAGCATCGGATATTGCGGACTTTAAAAAGCTC 180
Db	121 ACCATGAGCTACTGCTCTTATCGAACAAAGCATCGGATATTGCGGACTTTAAAAAGCTC 180
Qy	181 AAGTGCTCCAAAGAAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGGAGTGTGC 240
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Qy	241 TACTCTCCAAACCAAAAGGTCCTCGGTACTAGGCGACATCTCACAGAAAGTGAATCA 300
Db	241 TACTCTCCAAACCAAAAGGTCCTCGGTACTAGGCGACATCTCACAGAAAGTGAATCA 300
Qy	301 AGGCTAGAAAGACTGCGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG 360
Db	301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG 360
Qy	361 ATTTTGAANAATGGATTTCTTTACAGGATATAAAGCAATTTGTTAAAGGATTTTGTACAA 420
Db	361 ATTTTGAANAATGGATTTCTTTACAGGATATAAAGCAATTTGTTAAAGGATTTTGTACAA 420
Qy	421 GATAATGTCAATAAAGATCCGTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
Db	421 GATAATGTGAATAAAGATCCGTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
Qy	481 CTAACATTGAGACAGCATAGATAAAGTGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540
Db	481 CTAACATTGAGACAGCATAGATAAAGTGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540
Qy	541 GGTCAAAGACAGTTGACTGTATCGACGCTATGAGCCCGAGTGGCTCGTCCAGAGTCC 600
Db	541 GGTCAAAGACAGTTGACTGTATCGACGCTATGAGCCCGAGTGGCTCGTCCAGAGTCC 600
Qy	601 ACCTGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAAAACAACTGCCAGTTC 660
Db	601 ACCTGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAAAACAACTGCCAGTTC 660
Qy	661 AGTACGACGACATGACAGATCATATGCTCGCCATTAATGCAATGTGACCCCTCGCCCCCA 720
Db	661 AGTACGACGACATGACAGATCATATGCTCGCCATTAATGCAATGTGACCCCTCGCCCCCA 720
Qy	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTAATGGAGCAG 780
Db	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTAATGGAGCAG 780
Qy	781 AACAGACTGAAGAAATGTGACCGCGCTGTGCGGCAACACAGAAAGTTCCTGATCCGAGGCTC 840
Db	781 AACAGACTGAAGAAATGTGACCGCGCTGTGCGGCAACACAGAAAGTTCCTGATCCGAGGCTC 840
Qy	841 GTGTGGTACAGAGCGGATACGAGCGCTTCGGAAGAGGATCTCAAAAGGGGTGACGCGAG 900
Db	841 GTGTGGTACAGAGCGGATACGAGCGCTTCGGAAGAGGATCTCAAAAGGGGTGACGCGAG 900

Qy	901 ACTTGCAATCAGCAGATGAAGAAGCAGACTCAGACATGCCATTCCGCCAGATCACA 960
Db	901 ACTTGCAATCAGCAGATGAAGAAGCAGAACTCAGACATGCCATTCCGCCAGATCACA 960
Qy	961 GAAATGACCATCTCTCAGTACAGCTAATAGTCAGATTTTGCCTAAAGGCTTACCTGGTTTT 1020
Db	961 GAAATGACCATCTCTCAGTACAGCTAATAGTCAGATTTTGCCTAAAGGCTTACCTGGTTTT 1020
Qy	1021 TCAAAGTCTCAACCTGACCATCAATATTAAAGGCGATGCTCAAGCGAAGTGATG 1080
Db	1021 TCAAAGTCTCAACCTGACCATCAATATTAAAGGCGATGCTCAAGCGAAGTGATG 1080
Qy	1081 ATCTCGAGTACGAGGGGTACGAGCGGTGTGCGATAGCGTTTCTGTTGCGCAACAAC 1140
Db	1081 ATCTCGAGTACGAGGGGTACGAGCGGTGTGCGATAGCGTTTCTGTTGCGCAACAAC 1140
Qy	1141 CAGGCGGTACATCTCGCAACAACCTACCGAAGGGGGCATGCGCTTACGTCATCGAAGACCTG 1200
Db	1141 CAGGCGGTACATCTCGCAACAACCTACCGAAGGGGGCATGCGCTTACGTCATCGAAGACCTG 1200
Qy	1201 CTGCACTTCTGCGGCTGCGATGCTACTCGATGCGAACAACCTGATACGCGCTCCTC 1260
Db	1201 CTGCACTTCTGCGGCTGCGATGCTACTCGATGCGAACAACCTGATACGCGCTCCTC 1260
Qy	1261 ACTGCCATCGTTATATTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
Db	1261 ACTGCCATCGTTATATTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
Qy	1321 ATCCAGCGGTATTAACCTGGAACAACGCTGCGGGTGTACATCATGAACGACAGCGGCTCG 1380
Db	1321 ATCCAGCGGTATTAACCTGGAACAACGCTGCGGGTGTACATCATGAACGACAGCGGCTCG 1380
Qy	1381 CCGGTTGCGCGGCTCATCTACGGAAGATTCTGTCGGTGTCTACCGAGTTGCGGACGCTG 1440
Db	1381 CCGGTTGCGCGGCTCATCTACGGAAGATTCTGTCGGTGTCTACCGAGTTGCGGACGCTG 1440
Qy	1441 GGATGACAGAAATTCGAAACATGTCATCTCGCTGAAGCTCAAGAACAGAAAGCTGCCCGCG 1500
Db	1441 GGATGACAGAAATTCGAAACATGTCATCTCGCTGAAGCTCAAGAACAGAAAGCTGCCCGCG 1500
Qy	1501 TTCTCGAGGAGATCTCGGACGCTG 1524
Db	1501 TTCTCGAGGAGATCTCGGACGCTG 1524

RESULT 2

ADP49192

ID ADP49192 standard; DNA; 1767 BP.

XX

AC ADP49192;

XX

DT 12-FEB-2004 (first entry)

XX

DE Ecdysone receptor/VP16 transactivation domain DNA seq id 120.

XX

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain; hinge domain; ecdysone receptor; Ecr; ligand binding domain; activation domain; transgenic seed; transgenic plant; plant line; herbicide; pesticide; chimeric ecdysone receptor; Ecr;

KW

Yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.

XX

OS Synthetic.

OS Manduca sexta.

OS Ascomycota.

OS Ostrinia nubilalis.

OS Herpes simplex virus unknown type.

XX

US2003154509-A1.

XX

14-AUG-2003.

XX

24-OCT-2001; 2001US-00087167.

PF

XX 24-OCT-2001; 2001US-00087167.
 PR (PASC/) PASCAL E J.
 XX (VALE/) VALENTINE S A.
 PA (BROW/) BROWN J A.
 PA (COCK/) COCKRELL A S.
 PA (JOHN/) JOHNSON B D.
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI WPI; 2003-897756/82.
 XX P-PSDB; ADF49193.
 DR
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX
 PS Example 23; SEQ ID NO 120; 186pp; English.
 XX
 CC The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-Vp16
 CC transactivation domain fusion protein.
 XX
 SQ Sequence 1767 BP; 474 A; 438 C; 473 G; 382 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1524; DB 10; Length 1767;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCTTATAGCTATTTATTTGCTGG 60
 DB 1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCTTATAGCTATTTATTTGCTGG 60
 QY 61 TACTGTTCTTTTGTGATGCTCACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 DB 61 TACTGTTCTTTTGTGATGCTCACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 QY 121 ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 DB 121 ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 QY 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240
 DB 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240
 QY 241 TACTCTCCCAAAACCAAAAGGTTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
 DB 241 TACTCTCCCAAAACCAAAAGGTTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
 QY 301 AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCGAGAAAGCTTTGACATG 360
 DB 301 AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCGAGAAAGCTTTGACATG 360
 QY 361 ATTTTGAAGATGATTTCTTTACAGGATATTAAGAGCATTTGTTAAAGATTTATTTGACAA 420
 DB 361 ATTTTGAAGATGATTTCTTTACAGGATATTAAGAGCATTTGTTAAAGATTTATTTGACAA 420
 QY 421 GATTAATGTGAATAAGATGCGGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCTT 480
 DB 421 GATTAATGTGAATAAGATGCGGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCTT 480
 QY 481 CTAACATTGAGACAGCATAGATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
 DB 481 CTAACATTGAGACAGCATAGATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540

RESULT 3
 ABT07369
 ID ABT07369 standard; DNA; 1782 BP.

QY 541 GGTCAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTGTCTCCAGAGTCC 600
 DB 541 GGTCAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTGTCTCCAGAGTCC 600
 QY 601 ACGTGCAAGAACAAAGAAAGAAAGAACACACAGAGAGAAAGAAAGAAAGAAAGAAAGTCCAGTCC 660
 DB 601 ACGTGCAAGAACAAAGAAAGAAAGAAAGAACACACAGAGAGAAAGAAAGAAAGAAAGTCCAGTCC 660
 QY 661 AGTACGACGACAGTGGACGATCATATGCTTCCCAATATGCAATGTGACCTCCGCCCCCA 720
 DB 661 AGTACGACGACAGTGGACGATCATATGCTTCCCAATATGCAATGTGACCTCCGCCCCCA 720
 QY 721 GAGCGCGCAAGGATTTACGAAAGTGGTCCCGAGGTTCTTAACGAGAGAAAGTAAATGAGAGCAG 780
 DB 721 GAGCGCGCAAGGATTTACGAAAGTGGTCCCGAGGTTCTTAACGAGAGAAAGTAAATGAGAGCAG 780
 QY 781 AACAGACTGAAGAATGTGACCGCTGTCGGGAAACACAGAAAGTCCCTGATCGCGAGGCTC 840
 DB 781 AACAGACTGAAGAATGTGACCGCTGTCGGGAAACACAGAAAGTCCCTGATCGCGAGGCTC 840
 QY 841 GTGTGTTACCAAGGACGATACGACGAGCTTCCGGAAGAGGATCTCAAAGGGGTGACGAG 900
 DB 841 GTGTGTTACCAAGGACGATACGACGAGCTTCCGGAAGAGGATCTCAAAGGGGTGACGAG 900
 QY 901 ACTTGCCCAATCAGCAGATGAAGAAGACGAAAGACTCAGACATGCCATTCGCGCAGATCACA 960
 DB 901 ACTTGCCCAATCAGCAGATGAAGAAGACGAAAGACTCAGACATGCCATTCGCGCAGATCACA 960
 QY 961 GAAATGACCATCTCTCAAGTACAGTAAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTT 1020
 DB 961 GAAATGACCATCTCTCAAGTACAGTAAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTT 1020
 QY 1021 TCAGAGATCTCAGACCTGACAGATCAGATCATTTATTAAGGAGGATGCTCAAGCGAAGTATG 1080
 DB 1021 TCAGAGATCTCAGACCTGACAGATCAGATCATTTATTAAGGAGGATGCTCAAGCGAAGTATG 1080
 QY 1081 ATGCTGCGAGTAGCAGGCGGTACGACGCGGTGTCGGATAGCGTTCTGTTGCGCAACAAC 1140
 DB 1081 ATGCTGCGAGTAGCAGGCGGTACGACGCGGTGTCGGATAGCGTTCTGTTGCGCAACAAC 1140
 QY 1141 CAGGCGTACACTCGCGACAACTACCGCAAGGCGGGCATGGCCCTACGTCATCGNAGACCTG 1200
 DB 1141 CAGGCGTACACTCGCGACAACTACCGCAAGGCGGGCATGGCCCTACGTCATCGNAGACCTG 1200
 QY 1201 CTGCACTTCTGCGGCTGCAATGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 1260
 DB 1201 CTGCACTTCTGCGGCTGCAATGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 1260
 QY 1261 ACTGCCATCGTTATTTCTCGGATCGGCGGCGCTAGAGCAGCCACAGCTAGTAGAAGAG 1320
 DB 1261 ACTGCCATCGTTATTTCTCGGATCGGCGGCGCTAGAGCAGCCACAGCTAGTAGAAGAG 1320
 QY 1321 ATCCAGCGGTATTAACCTGAACACGCTGCGGTTGTCATCATGAAACAGACAGCGCGTGC 1380
 DB 1321 ATCCAGCGGTATTAACCTGAACACGCTGCGGTTGTCATCATGAAACAGACAGCGCGTGC 1380
 QY 1381 CCGCGTTGCGCGCTCATCTACCGGAGATTTCTGCGTCTTACCGAGTTGCGGAGCTG 1440
 DB 1381 CCGCGTTGCGCGCTCATCTACCGGAGATTTCTGCGTCTTACCGAGTTGCGGAGCTG 1440
 QY 1441 GGCATGCAAGTTCGAAACATGTCATCTCGCTGAAGCTCAAGAAACAGAGAGCTGCGCGCG 1500
 DB 1441 GGCATGCAAGTTCGAAACATGTCATCTCGCTGAAGCTCAAGAAACAGAGAGCTGCGCGCG 1500
 QY 1501 TTCTCGGAGGAGATCTGGGACGTTG 1524
 DB 1501 TTCTCGGAGGAGATCTGGGACGTTG 1524

XX ABT07369;
AC
XX
XX 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
DT
XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 124.
DE
XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.
KW
XX Ostrinia nubilalis.
OS Ostrinia nubilalis.
OS Chimeric.
XX
XX WO200261102-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 24-OCT-2001; 2001WO-US051417.
PF
XX
XX 24-OCT-2000; 2000US-0242969P.
PR
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
PI
XX
XX WPI; 2002-619259/66.
DR P-PSDB; ABJ05375.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
PT
XX Example 23; Page 280-283; 319pp; English.
PS
XX
XX The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
CC domain of an insect EcR, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
SQ Sequence 1782 BP; 475 A; 445 C; 475 G; 387 T; 0 U; 0 Other;

Query Match 92.8%; Score 1414.2; DB 6; Length 1782;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1471; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATCAGCAGCTATATGTGGATTTTATAGCCCTGCCCTTCATACGGTATTATTGCTTGG 60
DB 1 ATCAGCAGCTATATGTGGATTTTATAGCCCTGCCCTTCATACGGTATTATTGCTTGG 60

QY 61 TACTGTTCTTTTGTGATGCTCACCTGTGTTGGTGTACTTCTGAGGGATCCGCC 120
DB 61 TACTGTTCTTTTGTGATGCTCACCTGTGTTGGTGTACTTCTGAGGGATCCGCC 120

QY 121 ACCATGAAGTACTGTCTTCTATCGAACAGCATGCGATATTGCGGACTTAAAAAGCTC 180
DB 121 ACCATGAAGTACTGTCTTCTATCGAACAGCATGCGATATTGCGGACTTAAAAAGCTC 180

QY 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACTGGGAGTGTGC 240
DB 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACTGGGAGTGTGC 240

QY 241 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCA 300
DB 241 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCA 300

QY 301 AGCTAGAAAGACTGGAACAGCTATTCTTACTGATTTTCTCGAGAGACCTTGACATG 360
DB 301 AGCTAGAAAGACTGGAACAGCTATTCTTACTGATTTTCTCGAGAGACCTTGACATG 360

QY 361 ATTTTGAATAATGGATTCTTTTACAGGATATAAAGCATTTGTTAACAGGATATTGTACAA 420
DB 361 ATTTTGAATAATGGATTCTTTTACAGGATATAAAGCATTTGTTAACAGGATATTGTACAA 420

QY 421 GATAATGTGAATAAAGATGCCGTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
DB 421 GATAATGTGAATAAAGATGCCGTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480

QY 481 CTAACATTGAGACAGCATAGAATAAGTGGCAGCATCATTCGGAAGAGAGTAGTAACAAA 540
DB 481 CTAACATTGAGACAGCATAGAATAAGTGGCAGCATCATTCGGAAGAGAGTAGTAACAAA 540

QY 541 GGTCAAAGACAGTTGACTGTATCGACCGCTATGAGCCCGAGTGCCTCGTCCAGAGATCC 600
DB 541 GGTCAAAGACAGTTGACTGTATCGACCGCTATGAGCCCGAGTGCCTCGTCCAGAGATCC 600

QY 601 ACCTGCAAGAACAAAGAGAGAAAGAGACACAGAGAGAAAGACAAACTGCCAGTC 660
DB 601 CAGTGTGCGCAAAAAGAGAGAAAGAGACACAGAGAGAAAGACAAACTGCCAGTC 660

QY 661 AGTACGACGACAGTGGACGATCATATGCTGCTGCCATTAATGCAATGTGACCTTCGCCCCCA 720
DB 661 AGCACAACGACAGTACGATCATATGCTGCCCAATCATGCACTGTGATCCACCACCCCG 720

QY 721 GAGCGCGCAAGGANT-----CAGCAAGTGTGCTCCGAGGTTCCTAAACGAG 765
DB 721 GAGCGCGCAAGGANTTTCTGGAATGTTTGGAGCATGAAGTGTGCTCCGAGGTTCCTTCCGAG 780

QY 766 AAGCTAATGAGCAGAACAGACTGAAGAATGTGACCGCTGTGCGGGAACCAAGAGATCC 825
DB 781 AAGCTAATGAGCAGAACATCGCTGAAGAACATATACCCCTCACCGCAACACGAGATTC 840

QY 826 CTGATCGCAGGCTGCTGTTACCGAGCAGGATAGCAGCAGCTTCGGAGAGGATCTC 885
DB 841 CTGATCGCAGGCTGCTGTTACCGAGCAGGATAGCAGCAGCTTCGGAGAGGATCTC 900

QY 886 AAGAGGTGACGAGACTTGGCAATCAGCAGATGAAGAACGAAAGACTCAGACATGCCA 945
DB 901 AAGAGGTGACGAGACTTGGCAATCAGCAGATGAAGAACGAAAGACTCAGACATGCCA 960

QY 946 TTCGCCCAGATCAAGAAATGACCATCCTCACAGTACAGCTAATAGTCGAGTTTGCCTCAA 1005
DB 961 TTCGCCCAGATCAAGAAATGACCATCCTCACAGTACAGCTAATAGTCGAGTTTGCCTCAA 1020

QY 1006 GGCCTACCTGGTTTTCAAAGATCTCAACCTGACCCAGATCACATTTATTAAGGCGATGC 1065
DB 1021 GGCCTACCTGGTTTTCAAAGATCTCAACCTGACCCAGATCACATTTATTAAGGCGATGC 1080

QY 1066 TCAAGCAAGTGAATGCTGCGAGTAGCAGAGCGGTACGACGCGGTGTGCGATAGCGTT 1125
DB 1081 TCAAGCAAGTGAATGCTGCGAGTAGCAGAGCGGTACGACGCGGTGTGCGATAGCGTT 1140

QY 1126 CTGTTCCGCAACAAAGCGGTACACTCGGCAAACTACCGCAAGCGGGGATGGCTTAC 1185
DB 1141 CTGTTCCGCAACAAAGCGGTACACTCGGCAAACTACCGCAAGCGGGGATGGCTTAC 1200

QY 1186 GTCATCGAAGACCTGCTGCACTTCTGCGCTGCACTGCTGATGTCGATGTCGACAAACGTG 1245
DB 1201 GTCATCGAAGACCTGCTGCACTTCTGCGCTGCACTGCTGATGTCGATGTCGACAAACGTG 1260

QY 1246 CATTCAGCGCTCTCTCACTGCCATCGTTATATTCCTCGGATCGCGCGGCTTAGAGAGCCA 1305
DB 1261 CATTCAGCGCTCTCTCACTGCCATCGTTATATTCCTCGGATCGCGCGGCTTAGAGAGCCA 1320

QY 1306 CAGCTAGTAGAAGAGATCCAGCGGTATTAACCTGAACAGCTGCGGGTGTACATCATGAAC 1365
DB 1321 CAGCTAGTAGAAGAGATCCAGCGGTATTAACCTGAACAGCTGCGGGTGTACATCATGAAC 1380

QY 1366 CAGCACAGCGCTCGCGCGTTGCGCGTCATCTACGGAGATCTGTGCGTGTACC 1425
DB |||||
QY 1381 CAGCACAGCGCTCGCGCGTTGCGCGTCATCTACGGAGATCTGTGCGTGTACC 1440
DB |||||
QY 1426 GAGTTGCGGACCTCGGCATGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAC 1485
DB |||||
QY 1441 GAGTTGCGGACCTCGGCATGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAC 1500
DB |||||
QY 1486 AGGAAGTGCCTCGCTTCCTGAGAGAGATCTGGGAGTG 1524
DB |||||
QY 1501 AGGAAGTGCCTCGCTTCCTGAGAGAGATCTGGGAGTG 1539
DB |||||

RESULT 4

ADF49196

ID ADF49196 standard; DNA; 1782 BP.

XX AC

XX ADF49196;

XX DT

XX 12-FEB-2004 (first entry)

XX Ecdysone receptor/VP16 transactivation domain DNA seq id 124.

XX KW

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW KW

KW hinge domain; ecdysone receptor; EcR; ligand binding domain;

KW KW

KW activation domain; transgenic seed; transgenic plant; plant line;

KW KW

KW herbicide; pesticide; chimeric ecdysone receptor; EcR;

KW KW

KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.

XX OS

OS Synthetic.

OS OS

OS Ostrinia nubilalis.

OS OS

OS Ascomycota.

OS OS

OS Herpes simplex virus unknown type.

XX PN

PN US2003154509-A1.

XX XX

XX 14-AUG-2003.

XX XX

XX 24-OCT-2001; 2001US-00087167.

XX XX

XX 24-OCT-2001; 2001US-00087167.

XX PA

PA (PASC/) PASCAL E J.

XX PA

PA (VALE/) VALENTINE S A.

XX PA

PA (BROW/) BROWN J A.

XX PA

PA (COCK/) COCKRELL A S.

XX PA

PA (JOHN/) JOHNSON B D.

XX PI

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX PI

PI WPI; 2003-897756/82.

XX DR

DR P-PSDB; ADF49197.

XX XX

XX New receptor cassette encoding a chimeric receptor polypeptide, useful

XX PT

PT for regulating the expression of target polypeptides in plants in the

XX PT

PT presence of appropriate chemical ligands.

XX XX

XX Example 23; SEQ ID NO 124; 186pp; English.

XX PS

XX CC

CC The invention describes a receptor cassette encoding a chimeric receptor

XX CC

CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge

XX CC

CC (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding

XX CC

CC (E) domain that is heterologous with respect to the D domain, and an

Query Match 92.8%; Score 1414.2; DB 10; Length 1782;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1471; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
QY 1 ATGAGCAGCTATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTCTTGG 60
DB |||||
QY 61 TACTGTTTCTTTTGTGCGATGTCCACCTGTTGTTGTTGTTGTTACTTCTCGAGGATCCGCC 120
DB |||||
QY 61 TACTGTTTCTTTTGTGCGATGTCCACCTGTTGTTGTTGTTGTTACTTCTCGAGGATCCGCC 120
DB |||||
QY 121 ACCATGAAGCTACTGTTCTTATCGAACCAAGCATCGGATATTTGCGGACTTAAAAAGCTC 180
DB |||||
QY 121 ACCATGAAGCTACTGTTCTTATCGAACCAAGCATCGGATATTTGCGGACTTAAAAAGCTC 180
DB |||||
QY 181 AAGTCTCCAAAGAAAAAACCAGAAAGTGCAGCAAGTCTTGAAGAACAACTGGGAGTGTCCG 240
DB |||||
QY 181 AAGTCTCCAAAGAAAAAACCAGAAAGTGCAGCAAGTCTTGAAGAACAACTGGGAGTGTCCG 240
DB |||||
QY 241 TACTCTCCAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGCAGAAAGTGAATCA 300
DB |||||
QY 241 TACTCTCCAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGCAGAAAGTGAATCA 300
DB |||||
QY 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTTACTGATTTTCTCGAGAAAGCTTGACATG 360
DB |||||
QY 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTTACTGATTTTCTCGAGAAAGCTTGACATG 360
DB |||||
QY 361 ATTTTGAAGATGGATTTCTTACAGGATATATAAGCATTTGTTAACAGGATTTTGTACAA 420
DB |||||
QY 361 ATTTTGAAGATGGATTTCTTACAGGATATATAAGCATTTGTTAACAGGATTTTGTACAA 420
DB |||||
QY 421 GATATGTTGAATAAAGATGCGCTGCAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
DB |||||
QY 421 GATATGTTGAATAAAGATGCGCTGCAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
DB |||||
QY 481 CTAACATTTGAGACAGCATAGAAATAGTGCACATCATCATCGAAGAGAGTAGTAAACAA 540
DB |||||
QY 481 CTAACATTTGAGACAGCATAGAAATAGTGCACATCATCATCGAAGAGAGTAGTAAACAA 540
DB |||||
QY 541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGGTCTCCAGAGTCC 600
DB |||||
QY 541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGGTCTCCAGAGTCC 600
DB |||||
QY 601 AGTGTCAAACAAAGAGAGAGAAAGGACACAGAGAGAAAGACAACTGCCAGTC 660
DB |||||
QY 601 AGTGTGTGCGCAAAAGAGAGAGAAAGGACACAGAGAGAGAAAGACAACTGCCAGTC 660
DB |||||
QY 661 AGTGTGACGACAGTGGACGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB |||||
QY 661 AGTGTGACGACAGTGGACGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB |||||
QY 721 GAGGCGGCAAGGATTT-----CAGCAAGTGGTCCGAGGTTCTTAAAGGAG 765
DB |||||
QY 721 GAGGCGGCAAGGATTTCTGGAATGTTTTCAGCATGAAAGTGGTCCCGGCTTCTCTCGGAG 780
DB |||||
QY 766 AAGCTAATCGAGCAGACAGACTGGAAGATGTGACCCCGCTGTGCGGCAAGACCAAGAGTCC 825
DB |||||
QY 781 AAGCTATGAGAGAGAAATCGGCTGGAAGAACATACCCCTCCACCCCAACAGCAGTTC 840
DB |||||
QY 826 CTGATCCGAGGCTCGTGTGGTACACGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTC 885
DB |||||
QY 841 CTGATCCGAGGCTCGTGTGGTACACGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTC 900
DB |||||
QY 886 AAAAGGCTGCGCAGACTTTGGCAATCAGCAGATGAAGAGACCAAGACTCAGACATGCCA 945
DB |||||
QY 901 AAAAGGCTGCGCAGACTTTGGCAATCAGCAGATGAAGAGACCAAGACTCAGACATGCCA 960
DB |||||
QY 946 TTCCGCGCATGACAGAAATGACCATCTCAGAGTACAGCTAATAGTTCGAGTTTGCACAA 1005
DB |||||
QY 961 TTCCGCGCATGACAGAAATGACCATCTCAGAGTACAGCTAATAGTTCGAGTTTGCACAA 1020
DB |||||
QY 1006 GGCCTACCTGTTTTCACAAAGATCTCACAACTGACAGATCACAATTTTAAAGGATGC 1065
DB |||||

Db 1021 GGCCTACTGTTTTCACAAATCTCAACCTGACAGATCAATATTAAAGGCATGC 1080
 Qy 1066 TCAAGCAGATGATGATCTCGAGTACGAGGCGGTACGACGCGGTGTCGATAGCGTT 1125
 Db 1081 TCAAGCAGATGATGATCTCGAGTACGAGGCGGTACGACGCGGTGTCGATAGCGTT 1140
 Qy 1126 CTGTTCCGCAACACAGCGGTACACTCGCGACAACTACCGCAAGCGGGCATGCGCTAC 1185
 Db 1141 CTGTTCCGCAACACAGCGGTACACTCGCGACAACTACCGCAAGCGGGCATGCGCTAC 1200
 Qy 1186 GTCTCGAAGACCTGCTGCTCACTTCTGCGCGTGCATGTACTCGATGTCGATGCAACAGTG 1245
 Db 1201 GTCTCGAAGACCTGCTGCTCACTTCTGCGCGTGCATGTACTCGATGTCGATGCAACAGTG 1260
 Qy 1246 CATTAACGCGCTCTCACTGCGCATGTTATATCTCGGATCGCGCGGCTAGAGCGCA 1305
 Db 1261 CATTAACGCGCTCTCACTGCGCATGTTATATCTCGGATCGCGCGGCTAGAGCGCA 1320
 Qy 1306 CAGCTAGTAGAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGATCATGAAC 1365
 Db 1321 CAGCTAGTAGAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGATCATGAAC 1380
 Qy 1366 CAGCACAGCGCTCGCGCGTTCGCGCTCATCTACGCGAAGATTCTGCGGTGCTTACC 1425
 Db 1381 CAGCACAGCGCTCGCGCGTTCGCGCTCATCTACGCGAAGATTCTGCGGTGCTTACC 1440
 Qy 1426 GAGTTGCGGACGCTGGGATGAGAAATTCGAACATGTCGATCTGCTGAAGCTCAAGAAC 1485
 Db 1441 GAGTTGCGGACGCTGGGATGAGAAATTCGAACATGTCGATCTGCTGAAGCTCAAGAAC 1500
 Qy 1486 AGGAGCTGCGCGCGTTCCTGGAGGAGATCTGGGACGTG 1524
 Db 1501 AGGAGCTGCGCGCGTTCCTGGAGGAGATCTGGGACGTG 1539

RESULT 5

ABT07376
 ID ABT07376 standard; DNA; 1848 BP.
 XX
 AC ABT07376;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 DE Chimeric ecdysone receptor coding sequence SEQ ID NO: 134.
 XX
 KW Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor; gene; ds.
 XX
 OS Manduca sexta.
 OS Chimeric.
 XX
 PN WO200261102-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 24-OCT-2001; 2001WO-US051417.
 XX
 PR 24-OCT-2000; 2000US-0242969P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX
 DR WPI; 2002-619259/66.
 DR P-PSDB; ABJ05378.
 XX
 PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX

PS Example 25; Page 296-298; 319pp; English.
 XX
 CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a coding sequence described in the exemplification of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
 Query Match 87.4%; Score 1332; DB 6; Length 1848;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
 Qy 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
 Db 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
 Qy 61 TACTGTTTTCTTTTGTTCGATGCTCACCTGTGTTTGTGTTACTTCTGCGGGATCCGCC 120
 Db 61 TACTGTTTTCTTTTGTTCGATGCTCACCTGTGTTTGTGTTACTTCTGCGGGATCCGCC 120
 Qy 121 ACCATGAAGTACTGTTCTTCTATCGAACAGCAGCAGATTTTCCGCACTTAAAGAGCTC 180
 Db 121 ACCATGAAGTACTGTTCTTCTATCGAACAGCAGCAGATTTTCCGCACTTAAAGAGCTC 180
 Qy 181 AAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAATGGGAGTGTGCG 240
 Db 181 AAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAATGGGAGTGTGCG 240
 Qy 241 TACTCTCCAAACCAAAAGGTCTCCGTGACTAGGGGCACATCTGCAGAGAGTGGATCA 300
 Db 241 TACTCTCCAAACCAAAAGGTCTCCGTGACTAGGGGCACATCTGCAGAGAGTGGATCA 300
 Qy 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGAGCTTGGACATG 360
 Db 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGAGCTTGGACATG 360
 Qy 361 ATTTTGAATAATGGATTCTTTACAGGATATAAAAGCAATTTGTTACAGGATTTTGTACAA 420
 Db 361 ATTTTGAATAATGGATTCTTTACAGGATATAAAAGCAATTTGTTACAGGATTTTGTACAA 420
 Qy 421 GATTAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
 Db 421 GATTAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
 Qy 481 CTAACATTGAGACAGCATAGAAATAGTGCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Db 481 CTAACATTGAGACAGCATAGAAATAGTGCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Qy 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCCGAGTGGTGGTCCCGAGAGTCC 600
 Db 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCCGAGTGGTGGTCCCGAGAGTCC 600
 Qy 601 ACGTGCAAGAACAAAAGAGAAAGAAAGAACACAGAGAGAGAAAGACAAACTGCCAGTC 660
 Db 601 ACGTGCAAGAACAAAAGAGAAAGAAAGAACACAGAGAGAGAAAGACAAACTGCCAGTC 660
 Qy 661 AGTACGACGACAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA 720
 Db 661 AGTACGACGACAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA 720
 Qy 721 GAGCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAAACGAGAAAGCTAATGAGGAG 780
 Db 721 GAGCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAAACGAGAAAGCTAATGAGGAG 780
 Qy 781 AACAGACTGAAGAATGTGACGCCCGCTGCGGCGAACACAGAGAGTCCCTGATCGCGAGGCTC 840

Db 781 AACGACTGAAGATGTAGCGCGTGTGCGGACCAAGATCCCTGATCGGAGGCTC 840
 QY 841 GTGTGGTACCGAGACGGATACAGAGAGGCTTCGGAAGAGATCTCAAAAGGTTGACGAG 900
 Db 841 GTGTGGTACCGAGAGGGGTACGAGAGCGGTGCGAGGAAGATCTCAAGAGAGTTACACAG 900
 QY 901 ACTTGGCAATCAGCAGATGAGAACGAGACTCAGACATGCCATTCCGCCAGATCACA 960
 Db 901 ACATGGCAATTAGAGAGAAAGAGAGGAGAACTGACATGCCCTTCGTGAGATCACA 960
 QY 961 GAAATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCACAAAGGCTTACCTGGTTTT 1020
 Db 961 GAGATGACGATCTTACAGTGCAGCTTATTTAGAAATTCGCAAGGGACTACCGGATTC 1020
 QY 1021 TCAAGATCTCAACACCTGACAGATCAATTAATTAAGGATGCTCAAGCGAAGTGATG 1080
 Db 1021 TCCAAGATATCTCAGTCCGATCAAAATTAATTAAGGCGTCATCAAGCGAAGTGATG 1080
 QY 1081 ATGCTCGAGTAGCGAGCGGTACGACGGGTGTCGATAGGTTCTGTTCCCAACAC 1140
 Db 1081 ATGCTCGAGTAGCGAGCGGTACGACGGCGGACGAGCGTGTGTTCCGGAACAC 1140
 QY 1141 CAGGCTACACTCGGACAACTACCGCAAGCGGCGATGCGCTTACATCAAGACCTG 1200
 Db 1141 CAGGCGTACACGGCGACAACTACCGCAAGCGGCGATGCTTACATCAAGACCTG 1200
 QY 1201 CTGCACTTCTGCGCTGTCATGTACTGATGTCGATGCAACAGTGCATTAACGGCTCTC 1260
 Db 1201 CTGCACTTCTGCGGTGTATGTACTTCCATGAGCATGGACAATGTGCACTACCGCTGCTC 1260
 QY 1261 ACTGCCATGTTATATCTCGGATCGGCGGCGCTAGACGCCACAGCTAGTAGAAGAG 1320
 Db 1261 ACCGCCATGTTATATCTCAGACCGGCGGCGCTCGACCAACCCCTTTTGTAGGAGAA 1320
 QY 1321 ATCCACGGTATTACCTGAACAGCTGCGGGTGTACATCATGAACGACAGCGCGTCTG 1380
 Db 1321 ATCCAGAGATATCTTGAAGACGCTGCGGGTTATATTTAATCAGCAGACGGCGTCTG 1380
 QY 1381 CCGCGTGGCGCGCTCATCTACGCGAAGATTCTGCGGTGCTTACCGAGTTGGGACGCTG 1440
 Db 1381 CCGTGGTGGCGGTGCTGTTGCGCAAGATCCTCGGCGTGTGACGGAACCTGCGCAGCTC 1440
 QY 1441 GGATCGAGAAATTCGAAACATGTCATCTGCTGAAGCTCAAGACAGGAGCTGCGCGCG 1500
 Db 1441 GGCACGAGAACTCCAAACATGTGCTCTGCTGAAGCTGAAGAAAGGAACTTCGCGCA 1500
 QY 1501 TTCCTGGAGAGATCTGGGACGTG 1524
 Db 1501 TTCCTGGAGAGATCTGGGACGTG 1524

RESULT 6

ADFA9206
 ID ADFA9206 standard; DNA; 1848 BP.

XX AC
 AC ADF49206;

XX 12-FEB-2004 (first entry)

XX Ecdysone receptor/C1 transactivation domain DNA seq id 134.

XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; C1 transactivation domain; ds; gene.

XX Synthetic.
 OS Manduca sexta.
 OS Ascomycota.
 OS Zea mays.

PN US2003154509-A1.
 XX 14-AUG-2003.
 XX 24-OCT-2001; 2001US-00087167.
 XX 24-OCT-2001; 2001US-00087167.
 XX (PASC/) PASCAL E J.
 PA (VALE/) VALENTINE S A.
 PA (BROW/) BROWN J A. S.
 PA (COCK/) COCKRELL A. S.
 XX (JOHN/) JOHNSON B D.
 PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX WPI; 2003-897756/82.
 DR New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX Example 25; SEQ ID NO 134; 186pp; English.
 XX The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-C1
 CC transactivation domain fusion protein.
 XX Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
 SQ
 Query Match 87.4%; Score 1332; DB 10; Length 1848;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
 QY 1 ATGCGACGACTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
 Db 1 ATGCGACGACTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
 QY 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTGAGGATCCGCT 120
 Db 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTGAGGATCCGCT 120
 QY 121 ACCATGAGCTACTGTCTTCTATCGAACAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 Db 121 ACCATGAGCTACTGTCTTCTATCGAACAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 QY 181 AAGTGTCTCCAAAGAAAAACCGAAGTGCAGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240
 Db 181 AAGTGTCTCCAAAGAAAAACCGAAGTGCAGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240
 QY 241 TACTCTCCAAACCCAAAAGGTCTCCGCTGACTAGGGCAGCATCTGCAGAGTGGAAATCA 300
 Db 241 TACTCTCCAAACCCAAAAGGTCTCCGCTGACTAGGGCAGCATCTGCAGAGTGGAAATCA 300
 QY 301 AGGCTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTGCATG 360
 Db 301 AGGCTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTGCATG 360
 QY 361 ATTTTGAAGATGGATTTCTTTACAGGATATAAAGCAATTTGTTACAGGATTTTGTACAA 420
 Db 361 ATTTTGAAGATGGATTTCTTTACAGGATATAAAGCAATTTGTTACAGGATTTTGTACAA 420
 QY 421 GATAATGTGAATAAAGATGCCGTTCAGATAGATTTGCTTCAGTGGAGACTGATATGCCCT 480
 Db 421 GATAATGTGAATAAAGATGCCGTTCAGATAGATTTGCTTCAGTGGAGACTGATATGCCCT 480

QY	481	CTAACATTGAGACAGCATAGAATAAGTGGCGACATCATCATCGAAGAGAGTAGTAAACAAA	540
DB	481		
QY	481	CTTAACATTGAGACAGCATAGAATAAGTGGCGACATCATCATCGAAGAGAGTAGTAAACAAA	540
DB	481		
QY	541	GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGCCCGAGTGGCGGTGGTCCCGACAGTCC	600
DB	541		
QY	541	GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGCCCGAGTGGCGGTGGTCCCGACAGTCC	600
DB	541		
QY	601	ACGTGCAAGAAACAAAAGAACAGAAAAGGAAGCAACAGAGAGAAAAGACAAAATGCCAGTTC	660
DB	601		
QY	601	ACGTGCAAGAAACAAAAGAACAGAAAAGGAAGCAACAGAGAGAAAAGACAAAATGCCAGTTC	660
DB	601		
QY	661	AGTACGACGACAGTGGACGATCATATATGCTCTGCCATTAATGCAATGTGACACCTCGGCCCCA	720
DB	661		
QY	661	AGTACGACGACAGTGGACGATCATATATGCTCTGCCATTAATGCAATGTGACACCTCGGCCCCA	720
DB	661		
QY	721	GAGCGGCAAGGATTACAGAAAGTGGTCCGAGGTTCTTAAACGAGAGAACTAATGGAGCAG	780
DB	721		
QY	721	GAGCGGCAAGGATTACAGAAAGTGGTCCGAGGTTCTTAAACGAGAGAACTAATGGAGCAG	780
DB	721		
QY	781	AACAGACTGAAGAAATGTGACCGCGCTGTCCGCGAAACAGAAAGTCCCTGATCGGAGGCTC	840
DB	781		
QY	781	AACAGACTGAAGAAATGTGACCGCGCTGTCCGCGAAACAGAAAGTCCCTGATCGGAGGCTC	840
DB	781		
QY	841	GTGTGTTACNAGGACGATACGACGACCTTCGGAAGAGGATCTCAAAAGGTTGACGACAG	900
DB	841		
QY	841	GTGTGTTACNAGGACGATACGACGACCTTCGGAAGAGGATCTCAAAAGGTTGACGACAG	900
DB	841		
QY	901	ACTTGGCAATCAGCAGATGAAGAGACGAAGA CTGACACATGCCATTCGCCACAGATCAACA	960
DB	901		
QY	901	ACTTGGCAATCAGCAGATGAAGAGACGAAGA CTGACACATGCCATTCGCCACAGATCAACA	960
DB	901		
QY	961	GAATATGACCATCTCTCAACGTACAGTAAATAGTCCGAGTTTCCCAAGGCTACCTGGTTT	1020
DB	961		
QY	961	GAGATGACGATCTTAAACAGTGCAGCTATTATGTAGAATTTCGCAAGGACCTACCGGATTC	1020
DB	961		
QY	1021	TCAAGATCTCAACACCTGCACCATCACTATTATTAAGGCATGCTCAAGCGAAGTGATG	1080
DB	1021		
QY	1021	TCAAGATATCTCAGTCCGATCAANTTACATATTAAAGGCGTCATCAAGCGAAGTGATG	1080
DB	1021		
QY	1081	ATGCTGCGAGTAGCAGGCGGTAACGACCGGTGTCGATAGCGTTCTGTTCGCCAACAAAC	1140
DB	1081		
QY	1081	ATGCTGCGAGTAGCAGGCGGTAACGACCGGTGTCGATAGCGTTCTGTTCGCCAACAAAC	1140
DB	1081		
QY	1141	CAGGCGTACACTCGGCAACACTACCGCAAGGCGGCGATGGCTACGTCATCGAAGACCTG	1200
DB	1141		
QY	1141	CAGGCGTACACTCGGCAACACTACCGCAAGGCGGCGATGGCTACGTCATCGAAGACCTG	1200
DB	1141		
QY	1201	CTGCACTTCTCGCGTGCATGTACTCGATGTCGATGGAACACGTGCAATACGGCTCCTC	1260
DB	1201		
QY	1201	CTGCACTTCTCGCGTGCATGTACTCGATGTCGATGGAACACGTGCAATACGGCTCCTC	1260
DB	1201		
QY	1261	ACTGCCATCGTTATATTCTCGATCGCGCGGCTAGACGAGCCACAGCTAGTAGAAGAG	1320
DB	1261		
QY	1261	ACTGCCATCGTTATATTCTCGATCGCGCGGCTAGACGAGCCACAGCTAGTAGAAGAG	1320
DB	1261		
QY	1321	ATTCAGCGGTATTACTCTGAACACGCTCGGGGTGATCATCATGAACACGACAGCGCTCG	1380
DB	1321		
QY	1321	ATTCAGAGATCTACTTGAAGCGTCTCGGGTTTACATTTTAAATCAGCACAGCGCTCG	1380
DB	1321		
QY	1381	CGCGTTGGCGCGTCACTAACGGAAGATTTGTCTCGGTGCTTACCGAGTTTCGGACGCTG	1440
DB	1381		
QY	1381	CCTCGCTGGCGCGTCTGTCTCGGCAAGATTCCTCGCGGTGCTGACGGAACTCGGCACGCT	1440
DB	1381		
QY	1441	GGCATGCAAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAACAGGAAGCTCCCGCG	1500
DB	1441		
QY	1441	GGCATGCAAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAACAGGAAGCTCCCGCG	1500
DB	1441		
QY	1501	TTCTCTGGAGGAGATCTGGGACGTG	1524
DB	1501		
QY	1501	TTCTCTGGAGGAGATCTGGGACGTG	1524
DB	1501		

RESULT 7
ABT07377
ID ABT07377 standard; DNA; 1863 BP.
XX AC
XX AC ABT07377;
XX DT
XX DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX XX
XX XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 136.
XX XX
XX XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.
XX XX
XX XX Manduca sexta.
OS Manduca sexta.
OS Chimeric.
XX XX
XX PN WO200261102-A2.
XX PD
XX PD 08-AUG-2002.
XX XX
XX PF 24-OCT-2001; 2001WO-US051417.
XX PR
XX PR 24-OCT-2000; 2000US-0242969P.
XX XX
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX DR
XX DR WPI; 2002-619259/66.
XX DR P-PSDB; ABJ05379.
XX XX
XX XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX XX
XX XX Example 25; Page 301-304; 319pp; English.
XX XX
XX XX The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX XX
XX XX Sequence 1863 BP: 487 A; 489 C; 510 G; 377 T; 0 U; 0 Other;

	Query Match	87.4%;	Score 1332;	DB 6;	Length 1863;
	Best Local Similarity	92.1%;	Pred. No. 0;		
	Matches 1404;	Conservative	0; Mismatches	120; Indels	0; Gaps
Qy	1	ATGCAGCAGCTATATGTGGATTTTTTTTAAAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60		
Db	1	ATGCAGCAGCTATATGTGGATTTTTTTTAAAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60		
Qy	61	TACTGTTTCTTTTGTTCGAGTCTACCCCTGTTGTTTGGTTTACTTCTCGAGGATCCGCC	120		
Db	61	TACTGTTTCTTTTGTTCGAGTCTACCCCTGTTGTTTGGTTTACTTCTCGAGGATCCGCC	120		
Qy	121	ACCATGAGCTACTGTCCTTCTATCGAAACAAGCATCGCATATTTGCCGACTTTAAAAAGCTC	180		
Db	121	ACCATGAGCTACTGTCCTTCTATCGAACAAGCATCGCATATTTGCCGACTTTAAAAAGCTC	180		
Qy	181	AAGTGCTCCAAAGAAAAACCGAAGTGTGGCCAAAGTGTCTGAGACAAACATGGGAGTGTGCG	240		
Db	181	AAGTGCTCCAAAGAAAAACCGAAGTGTGGCCAAAGTGTCTGAGACAAACATGGGAGTGTGCG	240		

241 TACTCTCCAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGCAGAGAAGTGAATCA 300
Db |
241 TACTCTCCAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGCAGAGAAGTGAATCA 300
Qy |
301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTCTTCGAGAAAGACCTTGACATG 360
Db |
301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTCTTCGAGAAAGACCTTGACATG 360
Qy |
361 ATTTGAAATGGATTCTTTTACAGGATATAAAGCAATTTGTTAAACAGGATTATTTGTACAA 420
Db |
361 ATTTTGAATGGATTCTTTTACAGGATATAAAGCAATTTGTTAAACAGGATTATTTGTACAA 420
Qy |
421 GATATGTCAATAAAGATGCCCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCT 480
Db |
421 GATATGTCAATAAAGATGCCCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCT 480
Qy |
481 CTAACATTGAGACAGCATAGATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
Db |
481 CTAACATTGAGACAGCATAGATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
Qy |
541 GGTCAAAGACAGTTGACTGTATCGACGCGTATAGGCGCGAGTGCCTGCCAGAGTCC 600
Db |
541 GGTCAAAGACAGTTGACTGTATCGACGCGTATAGGCGCGAGTGCCTGCCAGAGTCC 600
Qy |
601 ACGTGAAGCAAAAG 660
Db |
601 ACGTGAAGCAAAAG 660
Qy |
661 AGTACGACGACAGTGCAGCATCATATGCTGCGCATATGCAATGTCACCTCGCGCCCA 720
Db |
661 AGTACGACGACAGTGCAGCATCATATGCTGCGCATATGCAATGTCACCTCGCGCCCA 720
Qy |
721 GAGCGCGCAAGGATTCACGAAGTGTGTCGAGGTTCTTAAACGGAAGCTATTCGAGCAG 780
Db |
721 GAGCGCGCAAGGATTCACGAAGTGTGTCGAGGTTCTTAAACGGAAGCTATTCGAGCAG 780
Qy |
781 AACAGACTGAAGATGTGACGCGCTGTGCGGCAACGAGAGTCCCTGATCGCGAGGCTC 840
Db |
781 AACAGACTGAAGATGTGACGCGCTGTGCGGCAACGAGAGTCCCTGATCGCGAGGCTC 840
Qy |
841 GTGTGTACAGGACGGATACGAGCAGCTTCGGAAGAGGATCTCAAAAGGGTGCAGCAG 900
Db |
841 GTGTGTACAGGAGGGGTACGAGCAGCTTCGGAAGAGGATCTCAAGAGAGTTACACAG 900
Qy |
901 ACTTGGCAATCAGCAGATGAAGAAGACGAAGACTCAGACATGCCATTCGCGCAGATCACA 960
Db |
901 ACATGGCAGTTAGAAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy |
961 GAATGACCATCTCAGCTACAGTAAATAGTTCGAGTTTGCAGAGGCTTACCTGGTGT 1020
Db |
961 GAGATGACGATCTTAAACAGTGCAGCTATTTGTAGAATTCGCAAGGAGACTTACCGGATTC 1020
Qy |
1021 TCAAGATCTCACAACTGACAGATCACATTTAAAGGCATGCTCAAGCGAAGTGATG 1080
Db |
1021 TCAAGATCTCAGTCCGATCAATATACATTTAAAGGCGTCATCAAGCGAAGTGATG 1080
Qy |
1081 ATGCTCGAGTACGAGCGGATACGACGCGGTGTCGATAGCTTTCGCAAGGCTTACCTGGT 1140
Db |
1081 ATGCTCGAGTACGAGCGGATACGACGCGGTGTCGATAGCTTTCGCAAGGCTTACCTGGT 1140
Qy |
1141 CAGCGTACACTCGCGCAACTACCGAGCGGCGATGCTACGTCATCGAAGACCTG 1200
Db |
1141 CAGCGTACACTCGCGCAACTACCGAGCGGCGATGCTACGTCATCGAAGACCTG 1200
Qy |
1201 CTGCACTTCTGCGCTCATGTTACTTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 1260
Db |
1201 CTGCACTTCTGCGCTCATGTTACTTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 1260
Qy |
1261 ACTGCCATCGTTATTTCTCGATTCGCGCGGCGCTTAGAGCGGACAGCTAGTAGAGAG 1320
Db |
1261 ACCGCCATCGTTATTTCTCAGACCGCGCGGCGCTTAGAGCGGACAGCTAGTAGAGAG 1320

Qy 1321 ATCCAGCGGTATTACCTGAACACACGCTCGGGTGTATCATCATGAACACGAGCGCGTCG 1380
Db |
1321 ATCCAGAGATACTACTTGAAGACGCTCGGGTGTATCATCATGAACACGAGCGCGTCG 1380
Qy 1381 CCGGTTCCGCGCTCATCTACGGAAGATTCTGTCGGTGTCTTACGAGTTCGGAGCGTG 1440
Db |
1381 CCGGTTCCGCGCTCATCTACGGAAGATTCTGTCGGTGTCTTACGAGTTCGGAGCGTG 1440
Qy 1441 GGCATGCAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAACAGGAAGTGCCTCG 1500
Db |
1441 GGCATGCAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAACAGGAAGTGCCTCG 1500
Qy 1501 TTCTCGAGGAGATCTCGGAGCTG 1524
Db |
1501 TTCTCGAGGAGATCTCGGAGCTG 1524

RESULT 8
ADP49208
ID ADF49208 standard; DNA; 1863 BP.
XX
AC ADF49208;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/Dof1 transactivation domain DNA seq id 136.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
KW yeast GAL4 DNA binding domain; Dof1 transactivation domain; ds; gene.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Zea mays.
XX
PN US2003154509-A1.
XX
PD 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.
XX
PR 24-OCT-2001; 2001US-00087167.
XX
PA (PASC/) PASCAL E. J.
PA (VALE/) VALENTINE S. A.
PA (BROWN/) BROWN J. A.
PA (COCK/) COCKRELL A. S.
PA (JOHN/) JOHNSON B. D.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
WP1; 2003-897756/82.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful
PT for regulating the expression of target polypeptides in plants in the
PT presence of appropriate chemical ligands.
XX
PS Example 25; SEQ ID NO 136; 186bp; English.
XX
CC The invention describes a receptor cassette encoding a chimeric receptor
CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
CC (E) domain that is heterologous with respect to the D domain, and an
CC activation domain. The receptor cassette and method are useful in
CC regulating the expression of target polypeptides in plants in the
CC presence of appropriate chemical ligands. The transgenic seeds and plants
CC can be used for the breeding of improved plant lines that, for e.g.,
CC increase the effectiveness of conventional methods such as herbicide or
CC pesticide treatment. This sequence encodes an ecdysone receptor-Dof1
CC transactivation domain fusion protein.

xx	Sequence	1863 BP;	487 A;	489 C;	510 G;	377 T;	0 U;	0 Other;
Qy	Query Match	87.4%;	Score 1332;	DB 10;	Length 1863;			
Qy	Best Local Similarity	92.1%;	Pred. No. 0;					
Qy	Matches 1404;	Conservative	0;	Mismatches	120;	Indels	0;	Gaps
Qy	0;							
Qy	1	ATCGACAGCTATATGTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60					
Qy	1	ATCGACAGCTATATGTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60					
Qy	61	TACTGTTCTTTTGTGATGCTCACCTGTTTGTGTTTGTGTTTACTTCTGACGGATCCGCC	120					
Qy	61	TACTGTTCTTTTGTGATGCTCACCTGTTTGTGTTTGTGTTTACTTCTGACGGATCCGCC	120					
Qy	121	ACCATGAAGCTACTGTCTTCTATCGAAACAGCAATGCGATATTTTCCGACTTAAAAAGCTC	180					
Qy	121	ACCATGAAGCTACTGTCTTCTATCGAAACAGCAATGCGATATTTTCCGACTTAAAAAGCTC	180					
Qy	181	AAGTGTCTCCAAAGAAAACCGAAGTGCCTGCTGAAGAAACAACTGGAGTGTGCG	240					
Qy	181	AAGTGTCTCCAAAGAAAACCGAAGTGCCTGCTGAAGAAACAACTGGAGTGTGCG	240					
Qy	241	TACTCTCCAAAACCAAAGGTCTCCGCTGACTAGGGCAGCATCTGACAGAGTGGAAATCA	300					
Qy	241	TACTCTCCAAAACCAAAGGTCTCCGCTGACTAGGGCAGCATCTGACAGAGTGGAAATCA	300					
Qy	301	AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCGAGAGACCTTGGACATG	360					
Qy	301	AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCGAGAGACCTTGGACATG	360					
Qy	361	ATTTTGGAAATGGATTTCTTACAGATATATAAGCATTGTTAAACAGGATATTGTGACAA	420					
Qy	361	ATTTTGGAAATGGATTTCTTACAGATATATAAGCATTGTTAAACAGGATATTGTGACAA	420					
Qy	421	GATAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT	480					
Qy	421	GATAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT	480					
Qy	481	CTAACNTTGACAGCAGTAGAATAAGTGGCAGCATCATCTCGGAAGAGAGTAGTAACAA	540					
Qy	481	CTAACNTTGACAGCAGTAGAATAAGTGGCAGCATCATCTCGGAAGAGAGTAGTAACAA	540					
Qy	541	GCTCAAGACAGTTGACTGTATCGACCGCTATGAGGCCCGAGTGCCTCCAGAGTCC	600					
Qy	541	GCTCAAGACAGTTGACTGTATCGACCGCTATGAGGCCCGAGTGCCTCCAGAGTCC	600					
Qy	601	ACGTGCAAGACAAAGAGAGAAAGAGAGCAGAGAGAAAGAGAAACAACTGCCAGTC	660					
Qy	601	ACGTGCAAGACAAAGAGAGAAAGAGAGCAGAGAGAAAGAGAAACAACTGCCAGTC	660					
Qy	661	AGTAGCAGCAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCGCCCA	720					
Qy	661	AGTAGCAGCAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCGCCCA	720					
Qy	721	GAGGGCGGAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAGAGCTAATGGAGCAG	780					
Qy	721	GAGGGCGGAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAGAGCTAATGGAGCAG	780					
Qy	781	ACACACTGAAAGATGTGACCGCGTGTGCGCGAACACAGAAAGTCCCTGATCGGAGGCTC	840					
Qy	781	ACACACTGAAAGATGTGACCGCGTGTGCGCGAACACAGAAAGTCCCTGATCGGAGGCTC	840					
Qy	841	GTGTGGTACCGAGCGGATACGAGCAGCTTCCGAAAGAGGATCTCAAAAGGAGTACCGCAG	900					
Qy	841	GTGTGGTACCGAGCGGATACGAGCAGCTTCCGAAAGAGGATCTCAAAAGGAGTACCGCAG	900					
Qy	901	ACTTGGCAATCAGCAGATGGAAGACCAAGACTCAGACATGCCATATCCCGCAGATCACA	960					
Qy	901	ACTTGGCAATCAGCAGATGGAAGACCAAGACTCAGACATGCCATATCCCGCAGATCACA	960					
Qy	961	GAAATGACCATCCTCACAGTAGCTAATAGTCGAGTTTGCAGAGGCTTACCTGGTGT	1020					

961	QY	DB	GAGATGACGATCTTAACAGTCGAGCTTATTTGTAGAAATTCGCAAGGGGACTACCGGGATTC	1020
1021	QY	DB	TCAAAGATCTCAACACCTGACAGATCACATTATTAAAGGCATGCTCAAGCGAAGTGATG	1080
1021	QY	DB	TCCAAAGATATCTCAGTCGGCATCAAATTTACATTTATTAAAGCGCTCATCAAGCGAAGTGATG	1080
1081	QY	DB	ATGCTGCCAGTAGCAGAGGCGGTACGACGCGGTGTGGATAGCGTTCTGTTTCGCCAACAAC	1140
1081	QY	DB	ATGCTGCCAGTAGCAGAGGCGGTACGACGCGGTGTGGATAGCGTTCTGTTTCGCCAACAAC	1140
1141	QY	DB	CAGGCGTACACTCGCGACAACCTACCGCAAGGCGGCATGGCCTCATCGAAGACCTG	1200
1141	QY	DB	CAGGCGTACACTCGCGACAACCTACCGCAAGGCGGCATGGCCTCATCGAAGACCTG	1200
1201	QY	DB	CTGCACTTCTGCGCGTGCATGTACTCGATGTGATGGACAAAGCTGCATTAACGCGCTCCTC	1260
1201	QY	DB	CTGCACTTCTGCGCGTGCATGTACTCGATGTGATGGACAAAGCTGCATTAACGCGCTCCTC	1260
1261	QY	DB	ACTGCCATCGTTATATTCCTGGATCGGCGCGGCTAGAGCAGCCACAGCTAGTAGAAGAG	1320
1261	QY	DB	ACGCCATCGTTATATTCCTGGATCGGCGCGGCTAGAGCAGCCACAGCTAGTAGAAGAG	1320
1321	QY	DB	ATCCAGCGGTATTAACCTGAACAGCTCGCGGTGTACATCATGAACACAGACAGCGCGCTG	1380
1321	QY	DB	ATCCAGCGGTATTAACCTGAACAGCTCGCGGTGTACATCATGAACACAGACAGCGCGCTG	1380
1381	QY	DB	CCGCGTTTGGCGCCGTCATCTACGCGAAGATTCTGTGCGTGCTTACCAGTTTGGGACGCTG	1440
1381	QY	DB	CCTCGTGGCGCGTCTGTTTGGCAAGATCTCTGGCGTGTGACGGAACCTGCGCAGCTC	1440
1441	QY	DB	GGATGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGGAAAGCTGCGCGCG	1500
1441	QY	DB	GGATGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGGAAAGCTGCGCGCG	1500
1501	QY	DB	TTCTTGGAGGAGATCTGGGACGTTG	1524
1501	QY	DB	TTCTTGGAGGAGATCTGGGACGTTG	1524
RESULT 9				
ABT07353				
ID	ABT07353 standard; DNA; 3972 BP.			
XX	ABT07353;			
XX				
DT	07-NOV-2002 (first entry)			
DE	Ecdysone receptor containing vector pCGS202 DNA SEQ ID NO: 104.			
XX	Plant; gene expression control; insect; hormone receptor; fertility;			
KW	ecdysone receptor; gene; ds.			
XX	Synthetic.			
XX	WO200261102-A2.			
PN	08-AUG-2002.			
PD	24-OCT-2001; 2001WO-US051417.			
XX	24-OCT-2000; 2000US-0242969P.			
PR	(SYGN) SYNGENTA PARTICIPATIONS AG.			
XX	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;			
PI	WPI; 2002-619259/66.			
DR	P-PSDB; ABJ05371.			
DR	New receptor cassette encoding a chimeric receptor polypeptide, useful in			
XX	regulating expression of target polypeptides in plants in the presence of			
PT	appropriate ligands that may be used in controlling plant fertility.			
XX				

Claim 28; page 255-258; 319pp; English.

The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecadysone receptor (ECR) of an insect, a ligand binding domain of an insect ECR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a coding sequence described in the exemplification of the invention.

Sequence 3972 BP: 1027 A; 895 C; 929 G; 1121 T; 0 U; 0 Other;

Query Match 87.4%; Score 1332; DB 6; Length 3972;
Best Local Similarity 92.1%; Pred. NO. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0

[illegible]

RESULT 11
 ABT07368
 ID ABT07368 standard; DNA; 1767 BP.
 XX AC
 XX ABT07368;
 XX AC
 XX 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 122.
 XX
 KW Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor; gene; ds.
 XX
 OS Manduca sexta.
 OS Spodoptera frugiperda.
 OS Chimeric.
 XX
 PN WO200261102-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 24-OCT-2001; 2001WO-US051417.
 XX
 XX 24-OCT-2000; 2000US-0242969P.
 PR
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PA
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI
 XX WPI; 2002-619259/66.
 DR P-PSDB; ABJ05374.
 XX
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX
 XX Example 23; Page 275-278; 319pp; English.
 PS
 XX The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a coding sequence described in the exemplification of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1767 BP; 476 A; 431 C; 477 G; 383 T; 0 U; 0 Other;
 Query Match 87.2%; Score 1328.8; DB 6; Length 1767;
 Best Local Similarity 92.0%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
 QY 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCAACGCTATTTTGTCTGG 60
 DB 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCAACGCTATTTTGTCTGG 60
 QY 61 TACTGTTTCTTTTGTGCTACCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 DB 61 TACTGTTTCTTTTGTGATGCTACCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 QY 121 ACCATGAAGCTACTGTTCTTCTCGAACAGCAATGCGATATTTCCGCACTTAAAGAGCTC 180
 DB 121 ACCATGAAGCTACTGTTCTTCTCGAACAGCAATGCGATATTTCCGCACTTAAAGAGCTC 180
 QY 181 AAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
 DB 181 AAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240

QY 241 TACTCTCCAAACCAAAAGGTCTCCGCTGACTAGGGCAATCTGACAGAAAGTGGAAATCA 300
 DB 241 TACTCTCCAAACCAAAAGGTCTCCGCTGACTAGGGCAATCTGACAGAAAGTGGAAATCA 300
 QY 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAAAGACTTCACATG 360
 DB 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAAAGACTTCACATG 360
 QY 361 ATTTTGAATAATGGATTTCTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTTGTACAA 420
 DB 361 ATTTTGAATAATGGATTTCTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTTGTACAA 420
 QY 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
 DB 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
 QY 481 CTAACATTGAGACAGCATAGATAAGTCGCGCATCATCATCGGAAGAGAGTAGTAACAAA 540
 DB 481 CTAACATTGAGACAGCATAGATAAGTCGCGCATCATCATCGGAAGAGAGTAGTAACAAA 540
 QY 541 GGTCAAAGACAGCTGACTGTATCGACGGTATGAGCCCGAGTGGCTGCTCCAGAGTCC 600
 DB 541 GGTCAAAGACAGCTGACTGTATCGACGGTATGAGCCCGAGTGGCTGCTCCAGAGTCC 600
 QY 601 ACCTGCAAGAAACAAAGAAAGAAAGAACACAGAGAGAAAAAGACAAACTGCCAGTTC 660
 DB 601 ACCTGCAAGAAACAAAGAAAGAAAGAACACAGAGAGAAAAAGACAAACTGCCAGTTC 660
 QY 661 AGTACGACGACAGTGGACGATCATATGCTGTCATTAATGCAATGTGACCTCCGCCCA 720
 DB 661 AGTACGACGACAGTGGACGATCATATGCTGTCATTAATGCAATGTGACCTCCGCCCA 720
 QY 721 GAGGCGGCAAGATTCACGAGTGGTCCGAGGTTCTTAACGGAGAGAGTAATGAGAGCAG 780
 DB 721 GAGGCGGCAAGATTCACGAGTGGTCCGAGGTTCTTAACGGAGAGAGTAATGAGAGCAG 780
 QY 781 AACAGACTGAAGAATGTGACGCGCTGTGCGGCGCTGTGCGGCGAACCAGAAAGTCCCTG 840
 DB 781 AACAGACTGAAGAATGTGACGCGCTGTGCGGCGAACCAGAAAGTCCCTGCGAGGCTC 840
 QY 841 GTGTGGTACAGGACGGATACAGCAGCTTCGGAAGAGAGTCTCAAAAGGTTGACGCGAG 900
 DB 841 GTGTGGTACAGGACGGGTTACAGCAGCGCTCGGAAGAGAGTCTCAAAAGAGTTACACAG 900
 QY 901 ACTTGCATACAGCAGATGAAGAAGAGAGAGTCTGACATGCTCATTTCCGCCAGATCACA 960
 DB 901 ACATGGCAGTTAGAAGAAGAGAGAGAGAGTCTGACATGCTCATTTCCGCCAGATCACA 960
 QY 961 GAAATGACCATCTCTCACAGTACAGCTAATAGTCGAGTTTGCCTCAAGGCTTACCTGTTT 1020
 DB 961 GAGATGACCATCTTAAACAGTGCAGCTTATTTGTAGAATTCGCAAGGAGTCTACCGGAT 1020
 QY 1021 TCAAGATCTCAACCTGACAGATACATTAATTAAGGAGTCTCAAGCGAGTGTGATG 1080
 DB 1021 TCAAGATATCTCAGTCCGATCAAAATTAATTAAGGAGTCTCAAGCGAGTGTGATG 1080
 QY 1081 ATGCTCGAGTACGAGCGGTACGAGCGGTGTCGATAGCGTCTGTTTCGCAACAAC 1140
 DB 1081 ATGCTCGAGTACGAGCGGTACGAGCGGTGTCGATAGCGTCTGTTTCGCAACAAC 1140
 QY 1141 CAGGCGGTACATCTCGCAACAACCTACCGAAGCGGGCATGGCTTACGTCATGCAAGACCTG 1200
 DB 1141 CAGGCGGTACATCTCGCAACAACCTACCGAAGCGGGCATGGCTTACGTCATGCAAGACCTG 1200
 QY 1201 CTGCACTTCTGCGCTGCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1260
 DB 1201 CTGCACTTCTGCGCTGCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1260
 QY 1261 ACTGCCATCGTTATATTTCTCGGATCGCGGGCTAGAGCAGCAGCAGCTAGTAGAAGAG 1320
 DB 1261 ACCGCCATCGTTATATTTCTCAGACCGCGGCTCGAGCAGCAGCTAGTAGAAGAG 1320

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:02:48 ; Search time 5198.63 Seconds
(without alignments)
11158.701 Million cell updates/sec

Title: US-10-087-167-120_COPY_1_1524
Perfect score: 1524
Sequence: 1 atgcagcagctatgtgga.....tggaggagatctggagcgtg 1524

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321.6	21.1	963	CNS0905M	BX067382 Single re
2	242.8	15.9	851	CNS011ME	AL100448 Drosophil
3	226.2	14.8	728	BM650826	BM650826 170006873
4	214.6	14.1	470	AA538642	AA538642 LD18219.5
5	183.6	12.0	607	AA664510	AA664510 ESTFrg2-
6	161.1	10.6	1050	CNS016YX	AL107379 Drosophil
7	159.6	10.5	574	AI258616	AI258616 LP01848.5
8	140.0	9.2	1031	BQ058428	BQ058428 AGENCOURT
9	139.6	9.2	842	CNS06JJC	AL401698 T7 end of
10	138.4	9.1	651	CNS09352	CNS09352 170005999
11	138.4	9.1	667	CD673041	CD673041 fg19q05.Y
12	138.4	9.1	867	BQ222200	BQ222200 AGENCOURT
13	138.4	9.1	918	BQ214241	BQ214241 AGENCOURT
14	138.4	9.1	1685	CR614375	CR614375 full-leng
15	138.4	9.1	1763	CR610600	CR610600 full-leng
16	138.4	9.1	1828	CR617823	CR617823 full-leng
17	138.4	9.1	1922	CR604070	CR604070 full-leng
18	138.4	9.1	1924	CR609885	CR609885 full-leng
19	138.4	9.1	1965	CR598124	CR598124 full-leng
20	138.4	9.1	1978	CR598123	CR598123 full-leng
21	138.4	9.1	2041	BC033500	BC033500 Homo sapi
22	138.2	9.1	721	BE382387	BE382387 601298693
23	133	8.7	1088	BX463524	BX463524 BX463524
24	127.6	8.4	1082	BX367164	BX367164 BX367164

25	127.4	8.4	866	4	BG675073
26	126.4	8.3	957	5	BE878950
27	125.8	8.3	1003	2	BX344136
28	125.8	8.3	1026	5	BQ052341
29	124.4	8.2	986	5	BQ877581
30	124.4	8.1	622	5	BQ636916
31	123.8	8.1	1135	5	BX365740
32	123.6	8.1	2035	3	CR749648
33	123.2	8.1	965	1	AL582953
34	122.6	8.0	972	1	AL522399
35	119.2	7.8	920	1	AL522738
36	118.8	7.8	1085	5	BX406790
37	118.6	7.8	1132	4	BM553603
38	117.6	7.7	1114	5	BX444140
39	117.6	7.7	1138	5	BM912640
40	117.6	7.7	1158	4	BM554635
41	117	7.7	1963	3	AK077620
42	115.6	7.6	649	6	CD304821
43	114.6	7.5	618	6	CD309514
44	113.6	7.5	444	9	AG215235
45	112.4	7.4	1074	5	BX342843

ALIGNMENTS

RESULT 1
CNS0905M 963 bp mRNA linear HTC 08-JAN-2003
LOCUS Single read from an extremity of a full-length cDNA clone made from
DEFINITION Anopheles gambiae total adult females. 5-PRIME end of clone
FKOAC51AC03 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
ACCESSION BX067382
VERSION BX067382.1 GI:27640663
KEYWORDS HTC.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 963)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (08-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
FEATURES
Location/Qualifiers
1..963
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FKOAC51AC03"
/plasmid="pME18S-EL"
/note="end : 5-PRIME"

QY	937	GACATGCCATCCCGCAGATCACAGAAATGACCATCTCCACAGTACAGCTAATAGTCGAG	996
DB	9	GAATTCACATTCGGGCACATACAGGAATACCATCTCCACAGTACAGCTAATAGTCGAG	68
QY	997	TTTTCGAAGGCCTACTCTGGTTTTCACAGATCTCACACCTGACAGATCATATTATTA	1056
DB	69	TTTCGGCAGGAGTCCGACATTCACCAAGATCCCGC-AGAGGATCAGATAACGTTACTA	127
QY	1057	AAGGATGCTCAAGCGAAGTATGATGCTGCAGTAGCAGCGGGTACACCGGGTGTGCG	1116
DB	128	AAGGCTCTCCAGTGAGGTGATGTTTGCAGATGGCCCGCGGTACGACCGCGAACC	187

Query Match 21.1%; Score 321.6; DB 3; Length 963;
Best Local Similarity 75.0%; Pred. No. 1.8e-77;
Matches 441; Conservative 0; Mismatches 144; Indels 3; Gaps 3;

1058	AGSCATGCTCAAGCGAAGTGAATGCTCGAGTAGCGAGCGGTACGACGCGGTCTCGG	1111
QY		
266	AGSCCTGCTCGTCGGAGGTGATGATCTCGTATGGCAGCAGCTATGACCAAGCTCGG	325
Db		
1118	ATAGCGTTCTGTTCGCCCAACACGAGCGGTACACTCGCAGCAAACTACCGCAAGCGCGGCA	1177
QY		
326	ACTCAATATTTCTTCGGGATATATAGATCAATATACGCGGGATTTCTTACAAATATGCCCGAA	385
Db		
1178	TGGCCTACGTCATTCGAAGACCTGCTGCACCTTTCGCGCTGTCATGTACTGATGTCATGG	1237
QY		
386	TGSCGTATAAACAATTGAAGACCTGCTGCAATTTCTGCCGCCAAATGTTTCTCGATGAAGGTGG	445
Db		
1238	ACAACTGCTATACGGCTCCTCACTGCCATCGTTATATTTCTCGGATCGCGCGGCGCTAG	1297
QY		
446	ACAACTCGAATAACGGCGCTTCTCACTGCCATTTGTGATCTTTCGACCGCGCGGCGCTCGG	505
Db		
1298	AGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACTCTGAACACGCTGCGGGTGTACA	1357
QY		
506	AGAGGCCCAACTAGTTCGAAGCGATCCAGAGCTACTACATCGACACGCTACGCAATTTATA	565
Db		
1358	TCATGAACACGACACAGGGCGTCCCGCGTTTGCCCGTCACTCTACGCGGAAGATCTGTGCGG	1417
QY		
566	TACTCAACCGCCACTGCGGACCTCAATG-AGCCTCGTCTTCTACGCAAGCTGCTCTCGA	624
Db		
1418	TGCTTACCGAGTTTGCGGACGCTGGGATGCAGAAATTCGAACATGTGCATCTCGCTGAAGC	1477
QY		
625	TCCTCACCGAGCTGCGTACGCTGGCAACCGAGATGTGTTTCTCACTAAAGC	684
Db		
1478	TCAAGAACACGAGAGCTGCCCGCTTCTTCGAGGAGATCTGGGACGT	1523
QY		
685	TCAAAAACCGCAAACTGCCCAAGTTCTCGAGAGATCTGGGACGT	730
Db		

RESULT 3	BM650826	728 bp	linear	EST 26-FEB-2002
LOCUS	BM650826		mRNA	
DEFINITION	17000687372602 A.Gam.ad.CDNA1 Anopheles gambiae cdna clone			
	19600449631714 5', mRNA sequence.			

ACCESSION	BM650826
VERSION	BM650826.1
KEYWORDS	GI:18950337
SOURCE	EST.
ORGANISM	Anopheles gambiae (African malaria mosquito)
	Anopheles gambiae
	Eukaryota; Metazoa
	Eukaryota; Arthropoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
	Anopheles.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 728)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charles, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004AYT row: E column: 24
Seq primer: M13 Reverse.

FEATURES	source
Location/Qualifiers	
1. 728	
/organism="Anopheles gambiae"	
/mol_type="rRNA"	
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"	
/db_xref="taxon:7165"	
/clone="19600449637314"	
/dev_stage="Adult"	
/lab_host="DH10b"	
/clone_lib="A.Gam.ad.cdNAl"	
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1."	

Qy	1117	GATAGCGTTCTGTTGCGCAACAACCGAGCGTACATCGCGAGCAACTACCGCAAGCGGC	1176
Dd	188	GACTCCATCCTCTTTGCGCAACAACCGATCGTACACGCGGACTCGTACAAGATGGCGGGC	247
Qy	1177	ATGGCCTACGTCATCGNAGACCTGCTGCACCTCTTCGCGCTGCATGTACTCGATGTCCGATG	1236
Dd	248	ATGGCGGACACGATCGAGGACCTGCTGCATCTTCTGCGGCGAGATGTACGCCTACGGTGG	307
Qy	1237	GACAACTGCATTACCGCGCTCCTCACTGCCATCGTTATATTCTCGGATCGCGCGGCGCTA	1296
Dd	308	GACAACTCGAGTACGCGCTGCTGACCGCGATCGTCACTCTTCTCCGACCGGCGCGGCTC	367
Qy	1297	GAGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACTGTGAACACGCTGCGGGTGTAC	1356
Dd	368	GAGAAAGCCGAGCTGGTGGAAAAGATCCAGAGCTACTACATCGACACGCTGCGCGCTAC	427
Qy	1357	ATCATGAACGAGCACAGGCGGTGCGCGGTGCGCGGTCACTATACGGGAAGATTCGTGCG	1416
Dd	428	ATCCTGAACCGGCACGGGGCGAC-CCGAAAGTGTAGCGTCAAGTTCGGGAA-CTGCTGTGCG	485
Qy	1417	GTGCTTACCGAGTTCGCGACGCTGGGATGCAGAAATTCGAAACATGTGCATCTCGCTGAAG	1476
Dd	486	ATCCTGACCGAGCTCGGACGCTCGGCAACGAGAACTCGGAGATGTGCTTCTCGTCAAG	545
Qy	1477	CTCAAGAACAGGAAGCTGCCGCCGTTCTTGGAGGAGATCTGGGACGTG	1524
Dd	546	CTGAGAACCTTAAGCTGCCCCGCTTCTTGGAGGAGATATGGGACGTG	593

RESULT 2	CNS011ME	851 bp	DNA	linear	GSS 26-JUL-1999
LOCUS	CNS011ME				
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN06K02 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				

ACCESSION	ALI00448
VERSION	ALI00448.1
KEYWORDS	GI:5612059
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyndroidea; Drosophilidae; Drosophila. 1 (bases 1 to 851) Genoscope.
REFERENCE	
AUTHORS	

TITLE	JOURNAL	COMMENT
Direct Submission		
Submitted (23-JUL-1999)	Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr	
	- Web : www.genoscope.cns.fr	
	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.abi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CDPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.	

```

FEATURES
source
Location/Qualifiers
1..851
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN06K02"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : Sp6"

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ORIGIN	Query Match	Score	DB	Length
	Best Local Similarity	71.5%		
	Pred. No. 1.2e-55;			
	Matches 333; Conservative	0; Mismatches 132;		
	Indels	1;		
	Gaps	1;		

Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org).

ORIGIN

Query Match 14.8%; Score 226.2; DB 4; Length 728;
Best Local Similarity 61.7%; Pred. No. 4.6e-51;
Matches 404; Conservative 0; Mismatches 233; Indels 18; Gaps 2;

Qy 551 AGTTGACTGTATCGACGCGTATGAGGCCGAGTGGTGTCTCCAGAGTCCACGTGCGAAGA 610
Db 79 AGAAGTGTCTCGCGTGTGCGTGTGCGGAGTGGTGTCTCCGAGAAATCAGTGTGCGCA 138
Qy 611 ACAAGAAGAGAAAGAGACACAGAGAGAAAGACAAACTGCCAGTCAATGACGCA 670
Db 139 TCAAGCGGAG 198
Qy 671 CAGTGGAGATCATATGCTGCTGCATATGCAATGTGACCTCCGCGCCAGAGAGCGGCA 730
Db 199 CCACCACCGTGTGATCAACAGAACAGCAGCAGTACAGTGTGAGTGTGCGGTGCTGA 258
Qy 731 GGATTACAGAAAGTGTCTCCGAG-----GTTCTTAACGAGAGAGTAAATGAGAGC 778
Db 259 TGAAGTGTGATCACCGCCCGCGCGATACCGCTACTGCGGAGAGAGTGTGTAACG 318
Qy 779 AGAACAGACTGAGAAATGTGAGCCCGCTGTGCGGCAACAGAGTCCCTGATCGCGAGC 838
Db 319 AAAACCGCAAGAAACATACCTCTGTGACGCGCAACAGATGCGCGTCTATCTACAAC 378
Qy 839 TCGTGTGTACAGCAGGATACGAGAGCGCTTCCGAGAGAGATCTCAAAAGGGTGAGC 898
Db 379 TGATCTGTACAGAGTGTCTACGAGAACCTGCGAGAGAGATCTCAAGAGGTAATGA 438
Qy 899 AGACTTGGCAATCAGCAGATGAAGAGACAGAGACTCAGACATGCCATTTCCGCCAGATCA 958
Db 439 TTA-----ACTCACCACAGAGAGAGAGATCCCCAGCAATCCACTTCGCGCACATA 492
Qy 959 CAGAAATGACCATCTCTCAGTACAGTAAATGATGAGTTTCCCAAGGCTACCTGTT 1018
Db 493 CGAAATCACCATCTCTCAGTACATCAATCTGCGAGTTCGCAAGGAGCTGCCAGAT 552
Qy 1019 TTTCAGAGATCTCAGAACCTGACAGATCAGATTTAAGGAGTGTCTCAAGCGAGTGA 1078
Db 553 TTACCAAGATCCCGAGAGAGATCAGATACGTTTCTAAGGCTGTCTCCAGTGAAGTGA 612
Qy 1079 TGATGTGCGAGTAGCGGCGGTACGACGCGGTGTGCGAGTGTGCGTGTGTTGCGCAACA 1138
Db 613 TGATGTGCGAATGGCCCGCGGTAGCAGCGCGAAACGACTCCATCTCTTTTGGCAACA 672
Qy 1139 ACCAGCGTACACTCGCGCAACTACCGCAAGCGCGGATGGCTACGTCATCGA 1193
Db 673 ACCGATCGTACACGCGCGACTCGTACAAGATGCGCGGATGGCGGACAGATCGA 727

RESULT 4
AA538642 470 bp mRNA linear EST 19-APR-2001
LOCUS LD18219.5prime LD Drosophila melanogaster embryo Bluescript
DEFINITION Drosophila melanogaster cDNA clone LD18219 5prime similar to M74078: Drosophila melanogaster ecdysone receptor (Ecr) mRNA, complete cds, mRNA sequence.

ACCESSION AA538642
VERSION AA538642.1 GI:2285158
KEYWORDS EST.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 470)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Teang, G., Lewis, S., and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project

JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 182 row: B column: 7
High quality sequence stop: 343.

FEATURES
source Location/Qualifiers
1..470
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="BDGP EST:BDcin017358"
/db_xref="taxon:7227"
/clone="LD18219"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/clone_lib="LD Drosophila melanogaster embryo Bluescript"
/note="Organ: embryo; Vector: Bluescript SK; Site 1:
EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-CDNA
Synthesis kit: Oligo dT-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)"

ORIGIN
Query Match 14.1%; Score 214.6; DB 1; Length 470;
Best Local Similarity 72.0%; Pred. No. 6.8e-48;
Matches 280; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 1135 AACACACGCGGTACATCGCGCAACATACCGCAAGCGCGGCATGCCCTACGTCTCGAA 1194
Db 1 AATAATAGATCATATACGCGGATTTCTACAAATGCGCGAATGGCTGATAACATTGAA 60
Qy 1195 GACCTGTGCACTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
Db 61 GACCTGTGCTATTTCTGCCGCCAAATGTTCTCGATGAAGGTGGAGCAAGTCAATACGCG 120
Qy 1255 CTCTCACTGCGATCGTTATATTTCTCGGATCGCGCGGCGCTAGACGACGACGCTAGTA 1314
Db 121 CTCTCACTGCGATGCTGATCTTCTCGACCGCGCGGCGCTGAGAGGCGCTTAACCTAGTC 180
Qy 1315 GAAGAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGTATCATCATGAACAGACAGC 1374
Db 181 GAAGGATCCAGAGCTACTACATCGACACGCTACGCAITTTATATATCTCAACGCCACTGC 240
Qy 1375 GGGTCCGCGGTGCGCGCTATCTACCGAGATTTCTGCTGCTGCTTACCGAGTTGCGG 1434
Db 241 GCGCACTCAATGAGCTGCTCTTCTACGCAAGCTGCTCTCGATCTTCAACGCAACCTG 300
Qy 1435 ACGCTGGGCATGCAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGGAGCTG 1494
Db 301 ACGCTGGGCAACCAAGACCGGAGATGTTTCTCACTAAAGCTCAAAAACCGCAACCTG 360
Qy 1495 CCGCGCTTCTCGGAGGAGATCTGGGACGT 1523
Db 361 CCCAAGTTCTCGAGAGATCTGGGACGT 389

RESULT 5
AA664510/c 607 bp mRNA linear EST 14-NOV-1997
LOCUS ESTFrg2- Human Brain, Clontech Homo sapiens cDNA clone pUC19-Frg2
DEFINITION 3', mRNA sequence.

ACCESSION AA664510
VERSION AA664510.1 GI:2619123
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 607)
AUTHORS Ming, H. and Huang, B.R.

TITLE	Research on mechanism of p75NTR induced apoptosis
JOURNAL	Unpublished (1997)
COMMENT	Other ESTs: ESTFrq2+

Contact: Ming Hong
National Laboratory of Medical Molecular Biology
Chinese Academic of Medical Sciences & PUMC
5 Dongdan Santiao, Beijing 100005, P.R.China

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model is designed for real-time processing, enabling immediate decision-making based on incoming data.	Model Performance Metrics
6. Integration with Existing Systems: The model seamlessly integrates with existing data management and analytics systems.	Model Performance Metrics
7. Customizable Parameters: The model offers customizable parameters to tailor its performance to specific use cases.	Model Performance Metrics
8. Regular Updates: The model is regularly updated with the latest data and algorithms to maintain its accuracy and relevance.	Model Performance Metrics
9. Compliance with Regulations: The model adheres to relevant data protection and privacy regulations, ensuring ethical data usage.	Model Performance Metrics
10. Support and Documentation: Comprehensive support and documentation are provided to assist users in utilizing the model effectively.	Model Performance Metrics

LOCUS CNS016YX 1050 bp DNA linear GSS 26-JUL-1999
DEFINITION *Drosophila melanogaster* genome survey sequence SP6 end of BAC BACN17G18 of DrosBAC library from *Drosophila melanogaster* (fruit fly), genomic survey sequence.

ACCESSION	AL107379
VERSION	AL107379.1
KEYWORDS	GI:5627062 GSS

SOURCE ORGANISM	REFERENCE
<i>Drosophila melanogaster</i> (fruit fly)	
<i>Drosophila melanogaster</i>	
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; <i>Drosophila</i> .	
1 (bases 1 to 1050)	

<http://www.edgp.ebi.ac.uk> - This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaud at CPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelBAC11.

FEATURES
source

ORIGIN

LOCUS
DEFINITION
AL258616 574 bp mRNA linear EST 19-APR-2001
L0101848.Sprime LP Drosophila melanogaster larval-early pupal pot2
Drosophila melanogaster cDNA clone L0101848 5prime similar to
M74078: ECR Fggn000546 PID:g157318 SWISS-PROT:P34021, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS

SOURCE	ORGANISM
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REFERENCE

AUTHORS	TITLE
...	...

END

JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic sequence DS05325
High quality sequence stop: 533.
Location/Qualifiers
1. 574
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LP01848"
/sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
/clone_lib="LP Drosophila melanogaster larval-early pupal
pOT2"
/note="Organ: whole body; Vector: pOT2; Site 1: EcoRI;
Site 2: XhoI; Sized fractionated cDNAs were directly
ligated into pOT2. Plasmid cDNA library."
"

ORIGIN
Query Match 10.5%; Score 159.6; DB 1; Length 574;
Best Local Similarity 61.1%; Pred. No. 1.2e-32;
Matches 280; Conservative 0; Mismatches 169; Indels 9; Gaps 1;
QY 753 GTTCTTAACGGAGACTAATGGAGCAGAACAGACTGAAGATGTGACCCCTGTGGC 812
Db 126 GCTACTACCTGTGAATATTGGCCAAAGTGTCAAGCGCGCAATATACCTTCTTAACGTA 185
QY 813 GAACAGAGTCTCGATCGCAGGCTCGTGTGTACAGGACGGATACGAGCGCTTC 872
Db 186 CAATCAGTTGGCGTTATATACAGTTAATTTGGTACAGGATGGCTATGACGAGCCATC 245
QY 873 GGAAGAGGATCTCAAAAGGGTGACGAGACTTTGGCAATCAGCAGATGAAGAAGACGAAGA 932
Db 246 TGAAGAGGATCTCAGCGGTATATGATCA-----ACCGATGAGAAGCAGAGCCA 296
QY 933 CTCAGACATGCCATTCGGCGAGATCAGAAATGACCATCTCTCAGATCAGCTAATAGT 992
Db 297 AACGGACGTGAGCTTTTCGGCATATAACCGAGATAACCATCTACCGGTCCAGTTGATGT 356
QY 993 CGAGTTTGGCAAGGCTACCTGTTTTCAAAGATCTCAACCTGACAGATCACAT 1052
Db 357 TGAGTTTGTAAAGGCTACCGCGTTTACAGGTTTACAAAGATACCCAGGAGACAGATCAGTT 416
QY 1053 ATTAAGGCGATGCTCAAGCGAAGTATGATGTCTGCGAGTAGCGAGCGGTACGACCGGT 1112
Db 417 ACTAAGGCGCTGCTCGTGGAGGTGATGATGTCTGCGTATGGCAGCGCTATGACACAG 476
QY 1113 GTCGAGTAGCGTTCTGTTTCCCAACACAGGCGGTACATCTCGGACAACTACCGAAGCC 1172
Db 477 CTCGGACTCAATATCTTCGCGAATAATAGATCATATACGCGGATTTCTTACAAATGCG 536
QY 1173 GGCATGGCTACGTATCAAGACCTGCTGCACTTCT 1210
Db 537 CGGAATGGCTGATAACAATTGAAGACCTGCTGCACTTCT 574

RESULT 8
LOCUS BQ058428 1031 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6794704 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814274
5', mRNA sequence.
ACCESSION BQ058428
VERSION BQ058428.1 GI:19817768
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1031)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM2067 row: k column: 11
High quality sequence stop: 634.
Location/Qualifiers
1. 1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5814274"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and SuperScript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 9.2%; Score 140; DB 5; Length 1031;
Best Local Similarity 56.3%; Pred. No. 3.9e-27;
Matches 329; Conservative 0; Mismatches 240; Indels 15; Gaps 3;
QY 946 TTCCGCCAGATCACAGAATGACCATCTCTCAGTACAGTAAATAGTCGAGTTTGC AAA 1005
Db 194 TTTGCCCACTTCACGAGCTGGCCATCATCTCAGTCCAGAGATCGTGGACTTCGCTAAG 253
QY 1006 GGCCTACCTGTTTTTAAAGATCTCAACCTGACAGATCACATTTAAGGCATGC 1065
Db 254 CAAGTGCCTGTTTCTCTGAGCTGGGCGGAGACCATGATCGCCCTCTCGAAGGATCC 313
QY 1066 TCAAGCGAAGTATGATGTCGAGTAGCGAGCGGTACGCGCGGTGTCGATAGCGTT 1125
Db 314 ACTATGAGATCATGCTGTAGACAGCAGCAGCGCTACAAACGAGACAGAGTGTATC 373
QY 1126 CTGTTCCGCAACCAACAGCGGTACACTCCGCAAACTACCGAAGCGGGCAT---GGCC 1182
Db 374 ACCTTCTTGAAGACTTCACTACAGCAAGGACGACTTCCACGTCGAGCGCTCGAGGTG 433
QY 1183 TAGTCATCGAAGACCTGCTGCACTTCTGCGCTGATGTACTCGATGTCGATGGACAAC 1242
Db 434 GAGTTTCATCAACCCCATCTTTCGAGTTCTCGCGGCGCATCGGCGCTTGGACGAC 493
QY 1243 GTGCATTACGCGCTCCTCACTGCTTATATTCTCG---GATCGCGCGGCGCTTAGAG 1299
Db 494 GCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCAACGTCGAG 553
QY 1300 CAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACACAGCTGCGGGTGTATC 1359
Db 554 GAGCGGGCGCGTGGAGCGGTTCGACAGAGCCCTACGTGGAGGCGCTGCTGTCTCTACAC- 612
QY 1360 ATGAACACAGACAGCGCGCTGCGCGGTTCGCGGTTCATCTACGCGAAGATTCGTGCGTG 1419
Db 613 -----GCGCATCAAGAGGCGCGAGGACGAGCTCGCTTCCCGCGCATGCTCATGAAG 664

Db	77	TTTGCCCACTTCAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG	136
Qy	1006	GGCTACCTGTTTTCAGAGATCTCAACCTGACGACATACATTAATTAAGGCATGC	1065
Db	137	CAAGTGCCTGTTCTCGAGCTGGCCGGAGGACCAAGATCGCCCTCTGAAGCATCC	196
Qy	1066	TCAACGGAAGTATGATGATCTGCGAGTACGAGCGGTACGAGCGGTGTGCGATAGCGTT	1125
Db	197	ACTATCGAGATCATCTGCTAGACAGACGCGGCTACACCAAGACAGAGTGTATC	256
Qy	1126	CTGTTTGGCAACAAACAGCGGTACACTCGCGAACAATCAACGCAAGCGGGCAT----	GGCC 1182
Db	257	ACCTTCTTGAAGACTTCACTTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAGGTG	316
Qy	1183	TACGTCATCGAAGACTGTCGACTTCTCCGCTGCATGTACTCGATGTCGATGACAAAC	1242
Db	317	GAGTTCATCAACCCCATCTTCAGTTCCTCGCGGGCCATCGCGCGTGGGCCCTGACACG	376
Qy	1243	GTGCAATACGCTCTCACTGCTCATCTGTTATATCTCG-----GATCGCGCGGCTAGAG	1299
Db	377	GCTGAGTACGCCCTGCTCATCTGCTCAATCAACATCTCTCGCGCGACCGGCCCAAGTGCAG	436
Qy	1300	CAGCCACAGCTAGTAGAAGATCCAGCGGTATTAACCTGAACACGCTGCGGTGTACATC	1359
Db	437	GAGCGGGCGGTGGAGCGTTGAGCAGACGCTAGTGGAGCGCTGCTGCTTACAC-	495
Qy	1360	ATGAACAGACAGCGCGTTCGCGGTTCGCGGTTCATCTACGCAAGATTCCTGTCGTTG	1419
Db	496	-----CGCATCAAGAGCGCGCAGGACCAAGTCTGCGCTTCCGCGCATGCTCATGAAG	547
Qy	1420	CTTACCGAGTTCGGAGCGTGGCGATGCAAGATTCGAACATGTGCATCTCGTGAAGCTC	1479
Db	548	CTGGTGAGCTGCGACGCTGAGCTCTGTGCACTCGAGCAGGTCTTTCGCTTGGCTTC	607
Qy	1480	AAGAACAGGAAGCTGCGCGCTTCTCTGAGGAGATCTGGGAGCT	1523
Db	608	CAGGACAGAGCTGCGGCTCTGCTGTCGGAGATCTGGAGCT	651
RESULT 11			
CD673041			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
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LOCUS			
DEFINITION			
ACCESSION			
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MEDLINE			
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VERSION      BQ222200.1  GI:20403609
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 867)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13220 row: 1 column: 05
              High quality sequence stop: 674.
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               /clone_lib="NIH MGC 70"
               /note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: NotI;
               Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.1 kb. Library constructed by Life
               Technologies."
ORIGIN
Query Match      9.1%; Score 138.4; DB 5; Length 867;
Best Local Similarity 56.2%; Pred. No. 1e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

QY 946 TTCCGCCAGATCACAGAAATGACCATCTCTCAGTACAGTAAATAGTCGAGTTTGCCAAA 1005
DB 99 TTTCGCCACTTCAGGAGTGGCCATCTCTCAGTCCAGGAGATCGTGAGCTTCGCTAAG 158
QY 1006 GGCCTACTGTTTTCAGAAATCTCAACCTGACAGATCAATATTAAAGCATGC 1065
DB 159 CAAAGTGCCTGTTTCTCGAGTGTGGCGGGAGGACCAAGATCGCCCTCTCGAAGGCATCC 218
QY 1066 TCAGCGAAGTGCATGCTCGAGTACGAGGGGTACGACGGGTGTCGGATAGCGTT 1125
DB 219 ACTATCGAGATCATGCTGTAGAGACAGCGCGCTACAAACAGAGAGAGTGTATC 278
QY 1126 CTGTTTCGCCAACACAGCGGTACACTCGGACAACTACCGCAAGCGGGGCAT---GGCC 1182
DB 279 ACCTTCTTGAAGACTTCACCTACAGCAAGACGACTTCACCGGTGCAGGCTCGAGTG 338
QY 1183 TAGGTCATGAGACCTGCTGCACTTCGCGCTGCTGATGTAATGATGTCATGAGCAAC 1242
DB 339 GAGTTTCATCAACCCCATCTTCAGTTCCTCGGGGCGCATCGCGGCTGGGCTGAGCAGC 398
QY 1243 GTGCATTACGCGCTCTCACTGCCATCGTTATATTCTCG---GATCGCGCGGGCTAGAG 1299
DB 399 GCTGAGTAGCGGCTGCTCATGCCATCAACATCTTCTCGGCGGACCGGCCCAACGTGAG 458
QY 1300 CAGCCACAGCTAGTAGAAGAGATCAGCGGTATTACCTGAACAGCGCTCGGGGTGTATC 1359
DB 459 GAGCGCGCGCGTGGAGCGGTTCAGAGAGCCCTACGTTGAGGCGCTCTGTCCTACAC- 517
QY 1360 ATGAACACAGCAGCGCGTGCCTGCTGCGCGTTCATCTAGCGGAAAGATTCTGTCGCTG 1419
DB 518 -----GCGCATCAAGAGGCGGAGGACAGCTGCGCTTCCGCGCATGCTCATGAAG 569
QY 1420 CTTACCGAGTTCCGAGCGCTGGGCATGCGAATTCGAAATTCGATGCTCTCGTGAAGTCTC 1479

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Db 570 CTGCTGAGCTGCGCAGCTGAGCTCTGTGCTCGGAGGAGTCTTCGCTTCGGGCTC 629
QY 1480 AAGAACAGGAGTGGCGCGTTCCTCGGAGAGATCTGGGACGT 1523
DB 630 CAGGACAAAGAGTGGCGCTCTGCTGTCGGAGATCTGGGACGT 673

RESULT 13
LOCUS   BQ214241
DEFINITION BQ214241 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070455
5', mRNA sequence.
ACCESSION BQ214241
VERSION    BQ214241.1 GI:20395641
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 918)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: DCTD/DTF/Gazdar
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13354 row: m column: 16
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               /clone_lib="NIH MGC 68"
               /note="Organ: lung; Vector: pCMV-SPORT6; Site:1: NotI;
               Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.8 kb. Library constructed by Life
               Technologies."
ORIGIN
Query Match      9.1%; Score 138.4; DB 5; Length 918;
Best Local Similarity 56.2%; Pred. No. 1e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

QY 946 TTCCGCCAGATCACAGAAATGACCATCTCTCAGTACAGTAAATAGTCGAGTTTGCCAAA 1005
DB 35 TTTCGCCACTTCAGGAGTGGCCATCTCTCAGTCCAGGAGATCGTGAGCTTCGCTAAG 94
QY 1006 GGCCTACTGTTTTCAGAAATCTCAACCTGACAGATCAATATTAAAGCATGC 1065
DB 95 CAAAGTGCCTGTTTCTCGAGTGTGGCGGGAGGACCAAGATCGCCCTCTCGAAGGCATCC 154
QY 1066 TCAGCGAAGTGCATGCTCGGAGTACGAGGGGTACGACGGGTGTCGGATAGCGTT 1125
DB 155 ACTATCGAGATCATGCTGTGCTAGAGACAGCGCGCTACAAACAGAGAGAGTGTATC 214
QY 1126 CTGTTTCGCCAACACAGCGGTACACTCGGACAACTACCGCAAGCGGGGCAT---GGCC 1182
DB 215 ACCTTCTTGAAGACTTCACCTACAGCAAGACGACTTCACCGGTGCAGGCTCGAGTG 274
QY 1183 TAGGTCATGAGACCTGCTGCACTTCGCGCTGCTGATGTAATGATGTCATGAGCAAC 1242
DB 275 GAGTTTCATCAACCCCATCTTCGAGTTCCTCGGGGCGCATCGCGGCTGGGCTCGACGAC 334

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QY 1243 GTGCATTACGGCTCTCACTGCCATCGTTATATCTCG--GATCGCGCGGCTAGAG 1299
DB 335 GCTGAGTAGCCCTGCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCCAACGTGAG 394
QY 1300 CAGCCACAGCTAGTAGAAGAGATCAGCGCGTATTACCTGAACACACGCTGCGGTGTACATC 1359
DB 395 GAGCGGCGCGGTGGAGCGCTTGACAGCAGCCCTACGTGGAGCGCTGCTGTCTTACAC- 453
QY 1360 ATGAACACAGCAGCGCGCTGCGCGCTTGCGCGGTGATCTACGGAAGATTCTGTCGGTG 1419
DB 454 -----GCGCATCAAGAGGCGGACGACCACTGCGCTTCCGCGCATGCTCATGAAG 505
QY 1420 CTTACCGAGTTCGGGACGCTGGGCATGACAGATTGGAACATGTGATCTCGCTGAAGCTC 1479
DB 506 CTGGTGAGCTTCGGACGCTGAGCTCTGTGCACTCGGACGAGTCTTCCGCTTGGGCTC 565
QY 1480 AAGAACAGGAAGTCCGCGCGTTCCTGGAGGAGATCTGGGAGCT 1523
DB 566 CAGGACAGAGCTGCGGCTCTGCTGTGGAGATCTGGGAGCT 609

RESULT 14
CR614375 1685 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DM011YE14 of Fetal liver of Homo sapiens
(human).
DEFINITION
ACCESSION CR614375
VERSION 1 GI:50495182
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1685)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1685)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr]
- Web : www.genoscope.cns.fr]
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1. .1685
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/db_xref="taxon:9606"
/clone="CS0DM011YE14"
/tissue_type="Fetal liver"
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ORIGIN
Query Match 9.1%; Score 138.4; DB 3; Length 1685;
Best Local Similarity 56.2%; Pred. No. 1.2e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

QY 946 TTCGCCAGATCCAGAAATGACCATCTCACAGTACAGCTAATAGTCGAGTTGCCAAA 1005
DB 734 TTTGCCCACTTCAGGAGCTGGCCATCATCTCATGCCAGAGATCGTGGACTTCGCTAAG 793
QY 1006 GGCCTACTCTGTTTTTCAAGATCTCAACACCTGACCAGATCATATTATTAAAGGATGC 1065
DB 794 CAAGTGCTGTTTCTCTGCAGCTGGCGGGGAGGACCGAGATCGCCCTCTGGAAGCATCC 853

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QY 1066 TCAAGCGAAGTGATGATGCTCGAGTAGCGAGGCGGTACGACGCGGTTCGGAATAGCOTT 1125
DB 854 ACTATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAAACCCAGACAGAGTGTATC 913
QY 1126 CTGTTGGCCAAACACAGGCGGTACTCTCGACAACTACCGCAAGCGCGGCAT---GGCC 1182
DB 914 ACCTTTCTTGAAGGACTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCGCTGAGGTG 973
QY 1183 TACGTCATCGAAGACCTGCTGCACATTTCTGCGCTGTCATGTAATCTGATGTCCGATGACAAAC 1242
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DB 1034 GCTGAGTAGCGCTGCTCATGCCATCAACATCTTCTCGCGCGACCGGCCCAACGTCGAC 1093
QY 1300 CAGCCACAGCTAGTAGAAGATCAGCGGTATTACCTGAACACACGCTGCGGTGTACATC 1359
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QY 1360 ATGAACACAGCAGCGCGCTGCGCGCTGCGCGCTCATCTACGCGAAGATTCTGTCGGTG 1419
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RESULT 15
CR610600 1763 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DJ010YB16 of T cells (Jurkat cell line)
DEFINITION Cot 10-normalized of Homo sapiens (human).
ACCESSION CR610600
VERSION 1 GI:50491407
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1763)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1763)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr]
- Web : www.genoscope.cns.fr]
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Fri Apr 15 16:53:51 2005

ORIGIN

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Query Match      9.1%; Score 138.4; DB 3; Length 1763;
Best Local Similarity 56.2%; Pred. No. 1.2e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

Qy 946 TTCGCCGAGATCAGACAAATGACCATCTCTCAGTACAGCTAATAGTCGAGTTTGGCCAAA 1005
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Db 820 TTTGCCCACTTCACGGAGCTGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG 879

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Db 880 CAAGTGCCTGTTTTCTCAGCTGGCCGGGAGACCAAGATCGCCCTCTGAAAGGCATCC 939

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Db 940 ACTATCGAGATCATCTGCTAGAGACAGCCAGGCGCTACAACACGACAGACAGAGTGTATC 999

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Db 1000 ACCTTCTTGAAGGACTTCACCTACAGCAAGACGACTTCCACCGTGCAGGCCCTGCAGGTG 1059

Qy 1183 TACGTCATCGAAGACTCTGTCACATCTGCGCCTGCTATGATCGATCGATGGACAAC 1242
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Db 1060 GAGTTCAATCAACCCCATCTTCGAGTTCTCGGGGCCATGCGGGGCTGGGCTGGACGAC 1119

Qy 1243 GTGCATTACGCGCTCTCACTGCCATCGTTATATTCTCG---GATCGCCCGGCGCTAGAG 1299
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Db 1351 CAGGACAAGAGCTGCCGCTCTGCTGTCGGAGATCTGGGAGCT 1394
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	632.2	41.5	2711	3	US-08-891-298-2
3	623.2	40.9	2745	3	US-08-553-648A-4
4	623.2	40.9	2745	4	US-09-564-418-4
5	621.6	40.8	1934	3	US-08-553-648A-2
6	621.6	40.8	1934	4	US-09-564-418-2
C 7	621.6	40.8	1934	3	US-09-564-418-61
C 8	621.6	40.8	2463	3	US-08-553-648A-10
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14	617.2	40.5	948	4	US-09-564-418-6
C 15	617.2	40.5	948	4	US-09-564-418-63
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24	445.2	29.2	10060	4	US-09-484-997-25
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39	437.4	28.7	1919	4	US-08-840-713-34	Sequence 34, Appl
40	344.6	22.6	2241	3	US-09-144-759-17	Sequence 17, Appl
41	344.6	22.6	2241	4	US-09-570-267-17	Sequence 17, Appl
42	344.6	22.6	2295	3	US-09-144-759-19	Sequence 19, Appl
43	344.6	22.6	2295	4	US-09-570-267-19	Sequence 19, Appl
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45	344.6	22.6	2301	4	US-09-570-267-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-393-839-1
; Sequence 1, Application US/09393839
; Patent No. 6504082
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garnaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/09/393,839
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Ostrinia nubilalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (368)..(2005)
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence and deduced amino acid
; OTHER INFORMATION: sequence of Ecdysone receptor
US-09-393-839-1

Query Match	54.9%;	Score 836;	DB 4;	Length 2126;
Best Local Similarity	90.1%;	Pred. No. 7.5e-242;	Mismatches 85;	Indels 15; Gaps 1;
Matches 912;	Conservative 0;			
QY	528	GAGTAGTAAACAAGGTCAAGACAGTGTGACTGTATCGACCGCTATGAGCCCGAGTGCCT 587		
Db	940	GAATGTCAAGATCCGGTTGAAGAAGTGTAGCGTGGCATGAGCCCGAGTGCCT 999		
QY	588	CGTCCAGAGTCCACGTGCAAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647		
Db	1000	GGTCCAGAAACCGCAGTGTGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059		
QY	648	CAAACTGCCAGTCAGTACCGACAGTGCATCATATGCTTCCCTGCATATGCAATGATGTA 707		
Db	1060	CAAACTACCAGTGCAGCAACGACATAGACATATATGCCCCCAATCATGACGATGTA 1119		
-QY	708	CCCTCCGCCCCAGAGCGCGCAAGGATT-----CACGAAGTGTGTCGCGAG 752		
Db	1120	TCGCCACACCCCGAGGACGAGGATTCTGGAATGTTTGCAGCATGAAGTGTGTCGCGC 1179		
QY	753	GTTCTTAACGGAGAACCTAATGGAGCAGAACAGACTGAAGAAATGTGACGCGCTGTGCGC 812		
Db	1180	GTTCTCTCGGAGAGCTGATGGAGCAGAAATCGTTGAAAGAACATACCCCTCTACCCG 1239		

Db 1549 GTTCGCCAACAACAAAGCGGTACACGCGGCAACACTACCGCCCAAGGCGCATGCTACGT 1608
 Qy 1188 CATCGAAGACCTGTGCACTTCTGCGCTGTCATGTACTCGATGTCGATGCGACCAAGTGA 1247
 Db 1609 CATCGAAGACCTGCTACACTTCTGCGGTGTCATGTTCGCGATGCGCATGCGCAATGTGCA 1668
 Qy 1248 TTACGCGTCTCACTGCGCATGTTATATCTCGATGCGCGCGCTAGAGCAGCCACA 1307
 Db 1669 CTTTGCACTGTCTACGCGCATGTTATATCTCAGATCGCGCGCGCTCGAGCAGCGTC 1728
 Qy 1308 GCTAGTAGAAGATCCAGCGGTATTAATCTGAACAACGCTGCGGGTGTATCATCATGAACCA 1367
 Db 1729 GCTGTAGAGAGATCCAGAGATACCTAGACAGGTTGCGAATTTACATCATCAACCA 1788
 Qy 1368 GCACAGCGGTGCGCGCTGTCGCGCTCATCTACCGAAGATTTCTGTCGCTGCTTACCGA 1427
 Db 1789 GAAACAGCGCTGCTGCGCTGTCGCGCTGATCTACGCGCAGGATCTCTGAGCGTCTGACCGA 1848
 Qy 1428 GTTGGGAGCGTGGCGCATGCGAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAG 1487
 Db 1849 GCTACGCACTGCGCGCAGCAAACTCCAAACATGTGCATCTCGCTGAAGCTCAAGAACAG 1908
 Qy 1488 GAAGCTGCGCGCTTCTCGGAGGAGATCTGGGACGTG 1524
 Db 1909 GAAGCTGCGCGCTTCTCGAGAGATCTGGGACGTG 1945

RESULT 3

US-08-653-648A-4
 ; Sequence 4, Application US/08653648A
 ; Patent No. 6379945
 ; GENERAL INFORMATION:
 ; APPLICANT: Jepsen, Ian
 ; APPLICANT: Greenland, Andrew
 ; APPLICANT: Martinez, Alberto
 ; TITLE OF INVENTION: A Gene Switch
 ; FILE REFERENCE: PPD50047/US
 ; CURRENT APPLICATION NUMBER: US/08/653,648A
 ; PRIOR FILING DATE: 1996-05-24
 ; PRIOR APPLICATION NUMBER: GB 9510759.5
 ; PRIOR FILING DATE: 1995-05-26
 ; PRIOR APPLICATION NUMBER: GB 9605656.9
 ; PRIOR FILING DATE: 1996-03-18
 ; PRIOR APPLICATION NUMBER: GB 9513882.2
 ; PRIOR FILING DATE: 1995-07-07
 ; PRIOR APPLICATION NUMBER: GB 9517316.7
 ; PRIOR FILING DATE: 1995-08-24
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 2745
 ; TYPE: DNA
 ; ORGANISM: Heliothis virescens
 ; FEATURE:
 ; NAME/KEY: Unsure
 ; LOCATION: (2522)..(2522)
 ; OTHER INFORMATION: Unsure
 US-08-653-648A-4

Query Match 40.9%; Score 623.2; DB 3; Length 2745;
 Best Local Similarity 79.1%; Pred. No. 2e-177;
 Matches 777; Conservative 0; Mismatches 178; Indels 27; Gaps 2;
 Qy 558 TGATATCAACGCGGTATGAGGCGCGGTGCGTCCAGAGTCCACGTCGCAAGAACAAAAG 617
 Db 893 TCTTGGCGTGGCATGAGGCGCGGTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 952
 Qy 618 AAGAGAAAAGAGCAAGAGAGAAAAGAACTCCAGTACGTACGACGACGTGGA 677
 Db 953 GAAAGAGAAAAGGCGCAGAGGAAAAGAAAATTTCCCGCTCAGTACGACGACGTAGA 1012
 Qy 678 CGATCATATCGCTGCCATATGATGTGACCTTCGCGCCCGCAGAGCGCAAGGATT-- 735

Db 1013 CGATCACATGCTCCCATCATGCAATGTGACCTTCCGCCCCCAAGGCGCGCTAGATTCT 1072
 Qy 736 -----CACGAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATGAGACAGAA 782
 Db 1073 GGAATGTGTCAGACACGAGGTGGTCCACGATTTCTGATGAGAAGCTAATGGAACAGAA 1132
 Qy 783 CAGACTGAAGAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGGAGGCTCGT 842
 Db 1133 CAGATTGAAGAAAGTGGCCCGCTCACTGCGCAATCAGAAGTCTGTGATCGCAAGGCTCGT 1192
 Qy 843 GTGTACAGACCGATACGAGCAGCTTCCGAGAGAGATCTCAAAAAGGTTGACGACAC 902
 Db 1193 GTGTACAGAGAGGCTATGAACACCTTCGAGAGAGACCTGAAGAGGTTACACAG-- 1250
 Qy 903 TTGCAATCAGCAGATGAAGAAGACGAAAGATCTCAGACATGCGCATTTCCGCCAGATCACA 962
 Db 1251 -----TCGACGAGAGACGACGAGACTCGGATATGCGTTCCGTCAGATTACCGA 1300
 Qy 963 AATGACCATCTCAGTACAGCTAAATAGTCGAGTTTCCCAAGGCTTACCTGGTTTTTC 1022
 Db 1301 GATGACGATTCTCAGAGTCAGCTCATCGTAGAATTCGCTAAGGCGCTCCCGGCTTCGC 1360
 Qy 1023 AAAGATCTCAACCTGACCGATACATTAATAAGGCATGCTCAAGCGAAGTCAATGAT 1082
 Db 1361 CAAGATCTCGCAGTCGGACCATGACGTTATTAAGGCGTCTCAAGTGAGTGATGAT 1420
 Qy 1083 GCTGCGGTAGCGAGGCGGTACGACGCGGTGTCGATAGCGTTCTGTTCCGCAACCA 1142
 Db 1421 GCTCGAGTGGTGGCGGTATGACGCGCCACCGACAGCGTACTGTTCCGCAACCA 1480
 Qy 1143 GCGGTACACTCGCGCAAACTACCGCAAGCGGCGCATGCGCTACGTATCGTAAGACCTGCT 1202
 Db 1481 GCGGTACACTCGCGCAAACTACCGCAAGCGGCGCATGCGCTACGTATCGTAAGACCTGCT 1540
 Qy 1203 GCATTTGCGCGTGCATGTTACTCGATGCGACCAAGTGCATTAAGCGCTCTCTCAC 1262
 Db 1541 GCATTTGCTGCGTGCATGTTACTCCATGATGATGATGATGATGATGATGATGATGATGAT 1600
 Qy 1263 TGCCATCGTTATATTTCTCGATCGCGCGCGCTAGAGCAGCCACAGCTAGTAGAAGAT 1322
 Db 1601 AGCCATTGTCATTTCTCAGACCGCGCGCGCTTCCGCAACCCCTGTTGGTGGAGAGAT 1660
 Qy 1323 CCAGCGGTATTACCTGAACACGCTCGCGGTGTACATCATGAACACGACAGCGCTCGCC 1382
 Db 1661 CCAGAGATATTACCTGAACACGCTACGCGGTGTACATCTCTGAACACGACAGCGCTCGCC 1720
 Qy 1383 GCGTGGCGCGTCACTACGCGAAGATTTCTGCGGTGCTTACCGAGTTTCGAGACGCTGG 1442
 Db 1721 CCGCGCGCGCGTCACTTTCGCGGAGATCTCTGGGCTACTGACGAGATCCGACCGCTGG 1780
 Qy 1443 CATGAGAAATTCGAACATGTCATCTCGCTGAAGCTCAAGAAACAGGAAGCTGCGCGCTT 1502
 Db 1781 CATGAGAAATTCGAACATGTCATCTCTCGCTGAAGCTCAAGAAACAGGAAGCTGCGCGCTT 1840
 Qy 1503 CCTGGAGGAGATCTGGGACGTG 1524
 Db 1841 CCTCGAGGAGATCTGGGACGTG 1862

RESULT 4

US-09-564-418-4
 ; Sequence 4, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jepsen, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James
 ; TITLE OF INVENTION: A GENE SWITCH
 ; FILE REFERENCE: 1392/4/3
 ; CURRENT APPLICATION NUMBER: US/09/564,418
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/564,418

```

; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (2522)..(2522)
; OTHER INFORMATION: n=a, c, g, or t
US-09-564-418-4

```

Query Match	40.9%;	Score 623.2;	DB 4;	Length 2745;
Best Local Similarity	79.1%;	Pred. No. 2e-177;		
Matches 777;	Conservative 0;	Mismatch 178;	Indels 27;	Gaps 2;
Qy	558	TGTATCGAGCGGTATGAGCGCCGAGTGGGTGCTCCAGAGTCCAGTGCAGTGAAGACAAAAG	617	
Db	893	TCCTCGGCTGGGCATGAGCGCCGAGTGGGTGCTGGGAGAACCACTGTGCANTGAACG	952	
Qy	618	AAGAGAAAGGAAGCACAGAGAGAAAAGACAAACTGCCAGTTCAGTACGACGACAGTGG	677	
Db	953	GAAGAGAAAGAGCGCAGAGGAAAAAGACAAAATTGCCCGTCAGTACGACGACAGTAGA	1012	
Qy	678	CGATCATATGCTGCCCATTAATGCAATGTACCTTCGCCCCCGAGAGGCGGCAAGGATT--	735	
Db	1013	CGATCACATGCTCCCATCATGCAATGTGACCTTCGCCCCCGAGAGGCGCTAGAAATTC	1072	
Qy	736	-----CACGAAAGTGGTCCGAGGTTCTTAACGAGAAAGCTAAATCGAGCAGAA	782	
Db	1073	GGAAATGTGACAGCAGAGTGGTGCCACGATTCTGTATGAGAGCTAAATCGAAACAGAA	1132	
Qy	783	CAGACTGAAGAATGTGACCGCGCTGTGGCGAAACGAAAGTCCCTGATCGCAGGCTCGT	842	
Db	1133	CAGATTGAAGAAGCTGCCCGCCCTCACTGCCAATCAGAAAGTCGTTGATCGCAAGGCTCGT	1192	
Qy	843	GTGGTACCAAGGCGGATACGACGCGCTTCGGAAGAGGATCTCAAAGGGTCACGCAGAC	902	
Db	1193	GTGGTACCAAGGAGGCTATGAACACCTTCGAGGAGACCTGAGAGGGTTACAG--	1250	
Qy	903	TTGGCAATCAGCAGATGAAGAAGACGAAGACTCAGACATGCCATTCGCCAGATCACAGA	962	
Db	1251	-----TCGGACGAGGACGACGAAGACTCGGATATGCCGTTCCGTCAGATTACCGA	1300	
Qy	963	AATGACCATCTCACAGTACGCTATAGTCGAGTTTGCAAGGCTACCTGGTGTTC	1022	
Db	1301	GATGACGATTCTCACAGTGGAGCTCATCGTAGAATTCGCTTAGGGCTCTCCGGCTTCG	1360	
Qy	1023	AAAGATCTCAACACTGACACAGATCACATTATTTAAAGGCATGCTCAAGCGAAGTGATGAT	1082	
Db	1361	CAAGATCTCCGAGTCGGACACAGATCAGCTTATTTAAAGGCGTGCTCAAGTGAGTGATGAT	1420	
Qy	1083	GCTGCGAGTAGCAGGGGGTACGACGCGGTGTCGGATAGGTTCTGTTGCCACCAACCA	1142	
Db	1421	GCTCCGAGTGGCTCGGCGGTATGACGCGGCACCCGACGCTACTGTTCCGCAACAACCA	1480	
Qy	1143	GGCGTACACTCGCGACAACTPACCGAAGGGGGCATGGCTACGTCATCGAAGACCTGCT	1202	
Db	1481	GGCGTACACTCGCGACAACTPACCGAAGGCGACGATGGCGTAGCTCATCGAGACCTGCT	1540	
Qy	1203	GCACTTCTGCGCTGCTATGTAATCTGATGTCGATGGACAACGTCGATTTACGCGTCTCTAC	1262	
Db	1541	GCACCTTCTGCTGGTGCATGTACTCCATGATGATGGATAGCTGATTCGCTGCTGTAC	1600	
Qy	1263	TGCGATCGTTATATCTCGATCGCGCGGCGCTTAGAGCAGCCACAGCTAGTACGAAGAT	1322	
Db	1601	AGCCATGTGTCATCTTCTCAGACCGGCCCGGGCTTGAGCAACCCCTGTTGTGTGAGAGAT	1660	
Qy	1323	CCAGCGGTATTACTGAAACCGCTGCGGGGTGTATCATCATCAACCAAGCAGCGCTCGCC	1382	
Db	1661	CCAGAGATATTACTGAAACCGCTACGGGTGTATCATCTTGAACGAGCAGCGCTCGCC	1720	

903	TTGGCAATCAGCAGATGAAGAAGACCAAGACTCAGACATGCCATTCGCGCAGATCACGA	962
QY		
904	-----TGGACAGGACGACGAGACTCGGATGCGGTCCGTTCAGATTACGGA	963
DB		
905	AATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCCAAAGGCGCTACCTGGTTTTTC	1022
QY		
906	GATGACCATCTCACAGTGCAGCTCATCGTAGAAATTCGCTAAGGGCGCTCCGCGCTTCGC	1360
DB		
907	AAAGATCTCACAACTTGACCAAGATCACATTATTAAAGGCATGCTCAAGCGAAAGTGATGAT	1082
QY		
908	CAAGATCTTCGACTCGGACCGACGATCACGTTATTAAAGGCGTGCTCAAGTGAGTGTGATGAT	1420
DB		
909	GCTCGAGTAGCGAGGCGGTACGACGCGGTGTCGGATAGGTTCTGTTGCCCAACAACCA	1142
QY		
910	GCTCCGAGTGGCTCGGCGGTATGACCGGCGCAACGACAGCGTACTGTCGCAACAACCA	1480
DB		
911	GGCGTACACTCGGACAACTACCGCAAGCGGGCGCATGGCTACGTCTCATCGAAGACCTGCT	1202
QY		
912	GGCGTACACTCGGACAACTACCGCAAGCGGCGCATGGCGTACGTCTCATCGAAGACCTGCT	1540
DB		
913	GCATCTTCGCGGTGCATGTACTCGATGTCGATGGACAACGTCGATTAACGCGCTCCTCAC	1262
QY		
914	GCATCTTCGCGGTGCATGTACTCGATGATGATGGATTAACGTGCAATTATTCGCGCTGCTTAC	1600
DB		
915	TGCGCATCGTTATTCTTCGATCGCGCGCGCTTAGAGCAGCCACAGCTAGTACGAAGAT	1322
QY		
916	AGCCATTGTTCATCTTCTCAGACCGGCCCGCGGCTTGAGCAACCCCTGTTGGTGGAGAGAT	1660
DB		
917	CCAGCGGTATTACTGCAACCGCTGCGGGGTGTATCATCATGAACGACACAGCGCGTCGCC	1382
QY		
918	CCAGAGATATTACTGCAACCGCTACGSGGTGTATCATCTGAAACGACAAAGCGCGTCGCC	1720
DB		

QY	963	ATGACCATCTCCACAGTACAGCTAATAGTCGAGTTTCCAAAGSCCTACCTGGTTTTTC	1022
DB	1141	GATACGATTTCTCAGTCAGTCAGCTCATCGTAGAATTCGTATAGGCGCTCCCGGGCTTCGC	1200
QY	1023	AAAGATCTCACAACCTCGACAGATCACATTTATTAAGGCGATGCTCAAGCGAAGTGATGAT	1082
DB	1201	CAAGATCTCGAGTCGGACACAGATCACGTTTATTAAGGCGTCTCAAGTGAGGTGATGAT	1260
QY	1083	GTCGAGTAGGAGCGGTCAGACGCGGTGTGCGATAGCGTTCTGTTCCGCCAACACCA	1142
DB	1261	GCTCCGAGTGGTCGCGGTATGACGCGGCCACCGACAGCGTACTGTTCCGGAACACCA	1320
QY	1143	GCCTACACTCCGCGAACAACCTACGCAAGCGCGCATGGCTACGTCATCGAAGACTGCT	1202
DB	1321	GGCGTACACTCGCGAACAACCTACGCAAGCGCGCATGGCTACGTCATCGAAGACTGCT	1380
QY	1203	GCATTTCTCCCGCTGCATGCTACTCGATGTCGATGGACAACTGTCATAGCGCTCCTCAC	1262
DB	1381	GCATTTCTCGGTGCATGCTACTCCATGATGATGATGATGATGATGATGATGATGATGAT	1440
QY	1263	TGCCATCTGTTATTTCTCGATCGCGCGGCTAGAGCAGCCACAGCTAGTAGAAGAT	1322
DB	1441	AGCCATTTGTCATCTTCTAGACCGCGCGGCTTGAACAAACCCCTGTTGGTGAGGACAT	1500
QY	1323	CCAGCGGTATTACCTGAAACACGCTCGGGGTGTACATCATGAAACAGCAGCGGTGCGC	1382
DB	1501	CCAGAGATATTACCTGAAACACGCTACGGGTGTACATCTCTGAAACAGCAGCGGTGCGC	1560
QY	1383	GGTTGGCGGCTCATCTACCGCAAGATTTCTGTCGGTGTACCGAGTTCCGGAGCTGCGG	1442
DB	1561	CGCGCGCGCGTCACTTTCCGGCGAGATCCTGGGCTACTGACGGAGATCCGACGCTGGG	1620
QY	1443	CATGCGAATTCGAACATGTCATCTCGCTGAAGCTCAAGAAACAGGAAGCTGCGCGGTT	1502
DB	1621	CATGCGAATTCGAACATGTCATCTCCCTCAAGCTGAAGAAACAGGAAGCTGCGCGGTT	1680
QY	1503	CCTGGAGGAGATCTGGGAGTG	1524
DB	1681	CCTCGAGGAGATCTGGGAGTG	1702

RESULT 7
US-09-564-418-61/c
; Sequence 61, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James

Query Match 40.8%; Score 621.6; DB 4; Length 1934;
Best Local Similarity 79.0%; Pred. No. 4.9e-177;
Matches 776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;
QY 558 TGATCGACGCGTATGAGCCCGAGTCGTCGCCAGAGTCCACGTCGCAAGAACAAAG 617
DB 733 TCTTGGGTGGGATGAGGCGCGAGTCGTCGGTGGTCCCGAGAACAGTGTGCAATGAACG 792
QY 618 AAGAGAAAAGAGACACAGAGAAAAGAAACAAACTCCCACTGATGATGACGACGAGTGG 677

; TITLE OF INVENTION: A GENE SWITCH		Query Match		40.8%; Score 621.6; DB 4; Length 1934;	
; FILE REFERENCE: 1392/4/3		Best Local Similarity		79.0%; Pred. No. 4.9e-177;	
; CURRENT APPLICATION NUMBER: US/09/564,418		Matches		776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;	
; CURRENT FILING DATE: 2000-05-03					
; PRIOR APPLICATION NUMBER: US 09/564,418					
; PRIOR FILING DATE: 2000-05-03					
; NUMBER OF SEQ ID NOS: 63					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 61					
; LENGTH: 1934					
; TYPE: DNA					
; ORGANISM: Heliothis virescens					
US-09-564-418-61					
QY	558	TGTTATCGACGCGTATGAGCCCGAGTGGGTGCTGCTCCAGAGTCCACGTCGCAAGAACAAAAAG	617		
DB	1202	TCTTGGCGTGGCATGAGCCCGAGTGGGTGCTGCGGAGAACCCAGTGTGCAATGAAACG	1143		
QY	618	AAGAGAAAAAGGAAGACAGAGAGAAAAAGACAAATCCAGTACGACGACAGTAGA	677		
DB	1142	GAAAGAGAAAAAGGCGACAGAGGAAAAAGACAAATTTGCCGTACGTACGACGACAGTAGA	1083		
QY	678	CGATCATATGCTGCCATATGCAATGTGACCTCCGCCCCAGAGGGCGGCAAGGATT--	735		
DB	1082	CGATCAGTCCCTCCCATCATGCATGTGACCTCGCCCCAGAGGCGCGTAGAATCT	1023		
QY	736	-----CACGAAGTGGTCCCGAGGTTCCTAAACGAGAGAGCTAATGAGAGCAGAA	782		
DB	1022	GGAATGTGTGCAGCAGGAGTGTGTCACGATTCCTGAAATGAGAGAGCTAATGGAACAGAA	963		
QY	783	CAGACTGAAGATGTGACCCCGCTGTGCGGGAACAGAGAGTCCCTGATCGCGAGGCTCGT	842		
DB	962	CAGATTGAAGACGTGCCCGCCCTCACTGCCAATCAGAAAGTCTGTTGATCGCAAGGCTCGT	903		
QY	843	GTGTTACCAAGACGATACGACGAGCTTTCGGAAGAGGATCTCAAAAGGGTGAACGAC	902		
DB	902	GTGTTACCAAGAGGCTATGACAACTTTCGAGGAAGACCTGGAAGAGGGTTACACAG--	845		
QY	903	TTGGCAATCAGCAGATGAAGAGACGAGACTACACATGCCATTCGCCCGAGATCACAGA	962		
DB	844	-----TCGGACGAGGACGACGAGAGCTCGGATATGCCGTTCCTCGTCAAGATTACCGA	795		
QY	963	AATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCCAAAGGCTACCTGGTTTTTC	1022		
DB	794	GATGACGATTTCTACAGTGCAGCTCATCTAGNAATTCGTAAGGCGCTCCCGGGCTTCGC	735		
QY	1023	AAAGATCTCAACACCTGACAGATCAATTTAAAGGATGCTCAACGGCAAGTAGATAT	1082		
DB	734	CAAGATCTCGACGTCGACACAGATCACTGTTTAAAGGCGTCTCAAGTAGAGGTGATGAT	675		
QY	1083	GCTCGGAGTAGCAGGGGTACGACGCGGTGTGCGATACGTTCTGTTTCGCCAACACCA	1142		
DB	674	GCTCCGAGTGGCTTCGGCGGTATGACCGCGGCCACCGACGCTACTGTTTCGGACACCA	615		
QY	1143	GGGCTACACTCGGCAAACTACCGCAGGCGGCGCATGGCTTACGTCATCGAAGACCTGCT	1202		
DB	614	GGCGTACACTCGGCAAACTACCGAAGCAGGACATGGCGTACGTCATCGAGGACCTGCT	555		
QY	1203	GCATCTTCGCGGTGATGTACTGATGTGATGCGAACAGCTGCATTCAGCGCTCTCAC	1262		
DB	554	GCATCTTCGCGGTGATGTACTGATGTGATGCGAACAGCTGCATTCAGCGCTCTCAC	495		
QY	1263	TGCCATCGTTATTTCTTCGGAATCGCGCGGCGCTTAGAGCAGCCACAGCTAGTAGAAGAT	1322		
DB	494	AGCATTTGTCTCTTCAGACCGCGCGCGGCTTAGAGCAACCCCTGTTGTTGTTGAGGACAT	435		
QY	1323	CCAGCGGATTTACTGAAACACGCTGCGGGGTGATCATCATGAAACGACACAGCGCTCGCC	1382		
DB	434	CCAGAGATATTAATCTGAAACACGCTGCGGGGTGATCATCTGAAACGACGCGCTCGCC	375		

QY 903 TTGGCAATCAGCAGATGAAGAGACGAGAACTCAGACATGCTCCGCGACATCACAGA 962
DB 1494 -----TCGGACGAGGACGACGAAAGACTCGGATATGCCGTTCCGTCAGATTACCGA 1445
QY 963 AATGACCATCTCAGAGTACAGCTAATAGTCGAGTTTCCCAAAGGCCCTACCTGGTTTTC 1022
DB 1444 GATGACGATTTCTCAGAGTGAGCTCATCTGTAGAAATTCGTAAGGGCCCTCCGGGCTTCGC 1385
QY 1023 AAAGATCTCACAACCTGACAGATCACATATTATAAGGCATGCTCAACGGAAGTGATGAT 1082
DB 1384 CAAGATCTCGAGTCGGACCAAGATCACGTTATTAAAGCGTGCTCAAGTGAGGTGATGAT 1325
QY 1083 GCTCGAGTAGGAGCGGTACGACGCGGTGTCGATAGCGTTCTGTTCGCCCAACCA 1142
DB 1324 GCTCGAGTTGGCTCGCGGTATGACCGCGGTCACCGACAGCGTACTGTTTCGGCAACCA 1265
QY 1143 GCGGTACACTCGGCAAACTACCGCAAGCGCGGCATGCGCTACGATCGAAGACTGCT 1202
DB 1264 GCGGTACACTCGGCAAACTACCGCAAGCGCGGCATGCGCTACGATCGAAGACTGCT 1205
QY 1203 GCATTTCTGCGGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1262
DB 1204 GCATTTCTGCGGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1145
QY 1263 TGCCATCGTTATATTCTCGATCGCGCGGCTAGAGCGACCAAGCTAGTAGAGAT 1322
DB 1144 AGCCATTGTCTATCTCAGACCGCGCGGCTTGGAGAACCCCTGTTGGTGGAGGACAT 1085
QY 1323 CCAGCGGTATTACCTGMAACACGCTCGGGGTGATCATATGAAACCAAGCAGCGCTCGCC 1382
DB 1084 CCAGAGATATTACCTGMAACACGCTCGGGGTGATCATATGAAACCAAGCAGCGCTCGCC 1025
QY 1383 GCGTTGCGCGGTCACTACCGCAAGATTCTGTCGCTGCTTACCGAGTTTCGGAGCCTGGG 1442
DB 1024 CCGCGCGCGGTCACTTTCGGCGAGATCTTCGGGCATCTGCGGACATCGCGAGCTCGG 965
QY 1443 CATGCAAGATTCGAACATGTGATCTCGCTGAGCTCAAGAACAGGAGCTCGCGCGTT 1502
DB 964 CATGCAAGATTCGAACATGTGATCTTCCTCAAGCTGAAAGACAGGAGCTCGCGCGTT 905
QY 1503 CCGTGGAGGAGTCTGGAGGTG 1524
DB 904 CCTCGAGGAGATCTGGGAGCTG 883

RESULT 9

US-08-653-648A-3
; Sequence 3, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:

; NAME/KEY: Unsure
; LOCATION: (2241)..(2241)
; OTHER INFORMATION: Unsure
US-08-653-648A-3

Query Match 40.8%; Score 621.6; DB 3; Length 2464;
Best Local Similarity 79.0%; Pred. No. 5.7e-177;
Matches 776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;

QY 558 TGTATCCACGCGTATGAGCGCGGTGCTGCTCCAGAGTCCACGTCGAAAGAACAAAG 617
DB 612 TCTTCCGCGTGGGATGAGCGCGGTGCTGCTCCGAGAACCAAGTGTGCAATGAACG 671
QY 618 AAGAGAAAGAAAGACACAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 677
DB 672 GAAAGAGAAAGAAAGAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 731
QY 678 CGATCATATGCTGCCATTAATGCAATGACCTCCGCGCGCGCGCGCGCGCGCGCG 735
DB 732 CGATCATATGCTGCCATTAATGCAATGACCTCCGCGCGCGCGCGCGCGCGCGCG 791
QY 736 -----CACGAGTGGTCCGAGGTCTTACGAGAGAGCTTAATGGAGCAGAA 782
DB 792 GGAATGTGTGAGCAGCAGAGGTGGTCCACGATTTCTGAATGAGAGAGCTTAATGGAGCAGAA 851
QY 783 CAGACTGAAGAAATGTGACCGCGCTGTCCGCGAAACAGAAAGTCCCTGTATCGCGAGGCTCGT 842
DB 852 CAGATTGAAGAAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 911
QY 843 GTGGTACAGAGCAGATACGAGCAGCTTCGGAAGAGGATCTCAAAAGGTGACGAGAC 902
DB 912 GTGGTACAGAGAGGCTATGAACAACTTCGAGGAGAGACCTGAAAGAGGTTACACAG-- 969
QY 903 TTGGCAATCAGCAGATGAAGAGAGAGACTCAGACATGCTATTCGCCAGATCACAGA 962
DB 970 -----TCGGACGAGGACGAGAAAGCTCGGATATGCGGTTCCGTCAGATTACCGA 1019
QY 963 AATGACCATCTCAGAGTACAGCTAATAGTCGAGTTTCCCAAAGGCCCTACCTGGTTTTC 1022
DB 1020 GATGACGATTTCTCAGTGCGAGCTCATCTGTAGAAATTCGTAAGGGCCCTCCGCGGCTCGC 1079
QY 1023 AAAGATCTCACAACCTGACAGATCACATTTATTAAGGCATGCTCAAGGAAAGTATGAT 1082
DB 1080 CAAGATCTCGAGTCCGACAGATCACTGTTATTAAGGGCGTCTCAAGTGAGGTGATGAT 1139
QY 1083 GCTCGAGTAGGAGCGGTGTCGAGTACGCGGTGTCGATAGCGTTCTGTCGCCAACAACCA 1142
DB 1140 GCTCGAGTAGGCTCGCGGTATGACGCGGCGGCTATGACGCGGCGGCTGTTTCGCCAACAACCA 1199
QY 1143 GCGGTACACTCGGACAACTACCGCAAGCGCGGCTATGCGCTACGTCATCGAAGACCTGCT 1202
DB 1200 GCGGTACACTCGGACAACTACCGCAAGCGGAGCATGCGGTACGTCATCGAGGACCTGCT 1259
QY 1203 GCATTTCTGCGGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1262
DB 1260 GCATTTCTGCGGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1319
QY 1263 TGCCATCGTTATTTCTCGGATCGCGCGCGGCTTAGAGGAGCCACAGCTAGTAGAGAGAT 1322
DB 1320 AGCCATTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
QY 1323 CCAGCGGTATTACCTGMAACACGCTCGGGGTGATGAGTATGAGTATGAGTATGAGTAT 1382
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QY 1383 GCGTTGCGCGGTCACTTACCGGAAAGATTCTGCGGTGCTTACCGAGTTTCGGAGCGCTGGG 1442
DB 1440 CCGCGCGCGGTGCTGCTGCGGAGATCTTCGGGCACTACTGACGAGATCCGACGCTGGG 1499
QY 1443 CATGCAAGATTCGAACATGTGATCTCGCTGAGCTCAAGAACAGGAGCTCGCGCGTT 1502
DB 1500 CATGCAAGATTCGAACATGTGATCTTCCTCAAGCTGAAAGAACAGGAGCTCGCGCGTT 1559

Db 1733 CGATCATGCTCCCTCCATCATGCAATGACCTCCGCCCCACAGAGCGCGTAGAATTCT 1674
Qy 736 -----CAGGAAGTGGTCCCGAGGTTCCTAACGGAGAGCTAATGGAGCAGAA 782
Db 1673 GGAATGTGTGCAGCAGAGGTGGTCCACGATTCCTGAATGAGAGCTAATGGAAACAGAA 1614
Qy 763 CAGACTGAAGAAATGTGACCGCTGTCCGCGAACAGAAAGTCCCTGTGATCGCGAGGCTCGT 842
Db 1613 CAGATTGAAGAAAGTGGCCCTCCCTCACTGCGCAATCAGAAAGTGGTGAATGCAAGGCTGT 1554
Qy 843 GTGTGTACAGGACGAGATCAGAGCAGCTTCGGAAGAGGATCTCAAAAGGGTGAACAGAC 902
Db 1553 GTGTGTACAGGAGGCTATGAACACCTTCGAGGAGACCTGAAGAGGGTTACACAG-- 1496
Qy 903 TTGGCAATCAGCAGATGAAGAAGACGAGACTCAGACATGCCATTCGCCAGATCAGAGA 962
Db 1495 -----TCGGACGAGGAGCAGCAGAGACTCGGATATGCGGTTCCTGACAGATTACCGA 1446
Qy 963 AATGACCATCTCAGATACAGCTAATAGTGCAGTTTGGCAAGGCCCTACCTGGTTCCTTC 1022
Db 1445 GATGACGATCTCAGAGTGACCTCATCTGAGAAATTCGCTAAGGCGCTCCCGGGCTTCGC 1386
Qy 1023 AAAGATCTCACAACTGACAGATCAGATCACAATTAATAAGGCATCTCAAGCGAAGTGAAT 1082
Db 1385 CAGATCTCGAGTGGACACAGATCAGCTTATTAAGGCGTCTCAAGTGAGGTGATGAT 1326
Qy 1083 GTCGAGTAGGAGCGGTGACGCGGTGTCGAGTAGGATCTGTTTCGCCAAACCA 1142
Db 1325 GCTCGAGTGGTTCGCGGTATGACGCGGCCACCGACAGCGTACTGTTTCGCGAACCA 1266
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Qy 1203 GCACCTTCGCGGTGATGATCTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 1262
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Db 1145 AGCCATTGTCATCTCTCAGACCGCGCGGCTTAGAGCAACCCCTGTTGTTGGAGGACAT 1086
Qy 1323 CCAGGCTATTACCTGAACACCGTGGGCTGATCATGATGATGATGATGATGATGATGAT 1382
Db 1085 CCAGAGATATTACCTGAACACCGTGGGCTGATCATCTCTGAACACCAAGCGGTCGCC 1026
Qy 1383 GCGTTCGCGGTGATCTAGCGAAGATTCGTGCGGTGCTTACCGAGTTGCGGACGCTGGG 1442
Db 1025 CCGCGGCGCGTCACTTCGCGGAGATCCTGGGCACTACTGACGAGATCCGCAAGCTGGG 966
Qy 1443 CATGCAAGATTGCAATGTCATCTCGTGAAGCTTCAAGAGCTCAAGAGCTGCGCGCTT 1502
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Qy 1503 CCTGGAGGAGATCTGGAGCTG 1524
Db 905 CCTCGAGGAGATCTGGAGCTG 884

RESULT 12

US-08-653-648A-9/c
; Sequence 9, Application 'US/08653648A'
; Patent No. 637945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653, 648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26

; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-08-653-648A-9

Query Match 40.6%; Score 618.4; DB 3; Length 1934;
Best Local Similarity 78.8%; Pred. No. 4.5e-176;
Matches 774; Conservative 0; Mismatches 181; Indels 27; Gaps 2;
Qy 558 TGTATCGACGCGTATGAGGCCGAGTCCGTCCCGAGTCCAGTCCAGAGTCCAGTCCAGAGAACAAAG 617
Db 1202 TCTTGGCGTGGCATGAGGCCGAGTCCGTGCGCGAGAACCCAGTGTGCAATGAAACG 1143
Qy 618 AAGAAAGAAAGAACGACAGACAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 677
Db 1142 GAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1083
Qy 678 CGATCATATGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 735
Db 1082 CGATCATATGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1023
Qy 736 -----CAGCAAGTGGTCCGAGGTTCTTAACGGAGAAAGCTTAATGGAGCAGAA 782
Db 1022 GGAATGTGTGAGCAGCAGAGTGGTCCACGATTCCTGAATGAGAAAGCTTAATGGAGCAGAA 963
Qy 783 CAGACTGAAGAAATGTGACGCGCTGTCCGCGAACCAAGAGTCCCTGATCGCGAGGCTCGT 842
Db 962 CAGATTGAAGAAAGTGGCGGCGGCTCACTGCGCAATCAGAAAGTGGTGAATGCGAAGGCTCGT 903
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Db 902 GTGTGTACAGGAGGCTTATGAACACCTTCGAGGAGAGACCTGAAGAGGTTACACAG-- 845
Qy 903 TTGGCAATCAGCAGATGAAGAAGACGAGACTCAGACATGTCATTCGCGCAGATCAGAGA 962
Db 844 -----TCGGACGAGGACGACGAGACTCCGATATGCGGTTCCGTCAGATTACCGA 795
Qy 963 AATGACCATCTCAGACTAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1022
Db 794 GATGACGATTCCTCAGAGTGCAGCTCATCTAGAAATTCGCTAAGGGGCTCCCGGGCTTCGC 735
Qy 1023 AAGATCTCACAACCTGACCGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1082
Db 734 CAAGATCTCGAGTCCGAGCCAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 675
Qy 1083 GCTGCGAGTAGCAGGCGGTGACGCGGTGTCGATAGCGTTCGATAGCGTTCGATAGCGTTCG 1142
Db 674 GCTCGAGTGGCTCGCGGTGATGACGCGGCCACCGACAGCGTACTGTTCCGCAACCA 615
Qy 1143 GCGGTACACTCGCGCAACTACCGCAAGCGGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1202
Db 614 GCGGTACACTCGCGCAACTACCGCAAGCGGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 555
Qy 1203 GCATCTTCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
Db 554 ACCTTCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 495
Qy 1263 TGCCATCGTTATATTCCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAGAGAT 1322
Db 494 AGCCATTGTCATCTCTCAGACCGCGGCTTAGAGCAACCCCTGTTGGTGGAGGACAT 435
Qy 1323 CCAGCGGTATTACCTGAAACACCGTGGCGGTGATCATCATGAAACAGCAGCGCGTCCGC 1382
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QY 1383 GCGTTGCCCGCTCATCTACGCGAAGATTCTGTCCGTGCTTACCGAGTTGGCGGACGCTGGG 1442
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 QY 1503 CCTGGAGGAGATCTGGGACGTG 1524
 DB 254 CCTGGAGGAGATCTGGGACGTG 233

RESULT 13
 US-08-653-648A-6
 ; Sequence 6, Application US/08653648A
 ; Patent No. 6379945
 ; GENERAL INFORMATION:
 ; APPLICANT: Jenson, Ian
 ; APPLICANT: Greenland, Andrew
 ; APPLICANT: Martinez, Alberto
 ; TITLE OF INVENTION: A Gene Switch
 ; FILE REFERENCE: PP050047/US
 ; CURRENT APPLICATION NUMBER: US/08/653,648A
 ; CURRENT FILING DATE: 1996-05-24
 ; PRIOR APPLICATION NUMBER: GB 9510759.5
 ; PRIOR FILING DATE: 1995-05-26
 ; PRIOR APPLICATION NUMBER: GB 9605656.9
 ; PRIOR FILING DATE: 1996-03-18
 ; PRIOR APPLICATION NUMBER: GB 9513882.2
 ; PRIOR FILING DATE: 1995-07-07
 ; PRIOR APPLICATION NUMBER: GB 9517316.7
 ; PRIOR FILING DATE: 1995-08-24
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 948
 ; TYPE: DNA
 ; ORGANISM: Spodoptera exigua
 US-08-653-648A-6

Query Match 40.5%; Score 617.2; DB 3; Length 948;
 Best Local Similarity 79.8%; Pred. No. 6.7e-176;
 Matches 758; Conservative 0; Mismatches 178; Indels 14; Gaps 2;
 QY 574 AGGCCCGAGTGGGTGCTCCAGAGTCCAGTGTCAAGAACAAAGAGAGAGAGAGAGCA 633
 DB 1 AGGCCCGAGTGGGTGCTCCAGAGAACCAAGTGTGCAATGAAAGAGAGAGAGAGAGCA 60
 QY 634 CAG 693
 DB 61 CAAAGGAG 120
 QY 694 ATATGCAATGTGACCTCCGCGCCAGAGGGGCAAGGATTCAAGAGTGGTCCCGAGG 753
 DB 121 ATATGCAATGTGATCCACCGCTCCAGAGGGGCAAGGATTCAAGAGTGGTCCCGAG 180
 QY 754 TTCTTAACGAG 813
 DB 181 TTCTTAATGAAAG 238
 QY 814 AACCAGAGTCCCTGATCCGAGGCTCGTGTGTACAGAGAGAGAGAGAGAGAGAGAGAG 873
 DB 239 AACCAGAGTCCCTTAATAGAGGCTGGTGTGTACAGAGAGAGAGAGAGAGAGAGAGAG 298
 QY 874 GAAGAGAGTCTCAAAAGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 933
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 QY 934 TCAGAGATCCATTCGCGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993
 DB 347 TCAGAGATCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTT 406

QY 994 GAGTTTGCACAAAGGCTACCTGGTCTTTCACAAAGATCTCACAACTTACACAGATCACATTA 1053
 DB 407 GAATTCGCTAAAGGGCCCTACAGCGTTTCGCAAAAGATCTCAAGTCGGATCAGATCACATTA 466
 QY 1054 TTAAAGGCATGCTCAAGCGAAGTGTATGCTGCGAGTAGCGAGGCGGTAACGACGCGGTG 1113
 DB 467 TTAAAGGCCTGTTTCGAGTAGGTGATGATGTTGCGAGTAGTCTGCGCGGTACGACGCGCG 526
 QY 1114 TCGGATAGCGTTCTGTTTCGCGCAACACAGGCGGTACACTCGCGGCAAACTACCGCAAGGCG 1173
 DB 527 ACAGACAGCGGTGTTTCGCGCAACACAGGCGGTACACCGCGGACAACTACCGCAAGGCA 586
 QY 1174 GGCATGGCTTACGTTCGAGAGACCTGCTGCACTTCTGCGCTGCACTGATCTGATGTCG 1233
 DB 587 GGCATGGCTTACGTTCGAGAGACCTGCTGCACTTCTGCGCTGCACTGATGTCATGTCATG 646
 QY 1234 ATGGACAAAGTGCATTACGCGCTCTCACTGCCATCGTTATATTCGCGATCGGCGGCG 1293
 DB 647 ATGGATAACGTCCACTATGCACTGCTCACTGCCATCGTCACTTCTCAGACCGACCGCGG 706
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 DB 767 TACATCTGAAACAGAACAGCTCGGTGCGCGTGTGCTGCTGCTCATCTACGCTAAGATCCTC 826
 QY 1414 TCGGTGCTTACCGAGTTGCGGACGCTGGGATCGAGAAATTCGAAACATGTCATCTCGCTG 1473
 DB 827 GGCATCTGACGAGCTGCGGACCTCGGATCGAGAACTCCAACTGTCATCTCACTC 886
 QY 1474 AGCTCAAGAACAGGAGCTGCGCGCTTCTCTGAGAGATCTGGGACGT 1523
 DB 887 AAGCTGAAGAACAGGACGCTGCGCGCTTCTCTGAGAGATCTGGGACGT 936

RESULT 14
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 ; Sequence 6, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jenson, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James
 ; TITLE OF INVENTION: A GENE SWITCH
 ; FILE REFERENCE: 1392/4/3
 ; CURRENT APPLICATION NUMBER: US/09/564,418
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/564,418
 ; PRIOR FILING DATE: 2000-05-03
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 948
 ; TYPE: DNA
 ; ORGANISM: Spodoptera exigua
 US-09-564-418-6

Query Match 40.5%; Score 617.2; DB 4; Length 948;
 Best Local Similarity 79.8%; Pred. No. 6.7e-176;
 Matches 758; Conservative 0; Mismatches 178; Indels 14; Gaps 2;
 QY 574 AGGCCCGAGTGGGTGCTCCAGAGTCCAGTGTCAAGAACAAAGAGAGAGAGAGAGCA 633
 DB 1 AGGCCCGAGTGGGTGCTCCAGAGAACCAAGTGTGCAATGAAAGAGAGAGAGAGAGCA 60
 QY 634 CAG 693
 DB 61 CAAAGGAG 120

Db 62 AAGCTGAAGAACAGGAACTGCCGCCGTTCTTCGAGGATATCTGGACGT 13

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Job time : 267.175 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 14, 2005, 11:19:52 ; Search time 916.505 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	100.0	1767	16	US-10-087-167-120
2	1414.2	92.8	1782	16	Sequence 120, App
3	1332	87.4	1848	16	Sequence 124, App
4	1332	87.4	1863	16	Sequence 134, App
5	1332	87.4	1863	16	Sequence 136, App
6	1328.8	87.2	1767	16	Sequence 102, App
7	1311.2	86.0	1776	16	Sequence 122, App
8	1222.2	79.3	1800	16	Sequence 118, App
9	1209	79.3	1428	16	Sequence 126, App
10	1208.2	79.3	1809	16	Sequence 128, App
11	1073	70.4	1800	16	Sequence 142, App
					Sequence 147, App

12	955.6	62.7	1500	16	US-10-087-167-67	Sequence 67, Appl
13	848.8	55.7	1515	16	US-10-087-167-75	Sequence 75, Appl
14	836	54.9	2126	14	US-10-295-370-1	Sequence 1, Appl
15	836	54.9	2126	15	US-10-292-356-1	Sequence 1, Appl
16	836	54.9	2126	15	US-10-292-324-1	Sequence 1, Appl
17	763.6	50.1	1518	16	US-10-087-167-93	Sequence 93, Appl
18	763.6	50.1	2840	15	US-10-083-842A-6	Sequence 6, Appl
19	763.6	50.1	2840	16	US-10-087-167-1	Sequence 1, Appl
20	760.4	49.9	1500	16	US-10-087-167-69	Sequence 69, Appl
21	742.8	48.7	1509	16	US-10-087-167-65	Sequence 65, Appl
22	719.4	47.2	763	16	US-10-087-167-5	Sequence 5, Appl
23	656.8	43.1	1533	16	US-10-087-167-79	Sequence 79, Appl
24	638.6	41.9	838	16	US-10-087-167-7	Sequence 7, Appl
25	636	41.7	1524	16	US-10-087-167-77	Sequence 77, Appl
26	632.2	41.5	2711	9	US-09-952-559-2	Sequence 2, Appl
27	628	41.2	1110	9	US-09-965-703-2	Sequence 2, Appl
28	628	41.2	1110	17	US-10-239-134-2	Sequence 2, Appl
29	628	41.2	1288	9	US-09-965-703-1	Sequence 1, Appl
30	628	41.2	1288	17	US-10-239-134-1	Sequence 1, Appl
31	628	41.2	1288	17	US-10-468-199-59	Sequence 59, Appl
32	628	41.2	1542	9	US-09-965-703-58	Sequence 58, Appl
33	628	41.2	1542	17	US-10-239-134-49	Sequence 49, Appl
34	626.4	41.1	1290	9	US-09-965-697-4	Sequence 4, Appl
35	621.6	40.8	960	9	US-09-965-703-5	Sequence 5, Appl
36	621.6	40.8	960	17	US-10-239-134-5	Sequence 5, Appl
37	621.6	40.8	960	17	US-10-468-199-3	Sequence 3, Appl
38	621.6	40.8	1054	9	US-09-965-703-3	Sequence 3, Appl
39	621.6	40.8	1054	17	US-10-239-134-3	Sequence 3, Appl
40	621.6	40.8	1054	17	US-10-468-199-65	Sequence 65, Appl
41	621.6	40.8	1054	18	US-10-783-810-1	Sequence 1, Appl
42	621.6	40.8	1934	17	US-10-606-060A-2	Sequence 2, Appl
43	621.6	40.8	2464	17	US-10-606-060A-3	Sequence 3, Appl
44	621.6	40.8	2464	17	US-10-606-060A-4	Sequence 4, Appl
45	617.2	40.5	948	17	US-10-606-060A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-087-167-120
; Sequence 120, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)EV
US-10-087-167-120

Query Match 100.0%; Score 1524; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1441	GGCATGCGAATTCGAACATGTGCATCTCGCTGAAAGCTCAAGAACACAGGAAGCTGCCGCG	1500
Db	1441	GGCATGCGAATTCGAACATGTGCATCTCGCTGAAAGCTCAAGAACACAGGAAGCTGCCGCG	1500
Qy	1501	TTCTCTGGAGGAGATCTGGACGTG	1524
Db	1501	TTCTCTGGAGGAGATCTGGACGTG	1524
RESULT 2			
US-10-087-167-124			
; Sequence 124, Application US/10087167			
; Publication No. US20030154509A1			
; GENERAL INFORMATION:			
; APPLICANT: Pascal, Erica			
; APPLICANT: Valentine, Scott			
; APPLICANT: Brown, Jeffrey			
; APPLICANT: Cockrell, Adam			
; APPLICANT: Johnson, Brian			
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS			
; FILE REFERENCE: 50018A			
; CURRENT APPLICATION NUMBER: US/10/087,167			
; CURRENT FILING DATE: 2002-03-01			
; PRIOR APPLICATION NUMBER: US 60/242,969			
; PRIOR FILING DATE: 2000-10-24			
; NUMBER OF SEQ ID NOS: 148			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 124			
; LENGTH: 1782			
; TYPE: DNA			
; ORGANISM: Synthetic Construct			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(1782)			
; OTHER INFORMATION: Ecdysone receptor chimera G(E)EV			
US-10-087-167-124			
Query Match 92.8%; Score 1414.2; DB 16; Length 1782;			
Best Local Similarity 95.6%; Pred. No. 0;			
Matches 1471; Conservative 0; Mismatches 53; Indels 15; Gaps 1			
Qy	1	ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTCGCTTCATACGCTATTATTTCCTTGG	60
Db	1	ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTCGCTTCATACGCTATTATTTCCTTGG	60
Qy	61	TACTGTTCTTTTGTGATGCTACCCCTGTTGTTGTTGTTTACTTCTCAGGGATCCGCC	120
Db	61	TACTGTTCTTTTGTGATGCTACCCCTGTTGTTGTTGTTTACTTCTCAGGGATCCGCC	120
Qy	121	ACCATGAAGCTACTGTCTTCATCGAACACATGCGATATTTGCCGACTTAAAAAGCTC	180
Db	121	ACCATGAAGCTACTGTCTTCATCGAACACATGCGATATTTGCCGACTTAAAAAGCTC	180

181 AAGTCTCCAAAGAAACCGAAGTGGCCAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
Db |||||
181 AAGTCTCCAAAGAAACCGAAGTGGCCAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
Qy |||||
241 TACTCTCCAAACCAAAAGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGAATCA 300
Db |||||
241 TACTCTCCAAACCAAAAGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGAATCA 300
Qy |||||
301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAAGCTTGACATG 360
Db |||||
301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAAGCTTGACATG 360
Qy |||||
361 ATTTTGAATAAGTATCTTTACAGATATAAAGCAATTTGAACAGGATTTATTTGACAA 420
Db |||||
361 ATTTTGAATAAGTATCTTTACAGATATAAAGCAATTTGAACAGGATTTATTTGACAA 420
Qy |||||
421 GATAATGTGAATAAAGATGCGCTTCAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
Db |||||
421 GATAATGTGAATAAAGATGCGCTTCAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
Qy |||||
481 CTAACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
Db |||||
481 CTAACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
Qy |||||
541 GGTCAAAGACAGTTGACTGTATCGACGCGTATGAGCCCGAGTGGTCTCCAGAGTCC 600
Db |||||
541 GGTCAAAGACAGTTGACTGTATCGACGCGTATGAGCCCGAGTGGTCTCCAGAGAG 600
Qy |||||
601 AGCTGCAAGCAAAAGAGAGAGAAAGGAGACAGACAGAGAGAAAGACAAATGCCAGTC 660
Db |||||
601 AGCTGCGCCAAAGAGAGAGAAAGGAGACAGACAGAGAGAAAGACAAATGCCAGTC 660
Qy |||||
661 AGTACGACGACAGTGGACATCATATGCTGCGCATTAATGCAATGTGACCTCCGCCCA 720
Db |||||
661 AGCACAACGACAGTGGACATCATATGCTGCGCATTAATGCAATGTGACCTCCGCCCA 720
Qy |||||
721 GAGCGCGCAAGGATT-----CAGGAAGTGTCCCGAGTTCCTTAACGGAG 765
Db |||||
721 GAGCGACGAGGATTCTGGAATGTTTGGACGATGAAGTGTCCCGCGTTCCTCTCGGAG 780
Qy |||||
766 AGCTAATGGAGACAGACAGTGAAGATGTGACGCGCTGTGGCGGAACAGAGTGC 825
Db |||||
781 AAGCTGATGAGCAGAAATCGGCTGAAGAAACATACCCCTCTACCGCCCAACGACGTT 840
Qy |||||
826 CTGATCGCAGGCTCGTGTGTGACAGGACGATACGAGCAGCTTCGGAAGAGGATCTC 885
Db |||||
841 CTGATCGCAGGCTCGTGTGTGACAGGACGATACGAGCAGCTTCGGAAGAGGATCTC 900
Qy |||||
886 AAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGACGAACTCAGACATGCCA 945
Db |||||
901 AAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGACGAACTCAGACATGCCA 960
Qy |||||
946 TTCGCGCAGATCAGAAATGACCATCTCACAGTACAGTATAGTTCGAGTTTGCCAAA 1005
Db |||||
961 TTCGCGCAGATCAGAAATGACCATCTCACAGTACAGTATAGTTCGAGTTTGCCAAA 1020
Qy |||||
1006 GGCTACCTGTTTTCAAAGATCTCACAACTGACAGATCAATTTATTAAGGATGC 1065
Db |||||
1021 GGCTACCTGTTTTCAAAGATCTCACAACTGACAGATCAATTTATTAAGGATGC 1080
Qy |||||
1066 TCAAGCGAAGTGTGATGCTGCGAGTAGCGAGCGGTACGACCGGTGTCGATACGTT 1125
Db |||||
1081 TCAAGCGAAGTGTGATGCTGCGAGTAGCGAGCGGTACGACCGGTGTCGATACGTT 1140
Qy |||||
1126 CTGTTCCGCAACACAGGCGTACACTCGGACAGACTTACCGAGGCGGCGCATGGCTAC 1185
Db |||||
1141 CTGTTCCGCAACACAGGCGTACACTCGGACAGACTTACCGAGGCGGCGCATGGCTAC 1200
Qy |||||
1186 GTCATGGAAGACCTGTGCACTTCTGCGCGTGCATGTACTCGATGTGATGGAACAAGTG 1245
Db |||||
1201 GTCATGGAAGACCTGTGCACTTCTGCGCGTGCATGTACTCGATGTGATGGAACAAGTG 1260

1246 CATTACCGCTCTCTCACTGCGCATGTTATATTTCTCGATCGCGCGGCTTAGACAGCCA 1305
Db |||||
1261 CATTACCGCTCTCTCACTGCGCATGTTATATTTCTCGATCGCGCGGCTTAGACAGCCA 1320
Qy |||||
1306 CAGCTAGTAGAAGAGATCCAGCGGTATTTACCTGAACAGCGTGGGTTGTACATCATGAAC 1365
Db |||||
1321 CAGCTAGTAGAAGAGATCCAGCGGTATTTACCTGAACAGCGTGGGTTGTACATCATGAAC 1380
Qy |||||
1366 CAGCACAGCGCTCGCGCGTTCGCGCTATCTACGCGAAGATTTCTGTCGGTGTCTTACC 1425
Db |||||
1381 CAGCACAGCGCTCGCGCGTTCGCGCTATCTACGCGAAGATTTCTGTCGGTGTCTTACC 1440
Qy |||||
1426 GAGTTGGCGGACGCTGGGCAATCGAATTCGAACATGTGCATCTCGTGAAGCTCAAGAAC 1485
Db |||||
1441 GAGTTGGCGGACGCTGGGCAATCGAATTCGAACATGTGCATCTCGTGAAGCTCAAGAAC 1500
Qy |||||
1486 AGGAAGCTGCGCGCTTCCTGAGGAGATCTGGGACGTG 1524
Db |||||
1501 AGGAAGCTGCGCGCTTCCTGAGGAGATCTGGGACGTG 1539

RESULT 3

US-10-087-167-134
; Sequence 134, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1848)
; OTHER INFORMATION: Bodyson receptor chimera G(M)MC
US-10-087-167-134

Query Match 87.4%; Score 1332; DB 16; Length 1848;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Qy 1 ATGCAGCAGCTATATGTGGATTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
Db 1 ATGCAGCAGCTATATGTGGATTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
Qy 61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTTGGTGTACTTCTGCGAGGATCCGCC 120
Db 61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTTGGTGTACTTCTGCGAGGATCCGCC 120
Qy 121 ACCATGAGCTACTGTTCTTCTATCGAAACAGCATGGATATTTCCGCACTTAAAAAGCTC 180
Db 121 ACCATGAGCTACTGTTCTTCTATCGAAACAGCATGGATATTTTTCGCACTTAAAAAGCTC 180
Qy 181 AAGTGTCTCAAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
Db 181 AAGTGTCTCAAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
Qy 241 TACTCTCCCAAAACCAAAAGGTTCTCGCTGACTAGGGCACATCTGACAGAACTGGGAATCA 300
Db 241 TACTCTCCCAAAACCAAAAGGTTCTCGCTGACTAGGGCACATCTGACAGAACTGGGAATCA 300

Db 421 GATATGTGAATAAAGATGCCCTCAGATAGATTGGCTTCAGTGGAGATGATATGCT 480
 QY 481 CTAACATTGAGACAGCATAGATAAAGTGGCATCATCATCGAAGAGAGTAGTAACAAA 540
 Db 481 CTAACATTGAGACAGCATAGATAAAGTGGCATCATCATCGAAGAGAGTAGTAACAAA 540
 QY 541 GGTCAAGACAGTTCAGTGTATCGACGGTATGAGCCCGAGTGGTGGTCCAGAGTCC 600
 Db 541 GGTCAAGACAGTTCAGTGTATCGACGGTATGAGCCCGAGTGGTGGTCCAGAGTCC 600
 QY 601 AGCTGCAAGAAACAAAAGAGAGAAAGGAAGACACAGAGAGAGAGAGAGAGAGAGAG 660
 Db 601 AGCTGCAAGAAACAAAAGAGAGAAAGGAAGACACAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 AGTACGACAGAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACGCTCCGCG 720
 Db 661 AGTACGACAGAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACGCTCCGCG 720
 QY 721 GAGGCGGCAAGATTACGAAGTGGTCCGAGGTTCCCTAACGGAGAGCTAATGAGCAG 780
 Db 721 GAGGCGGCAAGATTACGAAGTGGTCCGAGGTTCCCTAACGGAGAGCTAATGAGCAG 780
 QY 781 AACAGACTGAAGATTGTACGCGCTGTGCGGGAACCAAGTCCCTGATCGAGGCTC 840
 Db 781 AACAGACTGAAGATTGTACGCGCTGTGCGGGAACCAAGTCCCTGATCGAGGCTC 840
 QY 841 GTGTGTGACAGGACGGATACAGAGCGCTTCGGAAGAGGATCTCAAAAGGTTGACGAG 900
 Db 841 GTGTGTGACAGGACGGATACAGAGCGCTTCGGAAGAGGATCTCAAAAGGTTGACGAG 900
 QY 901 ACTTGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 Db 901 ACTTGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 961 GAAATGACCATCTCAGCAGTACAGTAAATAGTGGAGTTTCCCAAGGCGCTACCTGTTT 1020
 Db 961 GAAATGACCATCTCAGCAGTACAGTAAATAGTGGAGTTTCCCAAGGCGCTACCTGTTT 1020
 QY 1021 TCAAGATCTCAACACTGACAGATCAATTAATTAAGGCGATGCTCAAGCGAGTGTATG 1080
 Db 1021 TCAAGATCTCAGTCCGATCAATTAATTAAGGCGATGCTCAAGCGAGTGTATG 1080
 QY 1081 ATGCTCGAGTACGAGGCGGTACGACGGGTGTCGGATAGCGTCTGTTCCGCAACAC 1140
 Db 1081 ATGCTCGAGTACGAGGCGGTACGACGGGTGTCGGATAGCGTCTGTTCCGCAACAC 1140
 QY 1141 CAGGCGTACACTCGGACAACTACCGAAGGCGGCGATGCGCTTACGTCATCGAAGACCTG 1200
 Db 1141 CAGGCGTACACTCGGACAACTACCGAAGGCGGCGATGCGCTTACGTCATCGAAGACCTG 1200
 QY 1201 CTGCACTTCTGCGGTGATGTACTCGATGTCGATGGAACAACTGATGAGCGCTCTCTC 1260
 Db 1201 CTGCACTTCTGCGGTGATGTACTCGATGTCGATGGAACAACTGATGAGCGCTCTCTC 1260
 QY 1261 ACTGCAATCGTTATTTCTGGATCGCGCGGCTTAGAGAGAGAGAGAGAGAGAGAGAG 1320
 Db 1261 ACTGCAATCGTTATTTCTGGATCGCGCGGCTTAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 ATCCAGCGGTATTTACCTGAACCGTTCGGGTGTACATCATATGAACGACGAGCGGTG 1380
 Db 1321 ATCCAGAGATCTACTTTGAAGAGCGTTCGGGTGTACATCATATGAACGACGAGCGGTG 1380
 QY 1381 CCGGTTGCGCGGTGATCTACGCGAAGATTCTGTGGTGTGTTACCGAGTTGCGGAGCG 1440
 Db 1381 CCGTGTGCGCGGTGATCTACGCGAAGATTCTGTGGTGTGTTACCGAGTTGCGGAGCG 1440
 QY 1441 GGCATGAGAAATTCGAACATGTCATCTCGTGAAGCTCAAGACAGAGAGCTGCGCGCG 1500
 Db 1441 GGCATGAGAAATTCGAACATGTCATCTCGTGAAGCTCAAGACAGAGAGCTGCGCGCG 1500
 QY 1501 TTCTGGAGAGATCTCGGACGTG 1524

Db 1501 TTCTCGAGGAGATCTCGGACGTG 1524

RESULT 5
 ; Sequence 104, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 104
 ; LENGTH: 3972
 ; TYPE: DNA
 ; ORGANISM: synthetic construct
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(3972)
 ; OTHER INFORMATION: GAL4-Manduca Ecr-VP16 fragment in pGGS202
 ; NAME/KEY: CDS
 ; LOCATION: (2007)..(3668)
 ; OTHER INFORMATION: GAL4-Manduca Ecr-VP16 chimera
 ; US-10-087-167-104

Query Match 87.4%; Score 1332; DB 16; Length 3972;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTGG 60
 Db 1884 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTGG 1943
 QY 61 TACTGTTTCTTTTGTGCTGCTCACCCTGTTGTTGGTGTACTTCTGAGGATCCGCC 120
 Db 1944 TACTGTTTCTTTTGTGCTGCTCACCCTGTTGTTGGTGTACTTCTGAGGATCCGCC 2003
 QY 121 ACATGAAGCTACTGCTCTTATCGAACAAGCATGGATTTTCCGCACTTAAAGAGCTC 180
 Db 2004 ACCATGAAGCTACTGCTCTTATCGAACAAGCATGGATTTTCCGCACTTAAAGAGCTC 2063
 QY 181 AAGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
 Db 2064 AAGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 2123
 QY 241 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAGTGAATCA 300
 Db 2124 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAGTGAATCA 2183
 QY 301 AGGTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTTCTCCGAGAGACCTTGGACATG 360
 Db 2184 AGGTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTTCTCCGAGAGACCTTGGACATG 2243
 QY 361 ATTTTGAAGTGAATCTTTTACAGGATATAAAAGCATTTGTAACAGGATTTATTTGTACAA 420
 Db 2244 ATTTTGAAGTGAATCTTTTACAGGATATAAAAGCATTTGTAACAGGATTTATTTGTACAA 2303
 QY 421 GATAATGTGAATAAAGATGCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCTC 480
 Db 2304 GATAATGTGAATAAAGATGCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCTC 2363
 QY 481 CTAACATTGAGACAGCATAGATAAAGTGGACATCATCATCGGAGAGAGAGTAGTAACAAA 540
 Db 2364 CTAACATTGAGACAGCATAGATAAAGTGGACATCATCATCGGAGAGAGAGTAGTAACAAA 2423

541 GGTCAAAGACAGTTGACTGTATCGACGGTATGAGCGCCGAGTGCCTGCTCCAGAGTCC 600
 2424 GGTCAAAGACAGTTGACTGTATCGACGGTATGAGCGCCGAGTGCCTGCTCCAGAGTCC 2483
 601 ACCTGCAAGAAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCCAGTC 660
 2484 ACCTGCAAGAAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCCAGTC 2543
 661 AGTACGACGACAGTGGACGATCATATGCTGCCATATGCAATGTAAGTGCCTCCGCCCCCA 720
 2544 AGTACGACGACAGTGGACGATCATATGCTGCCATATGCAATGTAAGTGCCTCCGCCCCCA 2603
 721 GAGCGCGCAAGGATTACGAAAGTGTCCCGAGGTTCTTAACGAGAAAGCTTAATGGAGCAG 780
 2604 GAGCGCGCAAGGATTACGAAAGTGTCCCGAGGTTCTTAACGAGAAAGCTTAATGGAGCAG 2663
 781 AACAGACTGAAGAAATGTGACGCGCTGTCCGGACACAGAAAGTCCCTGATCGCGAGGCTC 840
 2664 AACAGACTGAAGAAATGTGACGCGCTGTCCGGACACAGAAAGTCCCTGATCGCGAGGCTC 2723
 841 GTGTGGTACACGACGCGATACGAGCAGGCTTCCGGAAGAGGATCTCAAAAGGGTGACCGAG 900
 2724 GTGTGGTACACGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAG 2783
 901 ACTTGGCAATCAGCAGATGAAGAAGAAAGAAAGTCCGATGCGCGAGGCTC 960
 2784 ACATGGCAGTTAGAAGAAAGAAAGAAAGAAAGTCCGATGCGCGAGGCTC 2843
 961 GAATGACCATCTCACAGTACAGCTTAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTT 1020
 2844 GAGATGACCATCTTAACAGTGCAGCTTATTTAGAAATTCGAAAGGGCTCATCAAGCGAAGTATG 2903
 1021 TCAAGATCTCAACCTGACAGATCAATATTAAGAGGATGCTCAAGCGAAGTATG 1080
 2904 TCCAGATATCTCAGTCCGATCAATATTAAGAGGCTCATCAAGCGAAGTATG 2963
 1081 ATGTGCGAGTACGAGCGGTGACAGCGGTTGCGGATAGGTTCTGTTGCGCAACAC 1140
 2964 ATGTGCGAGTACGAGCGGTGACAGCGGTTGCGGATAGGTTCTGTTGCGCAACAC 3023
 1141 CAGGCGTACACTCGCAGCAACTACCGAAGCGGCGATGCGCTCATCGAAGACCTG 1200
 3024 CAGGCGTACACTCGCAGCAACTACCGAAGCGGCGATGCGCTCATCGAAGACCTG 3083
 1201 CTGCACTTCTGCGGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 1260
 3084 CTGCACTTCTGCGGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 3143
 1261 ACTGCCATCGTTATATCTCGGATCGGCGGCGCTAGAGCGCCACAGCTAGTAGAAG 1320
 3144 ACCGCCATCGTTATATCTCGAGACCGGCGGCGCTAGAGCGCCACAGCTAGTAGAAG 3203
 1321 ATCCAGCGGTATTACCTGAACAGCTGCGGGTGTACATCATGAACAGCAGCGCGTGG 1380
 3204 ATCCAGAGATCTACTTGAAGAGCTGCGGGTGTACATTTAAATCAGCAGCGCGTGG 3263
 1381 CCGCGTTGCGCGGTGATCTACGCGAAGATTCTGCGGTGTTACCGAGTTCGCGAGGCTG 1440
 3264 CCGCGTTGCGCGGTGATCTACGCGAAGATTCTGCGGTGTTACCGAGTTCGCGAGGCTG 3323
 1441 GGCATGAGAAATTCGAGAAATGTCATCTGCTGAAGCTCAAGAAACAGGAAGTTCGCGCG 1500
 3324 GGCATGAGAAATTCGAGAAATGTCATCTGCTGAAGCTCAAGAAACAGGAAGTTCGCGCG 3383
 1501 TTCTCTGAGGAGATCTGGGACGTTG 1524
 3384 TTCTCTGAGGAGATCTGGGACGTTG 3407

Publication No. US20030154509A1
 GENERAL INFORMATION:
 APPLICANT: Pascal, Erica
 APPLICANT: Valentine, Scott
 APPLICANT: Brown, Jeffrey
 APPLICANT: Cockrell, Adam
 APPLICANT: Johnson, Brian
 TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 FILE REFERENCE: 50018A
 CURRENT APPLICATION NUMBER: US/10/087,167
 CURRENT FILING DATE: 2002-03-01
 PRIOR APPLICATION NUMBER: US 60/242,969
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 148
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 122
 LENGTH: 1767
 TYPE: DNA
 ORGANISM: Synthetic Construct
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1767)
 OTHER INFORMATION: Ecdysone receptor chimera G(M)FV
 US-10-087-167-122

Query Match 87.2%; Score 1328.8; DB 16; Length 1767;
 Best Local Similarity 92.0%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
 Qy 1 ATCAGCAGCATATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTGG 60
 Db 1 ATCAGCAGCATATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTGG 60
 Qy 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTGCGAGGATCGCC 120
 Db 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTGCGAGGATCGCC 120
 Qy 121 ACCATGAAGCTACTGTCTTCTATCGAAACAGCATGCGATTTTGGCGACTTAAAGAGCTC 180
 Db 121 ACCATGAAGCTACTGTCTTCTATCGAAACAGCATGCGATTTTGGCGACTTAAAGAGCTC 180
 Qy 181 AAGTGTCCAAAGAAACCCGAGTGGCCAGTGTCTGAAGAACAACTCGGAGTGTGCG 240
 Db 181 AAGTGTCCAAAGAAACCCGAGTGGCCAGTGTCTGAAGAACAACTCGGAGTGTGCG 240
 Qy 241 TACTCTCCAAACCCAAAGGTCTCCGCTGACTAGGACATCTGACAGAGTGGAAATCA 300
 Db 241 TACTCTCCAAACCCAAAGGTCTCCGCTGACTAGGACATCTGACAGAGTGGAAATCA 300
 Qy 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTGACATG 360
 Db 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTGACATG 360
 Qy 361 ATTTTGAAGATGGATTTCTTACAGGATATAAGCACTGTTAAACAGGATTTATTTGTACAA 420
 Db 361 ATTTTGAAGATGGATTTCTTACAGGATATAAGCACTGTTAAACAGGATTTATTTGTACAA 420
 Qy 421 GATAATGTGAATAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGCTGATATGCTC 480
 Db 421 GATAATGTGAATAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGCTGATATGCTC 480
 Qy 481 CTAACTATGAGACAGCATAGAAATAGTTCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Db 481 CTAACTATGAGACAGCATAGAAATAGTTCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Qy 541 GGTCAAGACAGTGTGACTGTATCGACGGTATGAGGCCGAGTGCCTGCTCCAGAGTCC 600
 Db 541 GGTCAAGACAGTGTGACTGTATCGACGGTATGAGGCCGAGTGCCTGCTCCAGAGTCC 600
 Qy 601 ACGTGCAAGAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCCAGTC 660
 Db 601 ACGTGCAAGAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCCAGTC 660


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QY 661 AGTACGACGACGATGATGATGCTGCTCAATGCAATGACCTCCGCCCA 720
DB 661 AGTACGACGACGATGATGATGCTGCTCAATGCAATGACCTCCGCCCA 720
QY 721 GAGGCGGCAAGGATTCAGCAAGTGTCCGAGGTTCTTAACGAGAGGATTAATGAGCAG 780
DB 721 GAGGCGGCAAGGATTCAGCAAGTGTCCGAGGTTCTTAACGAGAGGATTAATGAGCAG 780
QY 781 AACAGATGAGAGATGTCAGCGCGTGTCCGACACCAAGTCCCTGATCGGAGGCTC 840
DB 781 AACAGATGAGAGATGTCAGCGCGTGTCCGACACCAAGTCCCTGATCGGAGGCTC 840
QY 841 GTGTGTACACGACGATACGACGATGCTCCGAGAGGATCTCAAAAGGATGACGACG 900
DB 841 GTGTGTACACGAGGGGTACGACGATGCTCCGAGAGGATCTCAAAAGGATGACGACG 900
QY 901 ACTTGGCAATCAGCAGATGAAGAAGACGAAGACTCAGACATGCCATTCGCCAGATCA 960
DB 901 ACATGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GAAATGACCATCTCAGCAGTACAGCTAATAGTCGAGTTTGCACAAAGGCTACCTGTTT 1020
DB 961 GAGATGACCATCTTAAACGATGAGCTTATTTAGAAATTCGCAAGGGGACTACCGGATTC 1020
QY 1021 TCAGAGATCTCAACCTGACGATCAATTAATTAAGGATGCTCAAGCGAAGTGTATG 1080
DB 1021 TCCAGATATCTCAGTCCGATCAATTAATTAAGGATGCTCAAGCGAAGTGTATG 1080
QY 1081 ATGCTCGAGTACGAGGCGGTACGACGCGGTGTCCGATAGCGTTCTGTTCCCAACAAC 1140
DB 1081 ATGCTCGAGTACGAGGCGGTACGACGCGGTGTCCGATAGCGTTCTGTTCCCAACAAC 1140
QY 1141 CAGGCGTATACCTCGGACAACTACCGCAAGGCGGCTACGCTATCGAAGACCTG 1200
DB 1141 CAGGCGTATACCTCGGACAACTACCGCAAGGCGGCTACGCTATCGAAGACCTG 1200
QY 1201 CTGCACTTCGCGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTC 1260
DB 1201 CTGCACTTCGCGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTC 1260
QY 1261 ACTGCCATCGTTATATCTCGGATCGCGCGGCTAGAGCAGCAGCAGCTAGTAGAAGAG 1320
DB 1261 ACCGCCATCGTTATATCTCAGACCGCGCGGCTAGAGCAGCAGCAGCTAGTAGAAGAG 1320
QY 1321 ATCCAGCGTATACCTGAACAGCTGCGGCTGATCATATGAAACGACAGCAGCGCTG 1380
DB 1321 ATCCAGAGATACCTGTAAGAGCTGCGGCTGATCATATGAAACGACAGCAGCGCTG 1380
QY 1381 CCGCGTTCGCGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTC 1440
DB 1381 CCGCGTTCGCGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTC 1440
QY 1441 GGCATGAGATTCGAACATGTCATCTCGCTGAACTCAAGAACGAGGAGCTGCGCGCG 1500
DB 1441 GGCACGAGATTCGAACATGTCATCTCGCTGAACTCAAGAACGAGGAGCTGCGCGCG 1500
QY 1501 TTCTCGAGGAGATTCGGACGCTG 1524
DB 1501 TTCTCGAGGAGATTCGGACGCTG 1524

```

RESULT 7

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US-10-087-167-118
; Sequence 118, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A

```

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; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1776)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)BV
US-10-087-167-118

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Query Match      86.0%; Score 1311.2; DB 16; Length 1776;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1398; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

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QY 1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
DB 1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
QY 61 TACTGTTTCTTTTGTGATGCTCACCTGTTTGTGTTTACTTCTCGAGGATCCGCC 120
DB 61 TACTGTTTCTTTTGTGATGCTCACCTGTTTGTGTTTACTTCTCGAGGATCCGCC 120
QY 121 ACCATGAAGCTACTGTTCTTATGAAACAGATGCGATATTTGCCGACTTAAAGCTC 180
DB 121 ACCATGAAGCTACTGTTCTTATGAAACAGATGCGATATTTGCCGACTTAAAGCTC 180
QY 181 AAGTCTCCAAAGAAACCCGAGTGCAGGCTGCTGAAGAACAACTGGGAGTGTGCG 240
DB 181 AAGTCTCCAAAGAAACCCGAGTGCAGGCTGCTGAAGAACAACTGGGAGTGTGCG 240
QY 241 TACTCTCCAAACCCGAGTGCAGGCTGCTGAAGAACAACTGGGAGTGTGCG 300
DB 241 TACTCTCCAAACCCGAGTGCAGGCTGCTGAAGAACAACTGGGAGTGTGCG 300
QY 301 AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTGACATG 360
DB 301 AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTGACATG 360
QY 361 ATTTTGAAGATGGAATTTTACAGGATATAAAGCATTTTAAACAGGATTTTCTGACAA 420
DB 361 ATTTTGAAGATGGAATTTTACAGGATATAAAGCATTTTAAACAGGATTTTCTGACAA 420
QY 421 GATATGTGAATGAAGATGCGCTCAAGATAGATTGGCTTTCAGTGGAGACTGATATGCT 480
DB 421 GATATGTGAATGAAGATGCGCTCAAGATAGATTGGCTTTCAGTGGAGACTGATATGCT 480
QY 481 CTAACTTGAAGATGGAATTAAGTGGACATCATTCGGAAGAGAGTAGTAACAAA 540
DB 481 CTAACTTGAAGATGGAATTAAGTGGACATCATTCGGAAGAGAGTAGTAACAAA 540
QY 541 GGTCAAGACAGTTCGATGTCAGCGCTGATGAGCGCGGCTGCTGCTCCAGAGTCC 600
DB 541 GGTCAAGACAGTTCGATGTCAGCGCTGATGAGCGCGGCTGCTGCTCCAGAGTCC 600
QY 601 ACCTGCAAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 ACCTGCAAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 AGTACGACGACAGTGGAGCATATGCTGCTGATGCTGATGCTGATGCTGCTGCTGCTG 720
DB 661 AGTACGACGACAGTGGAGCATATGCTGCTGATGCTGATGCTGATGCTGCTGCTGCTG 720
QY 721 GAGGCGGCAAGGATTCAGCAAGTGTCCGAGGTTCTTAACGAGAGAGTAGTAAGAGCAG 780
DB 721 GAGGCGGCAAGGATTCAGCAAGTGTCCGAGGTTCTTAACGAGAGAGTAGTAAGAGCAG 780
QY 781 AACAGACTGAAGATGTGACGCGCTGTCGCGGCAACAGAGAGTCCCTGATCGGAGGCTC 840

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Db 781 AACAGAGTGAAGAAATGTGACCGCTGTGCGGCAACAGAAAGTCCCTGTATCGGAGGCTC 840
Qy 841 GTGTGGTACCAAGGAGGATAGACAGCCTTTCGGAAGAGGATCTCAAAAGGGTGACGAG 900
Db 841 GTGTGGTACCAAGGAGGATAGAAACACCTTCAGAGGAGACCTCAAGAGGGTGACGAG 900
Qy 901 ACTTGGCAATCAGCAGATGAAGAGAGAGAAAGACTCAGACATGCCATTCGCGCAGATCACA 960
Db 901 ACTTGGCAGT---CGGACGAGGATGAAGAGGAGTCAAGATGCGGCTTCGCGCAGATCACC 957
Qy 961 GAATGACCATCTCAGACAGTACAGTAATAGTCAGATTGTCGAAGGCTTACCTGCTTTT 1020
Db 958 GAGATGACGATCTCGACATGTTCAACTCATCTAGAAATTCGCAAAAGGCTTCGCGAGGCTTC 1017
Qy 1021 TCAAGATCTCACAACCTGACAGATCACATTAATTAAGGATGCTCAAGCGAAGTGAATG 1080
Db 1018 GCCAAGATCTCGAGTCGATCAATCACTTACTTAAGGGGTGTTCAAGTGAGGTGATG 1077
Qy 1081 ATGCTGCGAGTAGCGAGCGGTAAGACCGGCTGCGATAGCGTTCGTCGCAACAAAC 1140
Db 1078 ATGCTCCTGAGTGGCCGCGGTACGACGCGCCACCGACAGGCTACTGTTTCGCAACAAAC 1137
Qy 1141 CAGGCGTACATCGCGCACTACCGCAAGGGGCGCATGCGTCACTGATCGAAGACTG 1200
Db 1138 CAGGCGTACTCCCGCGCACTACCGCAAGGGGCGCATGCTTCTGATCGAGATCTC 1197
Qy 1201 CTGCACTTCTGCGCTGATGATCTGATGCGATGCGATGCGAAGCGTTCGCTCCTC 1260
Db 1198 TTGCACTTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
Qy 1261 ACTGCCATGTTATATTCGAGATCGCGCGGCGCTAGAGAGCGCACACTAGTAGAAGAG 1320
Db 1258 ACGGCAATGTCTTCTCAGACCGGCGCTGCGCTCGAGCAACCTTATTCGTTGGAAGAA 1317
Qy 1321 ATCCAGCGGTATCTGCAACAGCTGCGGGGTATACATCATGCAACCAAGCGCGCTCG 1380
Db 1318 ATCCAGCGGTATCTGCAACAGCTGCGGGGTATACATCATGCAACCAAGCGCGCTCG 1377
Qy 1381 CCGCGTTCGCGCTCATCTACGCAAGATTCCTGCGGTCTTACGAGTTCGCGAGCGTG 1440
Db 1378 CCGCGTTCGCGGTAGTCTTCGCAAGATTCCTGGGATATTCGCGAGTTCGCGAGCTC 1437
Qy 1441 GGCATGCAAAATTCGAACATGTGATCTGCTGAGCTCAAGAACAGGAGTTCGCGCG 1500
Db 1438 GGCATGCAAACTCCAAACATGTGATCTCGTTGAAGCTGAAGATAGGAAGCTGCGCGCG 1497
Qy 1501 TTCCTCGAGGAGATCTGGGACGTG 1524
Db 1498 TTCCTCGAGGAGATCTGGGACGTG 1521

RESULT 8
US-10-087-167-126
; Sequence 126, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1800
; TYPE: DNA

; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1800)
; OTHER INFORMATION: Ecdysone receptor chimera G(E)MV
US-10-087-167-126

Query Match 80.2%; Score 1222.2; DB 16; Length 1800;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1351; Conservative 0; Mismatches 173; Indels 15; Gaps 1;

Qy 1 ATGCAGCAGCTATATGTGGATTTTTTATGCCCTTGCCTTCATACGCTATTTATTTGTTGG 60
Db 1 ATGCAGCAGCTATATGTGGATTTTTTATGCCCTTGCCTTCATACGCTATTTATTTGTTGG 60
Qy 61 TACTGTTTCTTTTGTGCGATGCTCACCTGTTGTTGTTGTTTCTCTGAGGATCCGCC 120
Db 61 TACTGTTTCTTTTGTGCGATGCTCACCTGTTGTTGTTGTTTCTCTGAGGATCCGCC 120
Qy 121 ACCATGAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTC 180
Db 121 ACCATGAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTC 180
Qy 181 AAGTGTCTCAAAAGAAAAAACCGAAGTGCCTCAAGTGTCTGAAGAAACAACCTGGGAGTGTGC 240
Db 181 AAGTGTCTCAAAAGAAAAAACCGAAGTGCCTCAAGTGTCTGAAGAAACAACCTGGGAGTGTGC 240
Qy 241 TACTCTCCCAAAACCAAAAGGCTCTCGCTGACTAGGGCACATCTGACAGAAAGTGAATCA 300
Db 241 TACTCTCCCAAAACCAAAAGGCTCTCGCTGACTAGGGCACATCTGACAGAAAGTGAATCA 300
Qy 301 AGCTAGAAAGACTGGAACAGCTATTTTCTACTGATTTTTCTCTCGAAGAAGCTTGACATG 360
Db 301 AGCTAGAAAGACTGGAACAGCTATTTTCTACTGATTTTTCTCTCGAAGAAGCTTGACATG 360
Qy 361 ATTTTGAAGATGATCTTTTACAGGATATAAAGAGCATTTGTTTACAGGATTTATTTGTACA 420
Db 361 ATTTTGAAGATGATCTTTTACAGGATATAAAGAGCATTTGTTTACAGGATTTATTTGTACA 420
Qy 421 GATAATGTGAATAAAGATGCGCTCAGAGATAGATTTGGCTTCAGTGGAGACTGATATGCTT 480
Db 421 GATAATGTGAATAAAGATGCGCTCAGAGATAGATTTGGCTTCAGTGGAGACTGATATGCTT 480
Qy 481 CTAACTATGAGACAGCATAGAATAAGTGCACATCATATCGAAAGAGAGTAGTAGTAAACAA 540
Db 481 CTAACTATGAGACAGCATAGAATAAGTGCACATCATATCGAAAGAGAGTAGTAGTAAACAA 540
Qy 541 GGTCAAAAGACAGTTGACTGTATCGACGCTATGAGCGCCGAGTGCCTGCCAGAGTCC 600
Db 541 GGTCAAAAGACAGTTGACTGTATCGACGCTATGAGCGCCGAGTGCCTGCCAGAGTCC 600
Qy 601 ACGTCAAGAAACAAAAGAGAAAAAGAGAACAGACAGAGAAAAAGAAAAAATGCGCAGTC 660
Db 601 ACGTCAAGAAACAAAAGAGAAAAAGAGAACAGACAGAGAAAAAGAAAAAATGCGCAGTC 660
Qy 661 AGTACGACGAGTGGAGCATATATGCTGCTCCATATGCAATGTCACCTCCGCCCCCA 720
Db 661 AGTACGACGAGTGGAGCATATATGCTGCTCCATATGCAATGTCACCTCCGCCCCCA 720
Qy 721 GAGCGCGCAAGGATT-----CAGCAAGTGGTCCGAGGTTCTTAACCGAG 765
Db 721 GAGCGCGCAAGGATT-----CAGCAAGTGGTCCGAGGTTCTTAACCGAG 765
Qy 766 AAGCTAATGAGCAGAAACAGACTGAAGAATGTGACGCGCTGTGCGGGAACCAAGAGTCC 825
Db 766 AAGCTAATGAGCAGAAACAGACTGAAGAATGTGACGCGCTGTGCGGGAACCAAGAGTCC 825
Qy 841 CTGATCGCAGGCTCGT 900
Db 841 CTGATCGCAGGCTCGT 900
Qy 886 AAAAGGGTGCAGAGACTTTGGCAATCAGCAGATGAAGAAAGACGAAGACTCAGACATGCCA 945
Db 886 AAAAGGGTGCAGAGACTTTGGCAATCAGCAGATGAAGAAAGACGAAGACTCAGACATGCCA 945

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Db 901 AAGAGATTACACAGACATGCGAGTTAGAGAGAGAGAGAGAGAGAACTGACATGCC 960
Qy 946 TTCGCCAGATACAGAAATGACCACTCTCAGAGTACAGCTAATAGTCAGCTTTGCCAAA 1005
Db 961 TTCCTCAGATCAGAGATGACGATCTTAACAGTGCAGCTTATTTGTAGAATTGCGAAAG 1020
Qy 1006 GGCCTACCTGGTTTTTCAAGATCTCACAACTGACACAGATCACATTTATAAGGCGATGC 1065
Db 1021 GACTACCGGANTCTCCAGATATCTCAGTCCGATCAANTTACATTTATAAGGCGTCA 1080
Qy 1066 TCAAGCGAGTATGATGCTCGAGTACGAGGCGGTACGACGCGGTTCGGAATAGCGTT 1125
Db 1081 TCAAGCGAGTATGATGCTCGAGTACGAGGCGGTACGACGCGGTTCGGAATAGCGTT 1140
Qy 1126 CTGTTGCGCAACCAACAGCGGTACACTCGGCACTACCGCACTACCGCGGCGGATGCGCTAC 1185
Db 1141 CTGTTGCGCAACCAACAGCGGTACACGCGGCACTACCGCACTACCGCGGCGGATGCGCTAC 1200
Qy 1186 GTCATCGAAGACCTCTGCACTCTGCGCGTCTGATGCTGATGCTGATGCTGATGCTGATG 1245
Db 1201 GTCATCGAAGACCTCTGCACTCTGCGCGTCTGATGCTGATGCTGATGCTGATGCTGATG 1260
Qy 1246 CATTACGGCGCTCTCACTGCCATCGTTATTTCTCGGATCGCGCGGCTAGAGCAGCCA 1305
Db 1261 CACTACGGCGTCTCACTGCCATCGTTATTTCTCGGATCGCGCGGCTAGAGCAGCCA 1320
Qy 1306 CAGTAGTAGAGATCAGCGGTATTTACCTGAACACGCTCGCGGCTAGAGCAGCCA 1365
Db 1321 CTTTGTAGTAGAGATCAGCGGTATTTACCTGAACACGCTCGCGGCTAGAGCAGCCA 1380
Qy 1366 CAGCAGCGCTCGCGGTTGCGCGTCTCACTGCGGAGATCTGCGGTGCTTACC 1425
Db 1381 CAGCAGCGCTCGCGTCTGCGCGGTTGCGCGTCTCACTGCGGAGATCTGCGGTGCTTACC 1440
Qy 1426 GAGTTGCGGACCTCGCGGTTGCGCGTCTCACTGCGGAGATCTGCGGTGCTTACC 1485
Db 1441 GAACTGCGGACCTCGCGGTTGCGCGTCTCACTGCGGAGATCTGCGGTGCTTACC 1500
Qy 1486 AGGAAGTTCGCGGTTCTCGGAGGATCTGCGGAGCTG 1524
Db 1501 AGGAAGTTCGCGGTTCTCGGAGGATCTGCGGAGCTG 1539

RESULT 9
US-10-087-167-128
; Sequence 128, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Eric
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
; OTHER INFORMATION: G(M)M (GALA DNA Binding Domain fused to the Manduca BcR Hinge and
; OTHER INFORMATION: Ligand Binding Domain)
US-10-087-167-128
Query Match 79.3%; Score 1209; DB 16; Length 1428;

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Best Local Similarity 91.4%; Pred. No. 0; Mismatches 120; Indels 0; Gaps 0;
Matches 1281; Conservative
Qy 124 ATGAGCTACTGCTCTTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG 183
Db 1 ATGAGCTACTGCTCTTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG 60
Qy 184 TGCTCCAAAGAAAACCGAAGTGCCTCAAGTGTCTGAAGAACAACTGGGAGTGCCTAC 243
Db 61 TGCTCCAAAGAAAACCGAAGTGCCTCAAGTGTCTGAAGAACAACTGGGAGTGCCTAC 120
Qy 244 TCTCCCAAAACCAAAAGTCTCCGCTGACTAGGCGACATCTGACAGAGTGCATCAAGG 303
Db 121 TCTCCCAAAACCAAAAGTCTCCGCTGACTAGGCGACATCTGACAGAGTGCATCAAGG 180
Qy 304 CTAGAAAGACTTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGCTTTGACATGAT 363
Db 181 CTAGAAAGACTTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGCTTTGACATGAT 240
Qy 364 TTGAAATGGATCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 423
Db 241 TTGAAATGGATCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300
Qy 424 AATGTGAATAAAGATGCCGTCACAGATAGATTGCTTTCAGTGGAGACTGATATGCTCTA 483
Db 301 AATGTGAATAAAGATGCCGTCACAGATAGATTGCTTTCAGTGGAGACTGATATGCTCTA 360
Qy 484 ACATTGAGACAGCATAGAAATAGTGCACATCATCTCGAAGAGAGTAGTAACAAGGT 543
Db 361 ACATTGAGACAGCATAGAAATAGTGCACATCATCTCGAAGAGAGTAGTAACAAGGT 420
Qy 544 CAAAGACAGTTGACTGTATCGACGCTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 603
Db 421 CAAAGACAGTTGACTGTATCGACGCTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 480
Qy 604 TGCAAGAACAAAGAGAGAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
Db 481 TGCAAGAACAAAGAGAGAGAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 664 ACGACAGAGTGGACGATCATATGCTGCCATTAATGCAATGTGACCTCCGCGCCACAG 723
Db 541 ACGACAGAGTGGACGATCATATGCTGCCATTAATGCAATGTGACCTCCGCGCCACAG 600
Qy 724 GCGGCAAGGATTCAGAAAGTGTGCCGAGGTTCTTAACGAGAGAGAGAGAGAGAGAG 783
Db 601 GCGGCAAGGATTCAGAAAGTGTGCCGAGGTTCTTAACGAGAGAGAGAGAGAGAGAG 660
Qy 784 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCGAGGCTCG 843
Db 661 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCGAGGCTCG 720
Qy 844 TGGTACCAAGGAGTACGAGCAGCTTCCGGAAGAGAGTCTCAAAAGGAGTGCAGAGACT 903
Db 721 TGGTACCAAGGAGTACGAGCAGCTTCCGGAAGAGAGTCTCAAAAGGAGTGCAGAGACT 780
Qy 904 TGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963
Db 781 TGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 964 ATGACATCTCTCAGAGTACAGCTAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTCA 1023
Db 841 ATGACATCTCTCAGAGTACAGCTAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTCA 900
Qy 1024 AAGATCTCAACACTGACAGATCATATTTAAAGGAGTGTCAAGCGAGTGTATGATG 1083
Db 901 AAGATCTCAACACTGACAGATCATATTTAAAGGAGTGTCAAGCGAGTGTATGATG 960
Qy 1084 CTGCGAGTAGCAGGCGGTACAGCAGGTTGCGGAGTAGGTTCTGTTCCGCAACACAG 1143
Db 961 CTGCGAGTAGCAGGCGGTACAGCAGGTTGCGGAGTAGGTTCTGTTCCGCAACACAG 1020
Qy 1144 GCGTACACTCGCGACAACTTACCGCAAGGCGGCGATGCGCTAGTCTATCGAAGACCTGCTG 1203

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Db	1021	CGGTACACGCGGCAAACTACCGCAAGCGGGGCGATGCTCTACGTATCGAGGACCTGCTG	1080
Qy	1204	CACCTTCTCCGCTGCATGCTACGTATCGATGCGATGGACAAACGTGCAATTACGGGCTCCTCACT	1263
Db	1081	CACCTTCTCGGTGTGTGTACTCCATGAGCATGCAATGTGCACTACGGGCTGCTCACC	1140
Qy	1264	GCCATCGTTATTTCTCGGATCGGCGGGCCCTAGAGCGCCACAGCTAGTAGAAGATC	1323
Db	1141	GCCATCGTTATTTCTAGACGGGCCAGGCTCGAGCAACCCCTTTTGTGGAGGAATC	1200
Qy	1324	CAGCGGTATTACCTGAAACACGCTCGGGGTGTACATCATGAACAGCACAGCGCGCTCGCG	1383
Db	1201	CAGAGATACTACTTGAAGACGCTCGGGTTTACATTTTAATTCAGCACAGCGCTCGCCT	1260
Qy	1384	CGTTTCGCGCGTCTACGCGAAGATTCTGTCGGTGTCTTACCGAGTTCGCGACCGCTGGGC	1443
Db	1261	CGCTGCGCGTCTGTTTCGGCAAGATCTCGGCGTGTGACGGAACCTGCGCACGCTCGGC	1320
Qy	1444	ATGCAAGATTCGAACATGTGCTCGCTGAAGCTCAAGAACAGGAGCTGCGCGCGTTC	1503
Db	1321	ACGCAGAACTCCAAATGTGCATCTCGTGAAGCTGGAAGACAGGAAACTTTCGCGCATTC	1380
Qy	1504	CTGGAGGAGATCTGGACGTG	1524
Db	1381	CTCAGGAGATCTGGACGTG	1401
RESULT 10			
US-10-087-167-142			
; Sequence 142, Application US/10087167			
; Publication No. US20030154509A1			
; GENERAL INFORMATION:			
; APPLICANT: Pascal, Erica			
; APPLICANT: Valentine, Scott			
; APPLICANT: Brown, Jeffrey			
; APPLICANT: Cockrell, Adam			
; APPLICANT: Johnson, Brian			
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS			
; FILE REFERENCE: 50018A			
; CURRENT APPLICATION NUMBER: US/10/087,167			
; CURRENT FILING DATE: 2002-03-01			
; PRIOR APPLICATION NUMBER: US 60/242,969			
; PRIOR FILING DATE: 2000-10-24			
; NUMBER OF SEQ ID NOS: 148			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 142			
; LENGTH: 1809			
; TYPE: DNA			
; ORGANISM: Synthetic Construct			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(1809)			
; OTHER INFORMATION: Ecdysone receptor chimera VG(N)M			
US-10-087-167-142			
Query Match 79.3%; Score 1208.2; DB 16; Length 1809;			
Best Local Similarity 90.9%; Pred. No. 0; Mismatches 128; Indels 0; Gaps 0;			
Matches 1285; Conservative 0			
Qy	112	GGATCCGCCACCATGAAGCTACTGTCTTCTATCGAAACAAAGCATGCGATATTTGCCGACTT	171
Db	370	GGGACGTGACTAGTAAGCTACTGTCTTCTATCGAACAAGCATGCGATATTTGCCGACTT	429
Qy	172	AAAAAGCTCAAGTGTCCAAAGAAAAACCGAAGTGGCGGCAAGTGTCTGAAGAACAACTGG	231
Db	430	AAAAAGCTCAAGTGTCCAAAGAAAAACCGAAGTGGCGGCAAGTGTCTGAAGAACAACTGG	489
Qy	232	GAGTGTGCTACTCTCCAAAACCAAAGGTCTCCGCTGACTAGGGCACTCTGCACAGAA	291
Db	490	GAGTGTGCTACTCTCCAAAACCAAAGGTCTCCGCTGACTAGGGCACTCTGCACAGAA	549
Qy	292	GTGGAATCAAGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTCTCTCGAAGAC	351

QY 1432 CGAGCGCTGGGATGCGAGATTCGAACATGTCATCTCGCTCAAGCTCAAGAACAGGAAG 1491
DB 1690 CGCAGCGCTGGGACGACGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGGAAG 1749
QY 1492 CTGCGCGCGTCTCTCGAGAGATCTGGGACGTCG 1524
DB 1750 CTTCCGCCATCTCTCGAGGAGATCTGGGACGTCG 1782

RESULT 11
US-10-087-167-147
; Sequence 147, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1800)
; OTHER INFORMATION: Ecdysone receptor chimera GV(M)M
US-10-087-167-147

Query Match 70.4%; Score 1073; DB 16; Length 1800;
Best Local Similarity 79.2%; Pred. No. 1.5e-311;
Matches 1404; Conservative 0; Mismatches 120; Indels 249; Gaps 1;

QY 1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATAGCTATTATTGCTGCG 60
DB 1 ATGCAGCAGCTATATGCGATTTTATAGCCCTGCTTCATAGCTATTATTGCTGCG 60
QY 61 TACTGTTCTTTTGTGCGATGCTCACCTGTTGTTGTTGTTACTTCTGCGAGGATCCGCC 120
DB 61 TACTGTTCTTTTGTGCGATGCTCACCTGTTGTTGTTGTTACTTCTGCGAGGATCCGCC 120
QY 121 ACCATGAAGCTACTGTTCTTATCGAAACAGCATGCGATATTTGCGAATTAAAGCTC 180
DB 121 ACCATGAAGCTACTGTTCTTATCGAAACAGCATGCGATATTTGCGAATTAAAGCTC 180
QY 181 AAGTGCTCCAAAGAAACCGAAGTGGCGCAAGTGTGTAAGAACAACTGGGAGTCTCGC 240
DB 181 AAGTGCTCCAAAGAAACCGAAGTGGCGCAAGTGTGTAAGAACAACTGGGAGTCTCGC 240
QY 241 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAATGGAATCA 300
DB 241 TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAATGGAATCA 300
QY 301 AGGCTAGAAAGACTGGAAACAGCTATTCTACTGATTTTCTCGAAGAACCTTGACATG 360
DB 301 AGGCTAGAAAGACTGGAAACAGCTATTCTACTGATTTTCTCGAAGAACCTTGACATG 360
QY 361 ATTTTGAAGATGATTTCTTTACAGGATATTAAGCATTTTAAACAGGATTTTGTACAA 420
DB 361 ATTTTGAAGATGATTTCTTTACAGGATATTAAGCATTTTAAACAGGATTTTGTACAA 420
QY 421 GATAATGTGAATAAGATGCGGTCCACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCT 480
DB 421 GATAATGTGAATAAGATGCGGTCCACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCT 480

QY 481 CTAACATTTGACACAGCATAGATAAGTCCGACATCATCATCGAAGAGAGTAGTAACAAA 540
DB 481 CTAACATTTGACACAGCATAGATAAGTCCGACATCATCATCGAAGAGAGTAGTAACAAA 540
QY 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGGTCTGCCAGATC- 599
DB 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGGTCTGCCAGATC- 600
QY 600 ----- 599
DB 601 ACGTGCAAGCTTGCCCGCCCGACCGATGTACGCTGGGGGACGAGCTCCACTTAGACGCG 660
QY 600 ----- 599
DB 661 GAGGACGTGGCGATGGCGCATGCCGCGCTAGACGATTTTCGATCTCGACATGTTGGGG 720
QY 600 ----- 599
DB 721 GACGGGGATTCCCGGGTCCGGATTTTACCCCCACGACTCCGCCCTTACGGCGCTCTG 780
QY 600 ----- 599
DB 781 GATATGGCCGACTTCGAGTTTGGAGCAGATGTTTACCGATGCCCTTGGAAATTGACAGTAC 840
QY 600 -----CAGTGCAGAAACAAAAGAGAGAAAGGAGGACACAGAGAGAAAGACAAA 651
DB 841 GGTGGGAACACGTGCAGAACAAAGAGAGAGAAAGGAGGACACAGAGAGAAAGACAAA 900
QY 652 CTGCGAGTCAGTACGACACAGTGGACGATCATATGCTGCGCATATGCAATGTGACCT 711
DB 901 CTGCGAGTCAGTACGACACAGTGGACGATCATATGCTGCGCATATGCAATGTGACCT 960
QY 712 CCGCCCCAGAGGCGGCGAAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTA 771
DB 961 CCGCCCCAGAGGCGGCGAAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTA 1020
QY 772 ATGGAGCAGAACAGACTGAAGATGTGACGCGCTGTGCGGCGAACAGAGTCCCTGATC 831
DB 1021 ATGGAGCAGAACAGACTGAAGATGTGACGCGCTGTGCGGCGAACAGAGTCCCTGATC 1080
QY 832 GCGAGGCTGTGTGTACGAGCAGGATACGAGCAGCTTCGGAAGAGAGATCTCAAAAGG 891
DB 1081 GCGAGGCTGTGTGTACGAGCAGGATACGAGCAGCTTCGGAAGAGAGATCTCAAGAGA 1140
QY 892 GTGACGCGACATTTGGCAATCAGCAGTGAAGAGACGAGACTCAGACATGCAATTCGCG 951
DB 1141 GTTACACAGACATGGCAGTTAGAAGAAAGAGAGAGGAGAACTGACATGCCCTTCCGT 1200
QY 952 CAGATCACAGAAATGACCACTCTCACAGTACAGCTAATAGTCCGAGTTTCCCAAAGGCTA 1011
DB 1201 CAGATCACAGATGACGATCTTACAGTGCAGCTTATTTGTAGAAATTCGCAAAGGACTA 1260
QY 1012 CCTGGTTTTTCAAAGATCTCAAACTGACAGATCACAATTAATAAGGATGCTCAAGC 1071
DB 1261 CCGGGATTCTCCAAGATATCTCAGTCCGATCAAAATTAATAAGGCGTCATCAAGC 1320
QY 1072 GAAGTATGATGCTCGAGTACGAGGCGGTACGACGCGGTGTCGAGATGCGTTCGTTTC 1131
DB 1321 GAAGTATGATGCTCGAGTACGAGGCGGTACGACGCGGTGTCGAGATGCGTTCGTTTC 1380
QY 1132 GCCAACAAACAGCGGTACACTCGCGACAACTACCGCAAGCGCGGCACTGGCCTACGTCATC 1191
DB 1381 GCGAACAAACAGCGGTACACTCGCGACAACTACCGCAAGCGCGGCACTGGCCTACGTCATC 1440
QY 1192 GAAGACCTGCTGCACTTCTGCCGTCATGTACTCGATGTGATGACAAAGCGATTTAC 1251
DB 1441 GAGGACCTGCTGCACTTCTGCCGTCATGTACTCGATGTGATGATCTCCATGAGCATGCAATGTCAC 1500
QY 1252 GCGCTCCTCAGTCCCATCGTTATATTTCTCGGATCGGCGCGGCTACGAGCGCCACAGCTA 1311
DB 1501 GCGCTCCTCAGTCCCATCGTTATATTTCTCAGACCGGCGCGGCTTCGAGCAACCCCTTTT 1560

		1312	GTAGAAGAGATCCAGCGGTTATTACCTTGAAACA	C	GCTGGGGTGTACATCATGAACCAGCAC	1371
Qy		1561	GTGGAGAAATTCAGAGATACTACTTGAAGACG	T	CTGGGGTTTTACATTTTAATAATCAGCAC	1620
Dd		1372	AGCGGTGCGCGGTTTCGCCGTCACTACGCNAGAN	T	CTGTCGGTGTCTTACCGAGTTG	1431
Qy		1621	AGCGGTGCGCTCGCTGCGCGGTGCTTGGCAAGAT	T	CTCGCGTGTGACGGAATCTG	1680
Dd		1432	CGGACGTGGGCATGCAAGATTGCAACATGTGCAT	T	CTCGTGAAGCTCAAAGAACAGGAAG	1491
Qy		1681	CGACGTTCGGCAGCGAAGACTCCAACATGTGCAT	T	CTCGTGAAGCTGAAGAACAGGAAA	1740
Dd		1492	CTCGCGCGTTCTGGAGGAGATCTGGACGTG			1524
Qy		1741	CTTCGGCCATTCTTCGAGGAGATCTGGACGTG			1773
Dd						
	RESULT 12					
	US-10-087-167-67					
	; Sequence 67, Application US/10087167					
	; Publication No. US20030154509A1					
	; GENERAL INFORMATION:					
	; APPLICANT: Pascal, Erica					
	; APPLICANT: Valentine, Scott					
	; APPLICANT: Brown, Jeffrey					
	; APPLICANT: Cockrell, Adam					
	; APPLICANT: Johnson, Brian					
	; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS					
	; FILE REFERENCE: 50018A					
	; CURRENT APPLICATION NUMBER: US/10/087,167					
	; PRIOR FILING DATE: 2002-03-01					
	; PRIORITY APPLICATION NUMBER: US 60/242,969					
	; PRIOR FILING DATE: 2000-10-24					
	; NUMBER OF SEQ ID NOS: 148					
	; SOFTWARE: PatentIn version 3.1					
	; SEQ ID NO 67					
	; LENGTH: 1500					
	; TYPE: DNA					
	; ORGANISM: Synthetic construct					
	; FEATURE:					
	; NAME/KEY: CDS					
	; LOCATION: (1)..(1500)					
	; OTHER INFORMATION: Ecdysone Receptor chimera MEV					
	US-10-087-167-67					
		Query Match	62.7%;	Score 955.6;	DB 16;	Length 1500;
		Best Local Similarity	99.6%;	Pred. No. 2.9e-276;		
		Matches 958; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	563	CGACGCGTATGAGCCCCGAGTGCCTGCCAGAGTCCAGAGTCCACGTGCNAGAACAAAGAAGAGAG	622			
Dd	296	CGGTGGGCATGAGGCCCGAGTGCCTGCCAGAGTCCACGTGCNAGAACAAAGAAGAGAG	355			
Qy	623	AANAAGRACACAGAGAAAAAGACAAACTGCCAGTCCAGTACGACGACGACGTGGACGATC	682			
Dd	356	AANAAGRACACAGAGAAAAAGACAAACTGCCAGTCCAGTACGACGACGACGTGGACGATC	415			
Qy	683	ATATGCTCTGCCATATGCAATGTGACCCCTCGCGCCCACGAGCGCGCAAGGATTTCACGAAG	742			
Dd	416	ATATGCTCTGCCATATGCAATGTGACCCCTCGCGCCCACGAGCGCGCAAGGATTTCACGAAG	475			
Qy	743	TGGTCCCAGGTTCTTAACGGAAGAAGCTTAATGGACAGAAACAGATGGAAGATGTGACGC	802			
Dd	476	TGGTCCCAGGTTCTTAACGGAAGAAGCTTAATGGACAGAAACAGATGGAAGATGTGACGC	535			
Qy	803	CGCTGTCCGCGAACACAGAAAGTCCCTGATCGCGAGGCTCGTGTGGTACACGAGACGGATACG	862			
Dd	536	CGCTGTCCGCGAACACAGAAAGTCCCTGATCGCGAGGCTCGTGTGGTACACGAGACGGATACG	595			
Qy	863	AGCAGCCTTCGGAACAGAGGATTCTCAAAAGGGTGAACGAGATTTGGCAATCAGCAGATGAAG	922			
Dd	596	AGCAGCCTTCGGAACAGAGGATTCTCAAAAGGGTGAACGAGATTTGGCAATCAGCAGATGAAG	655			

Query Match 55.7%; Score 848.8; DB 16; Length 1515;
Best Local Similarity 90.9%; Pred. No. 4.1e-244; Indels 15; Gaps 1;
Matches 920; Conservative 0; Mismatches 77;

QY 528 GAGTAGTAAAGAGTCAAGACAGTGTGACTGTATCGACGGGTATGAGCCCGAGTGGCT 587
DB 261 GAAATGTCAAGATCCCGTTGAAGAAGTGTGTAGCGGTGGCATGAGGCCGAGTGGCT 320

QY 588 GTCCACAGTCCAGTGTCAAGAACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
DB 321 GGTGCCAGAACCGATGTGCGCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380

QY 648 CAACTGCGCAGTCACTAGACACAGTGGACCATCATATGCTGCGCATTAATCAATGTGA 707
DB 381 CAACTACAGTGTGAGACACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 440

QY 708 CCTCCGCCCCCAGAGGGCGCAAGGATT-----CAGCAAGTGGTCCCGAG 752
DB 441 TCACACACCCCGAGGCGAGCGAGATTCTGGAATGTTTGCAGCATGAAGTGTCCCGCG 500

QY 753 GTTCTTAACGAGAGAGCTTAATGGAGCAAGACAGTGAAGATGTGAAGCGCTGTGCGC 812
DB 501 GTTCTCTCGGAGAGCTGATGGAGCAGAAATCGGCTGAAGAACATACCCCGCTCACCGC 560

QY 813 GAACCAAGATCCCTGATCGCAGGCTCGTGTGTACCAAGGAGGATACGACAGCCTTC 872
DB 561 CAACCAAGATCCCTGATCGCAGGCTGTGTGTGTACCAAGGAGGATACGACAGCCTTC 620

QY 873 GGAAGAGGATCTCAAAAGGCTGACGAGACATTTGGCAATCAGCAGATGAAGAGAGAGAG 932
DB 621 GGAAGAGGATCTCAAAAGGCTGACGAGACATTTGGCAATCAGCAGATGAAGAGAGAGAG 680

QY 933 CTCAGACATGCCATTCGCGCAGATCAAGAAATGACATCTTCAAGTACAGTAAATAGT 992
DB 681 CTCAGACATGCCATTCGCGCAGATCAAGAAATGACATCTTCAAGTACAGTAAATAGT 740

QY 993 CGAGTTTGCAGAGGCTACCTGTTTTCAGAGATCTCAGACCTGACAGATCAAT 1052
DB 741 CGAGTTTGCAGAGGCTACCTGTTTTCAGAGATCTCAGACCTGACAGATCAAT 800

QY 1053 ATTAAAGGATGCTCAAGGAGTGTATGATGCTGCGAGTAGCGAGCGGTACGACCGGT 1112
DB 801 ATTAAAGGATGCTCAAGGAGTGTATGATGCTGCGAGTAGCGAGCGGTACGACCGGT 860

QY 1113 GTCGATAGCGTTCTGTTCCGCAACAAACAGGCGGTACATCTGCGGACAACTACCGAAGGC 1172
DB 861 GTCGATAGCGTTCTGTTCCGCAACAAACAGGCGGTACATCTGCGGACAACTACCGAAGGC 920

QY 1173 GGCATGGCTAGCTCATCGAAGACCTGTGCACTTCTGCGCTGCTGCTGCTGCTGCTGCTG 1232
DB 921 GGCATGGCTAGCTCATCGAAGACCTGTGCACTTCTGCGCTGCTGCTGCTGCTGCTGCTG 980

QY 1233 GATGGACACGTCATTAACGCGTCTCTACTGCGATCGTTATATTTCTCGGATCGGCGGG 1292
DB 981 GATGGACACGTCATTAACGCGTCTCTACTGCGATCGTTATATTTCTCGGATCGGCGGG 1040

QY 1293 CCTAGAGCAGCCACAGCTAGTAGAAGATCCAGCGGTATTAACCTGAACACGCTGCGGGT 1352
DB 1041 CCTAGAGCAGCCACAGCTAGTAGAAGATCCAGCGGTATTAACCTGAACACGCTGCGGGT 1100

QY 1353 GTACATCATGAACAGACAGCGGCTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGT 1412
DB 1101 GTACATCATGAACAGACAGCGGCTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGT 1160

QY 1413 GTCGGTCTTACCGAGTTGCGGAGCTGGGCGATGAGAAATTCAGAAATGTGCAATCTCGCT 1472
DB 1161 GTCGGTCTTACCGAGTTGCGGAGCTGGGCGATGAGAAATTCAGAAATGTGCAATCTCGCT 1220

QY 1473 GAAGCTCAAGAACAGGAGCTGCGCGGTTCTTGGAGGAGATCTGGAGCGTG 1524
DB 1221 GAAGCTCAAGAACAGGAGCTGCGCGGTTCTTGGAGGAGATCTGGAGCGTG 1272

RESULT 14

US-10-295-370-1
; Sequence 1, Application US/10295370
; Publication No. US2003008890A1
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garnaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/10/295,370
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/393,839
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Ostrinia nubilalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (368)..(2005)
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence and deduced amino acid
; OTHER INFORMATION: sequence of Ecdysone receptor
US-10-295-370-1

Query Match 54.9%; Score 836; DB 14; Length 2126;
Best Local Similarity 90.1%; Pred. No. 3.6e-240;
Matches 912; Conservative 0; Mismatches 85; Indels 15; Gaps 1;

QY 528 GAGTAGTAAAGAGTCAAGACAGTGTGACTGTATCGACGGGTATGAGCCCGAGTGGCT 587
DB 940 GAAATGTCAAGATCCCGTTGAAGAAGTGTGTAGCGGTGGCATGAGGCCGAGTGGCT 999

QY 588 CQTCCAGAGTCCACGTGCAAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
DB 1000 GGTGCGAGAACGAGTGTGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059

QY 648 CAACTGCGCAGTCACTAGACACAGTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 707
DB 1060 CAACTGCGCAGTCACTAGACACAGTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 1119

QY 708 CCTCCGCCCCCAGAGGGCGCAAGGATT-----CAGCAAGTGGTCCCGAG 752
DB 1120 TCCGCCACCCCGAGGCGCAGGAGTCTGGAATGTTTGCAGCATGAAGTGTGCTCCGCG 1179

QY 753 GTTCTTAACGAGAGAGCTAAATGGAGCAGAACAGACTGAAGAAATGTGACCGCGCTGTCCGC 812
DB 1180 GTTCTTCTCGAGAGAGCTGATGGAGCAGAAATCGGTTGAAGAACATACCCCGCTCACCGC 1239

QY 813 GAAACCAAGATCCCTGATCGCAGGCTCGTGTGTTACCAAGGAGGATACGAGCAGCCTTC 872
DB 1240 CAAACCAAGATCCCTGATCGCAGGCTCGTGTGTTACCAAGGAGGATACGAGCAGCCTTC 1299

QY 873 GGAAGAGGATCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGAGAGAGAG 932
DB 1300 GGAAGAGGATCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGAGAGAGAG 1359

QY 933 CTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCTCACAGTACAGCTAATAGT 992
DB 1360 CTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCTCACAGTACAGCTAATAGT 1419

QY 993 CGAGTTTGCAGAGGCTACCTGTTTTCAGAAATCTCAAACTGACAGATCACAT 1052
DB 1420 CGAGTTTGCAGAGGCTACCTGTTTTCAGAAATCTCAAACTGACAGATCACAT 1479

QY 1053 ATTAAAGGATGCTCAAGGAGTGTATGATGCTGCGAGTAGCGGCGGTACGACCGGT 1112
DB 1480 ATTAAAGGATGCTCAAGGAGTGTATGATGCTGCGAGTAGCGGCGGTACGACCGGT 1539

1113	GT	CGGATAGCGTTCTGTTCCGCCAACAACAGGCGGTACACTCGCGACNACTACCGCAAGGC	1172
1540	GT	CGGATAGCGTTCTGTTCCGCCAACAACAGGCGGTACACTCGCGACNACTACCGCAAGGC	1599
1173	GG	CATGGCCCTACGTCTCATCGAAGACCTGCTGCACTTCTGCGCTGCAATGACTCGATGTC	1232
1600	GGG	CATGGCGTAGCTCATCGAGACCTGCTGCACTTCTGCGCTGCAATGACTCGATGTC	1659
1233	GAT	GGCAACCGTGCATTACCGCGCTCCTCACTGCCATCGTTATATTCTCGGATCGGCGGG	1292
1660	GAT	GGAACAACGTGCAATTACGCGCTCCTCACTGCCATCGTTATATTCTCGGATCGGCGGG	1719
1293	CCT	AGACGACGCAACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACAACGCTCGGGT	1352
1720	CCT	AGACGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACAACGCTCGGGT	1779
1353	GT	ATCATATGAACACAGACACGCGCTGCGCGCTGGCGGTATCTATCTACGCGAAGATTCT	1412
1780	GT	ATCATATGAACACAGACACGCGCTGCGCGGTATCTATCTACGCGAAGATTCT	1839
1413	GT	CGGTGCTTTACCGAGTTGCGGACGCTGGGCGATGCGAATTCGAACAATGTGCATCTCGCT	1472
1840	GT	CGGTGCTTTACCGAGTTGCGGACGCTGGGCGATGCGAATTCGAACAATGTGCATCTCGCT	1899
1473	GA	AGCTCAAGAAACAGGAAGCTGCGCGCTTCTCTGGAGGAGATCTGGGACGTG	1524
1900	GA	AGCTCAAGAAACAGGAAGCTGCGCGCTTCTCTGGAGGAGATTTGGGACGTG	1951

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RESULT 15
US-10-292-356-1
; Sequence 1, Application US/10292356
; Publication No. US20030110528A1
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garmaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/10/292,356
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/393,839
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Ostrinia nubilalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (368)..(2005)
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence and deduced amino acid
; OTHER INFORMATION: sequence of Ecdysone receptor
US-10-292-356-1

```

Query Match	54.9%	Score 836;	DB 15;	Length 2126;
Best Local Similarity	90.1%	Pred. No. 3.6e-240;		
Matches 912; Conservative	0;	Mismatches 85;	Indels 15;	Gaps 1;

Qy	528	GAGTAGTAACAAGGTCNAAGACAGAGTTGA	CTGTATCGACGGTATGAGGCCCGAGTCGCT	587
Db	940	GAATGTCAAGAAATGCCGGTTGAAGAAGTGT	TTTAGCGGTGGCGATGAGGCCCGAGTCGCT	999
Qy	588	CGTCCCAGAGTCCACGTGCAGAACAAAGAG	AGAAAGAAAGAACGACACAGAGAAAAAGA	647
Db	1,000	GGTGCCAGAAACGCAAGTGTGCGCAAAAG	AGAAAGAAAGAACGACACAGAGAAAAAGA	1,059
Qy	648	CAAACTGCCAGTCAGTAGCAGCAGATGGAC	CGATCATATGCTGCCCATATGCAATGTGA	707
Db	1060	CAAACTACCTGAGACCAACGACAGTAGAGAT	GCATATGCCCCCAATCATGCAAGTGTGA	1,119

Qy	708	CCCTCCGCCCCCAGAGCGCGCAAGATT-----CAGCAAGTGTCCCGAG	752
Db	1120	TCGCGCACCCCGGAGCGACGAGATTCGGAATGTTTGCAGCATGAAGTGTGCCGCG	1179
Qy	753	GTTCTCTAACGGAGAGCTAATGAGCAGAAACACATGAAGAAATGTGACGCGCTGTCCGG	812
Db	1180	GTTCTCTTCGGAGAGCTGATGAGCAGAGATCGGTTGAGNAATATACCCCCCTCACCGC	1239
Qy	813	GAACCAAGAGTCCCTGATCCGCGAGGCTCGTGTACCAAGGA CGGATACAGAGACGCTTC	872
Db	1240	CAACCAAGCTTCTCTGATCCGAGGCTGTGTGTACCAAGGACGGATACAGAGCGCTTC	1299
Qy	873	GGAAAGGAGTCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAAGCAAGA	932
Db	1300	GGAAAGGAGTCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAAGCAAGA	1359
Qy	933	CTCAGACATGCCATTTCGCGCCAGATCAAGAAAATGACCATCCTCACAGTACAGCTAATAGT	992
Db	1360	CTCAGACATGCCATTTCGCGCCAGATCAAGAAAATGACCATCCTCACAGTACAGCTAATAGT	1419
Qy	993	CGAGTTTGCACAAAGGCGCTACCTGGTTTTTCAAGAATCTCAACAACCTGACCAGATCACATT	1052
Db	1420	CGAGTTTGCACAAAGGCGCTACCTGGTTTTTCAAGAATCTCAACAACCTGACCAGATCACATT	1479
Qy	1053	ATTAAGGCATGCTCAAGCGAAGTGATGCTCGAGTAGCAGAGGCGGTACGACGCGGT	1112
Db	1480	ATTAAGGCATGCTCAAGCGAAGTGATGCTCGAGTAGCAGAGGCGGTACGACGCGGT	1539
Qy	1113	GTCCGATAGCGTTCTGTTCGCCAACCAACAGGCGGTACACTCGGACAACTACCGCAAGGC	1172
Db	1540	GTCCGATAGCGTTCTGTTCGCCAACCAACAGGCGGTACACTCGGACAACTACCGCAAGGC	1599
Qy	1173	GGGCATGGCGCTACGTCAATCGAAGACTGCTGCACTTCTGCGCGTGCATGTACTCGATGTC	1232
Db	1600	GGGCATGGCGCTACGTCAATCGAAGACTGCTGCACTTCTGCGCGTGCATGTACTCGATGTC	1659
Qy	1233	GATCGCAACGTCGATTACGCGCTCCTCACTGCCATCGTTATATTCTCGGATCGGCGCGG	1292
Db	1660	GATCGCAACGTCGATTACGCGCTCCTCACTGCCATCGTTATATTCTCGGATCGGCGCGG	1719
Qy	1293	CCTAGACGAGCCACAGCTAGTAGAAGAGATCCAGCGGTAATTACTGGAACAGCTGCGCGGT	1352
Db	1720	CCTAGACGAGCCACAGCTAGTAGAAGAGATCCAGCGGTAATTACTGGAACAGCTGCGCGGT	1779
Qy	1353	GTACATCATGNAACAGCACAGCGGTCGCGCGTTCGCGCTCATCTACCGGAAGATTCT	1412
Db	1780	GTACATCATGNAACAGCACAGCGGTCGCGCGTTCGCGCTCATCTACCGGAAGATTCT	1839
Qy	1413	GTCGGTGTCTTACCGAGTTGCGGACGCTGGGCGATCGAGAAATTCGAACATGTGCATCTCGCT	1472
Db	1840	GTCGGTGTCTTACCGAGTTGCGGACGCTGGGCGATCGAGAAATTCGAACATGTGCATCTCGCT	1899
Qy	1473	GAAGCTCAAGAACAAGGAGCTGCGCGGTTCTCTGGAGAGATCTGGGACGTG	1524
Db	1900	GAAGCTCAAGAACAAGGAGCTGCGCGGTTCTCTGGAGAGATCTGGGACGTG	1951

Search completed: April 14, 2005, 19:22:31
Job time : 922.505 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 09:56:57 ; Search time 7226.52 Seconds
(without alignments)
11144.035 Million cell updates/sec

Title: US-10-087-167-104_COPY_2007_3668
Perfect score: 1662
Sequence: 1 atgaagctactgtcttctat.....ttgacgagtagcgtgggttag 1662

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_ey.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1662	100.0	3972	6	AX555352 Sequence
2	1612.8	97.0	1767	6	AX555370 Sequence
3	1552.2	93.4	1800	6	AX555374 Sequence
4	1441.6	86.7	1776	6	AX555366 Sequence
5	1431.8	86.1	1863	6	AX555384 Sequence
6	1426.6	85.8	1848	6	AX555382 Sequence
7	1425	85.7	1428	6	AX555376 Sequence
8	1424	85.7	1767	6	AX555368 Sequence
9	1422	85.6	1809	6	AX555390 Sequence
10	1314.2	79.1	1782	6	AX555372 Sequence
11	1316.6	73.2	1518	6	AX555341 Sequence
12	1167.4	70.2	1500	6	AX555317 Sequence
13	1166	70.2	1800	6	AX555395 Sequence
14	1109.8	66.8	1533	6	AX555327 Sequence
15	996.2	59.9	1509	6	AX555313 Sequence
16	978.6	58.9	1500	6	AX555315 Sequence
17	976.6	58.8	2840	3	MSU19812
18	976.6	58.8	2840	6	AX555249 Sequence
19	954.6	57.4	1551	6	AX555319 Sequence

20	954.6	57.4	1566	6	AX555337	Sequence
21	951.8	57.3	1464	6	AX555331	Sequence
22	899.4	53.5	1524	6	AX555325	Sequence
23	871.8	52.5	1515	6	AX555323	Sequence
24	831.6	50.0	838	6	AX555255	Sequence
25	799.8	48.1	1506	6	AX555311	Sequence
26	760.2	45.7	1503	6	AX555339	Sequence
27	734.2	44.2	1542	6	AX555321	Sequence
28	715	43.0	1491	6	AX555333	Sequence
29	683.6	41.1	1017	3	PCO251809	Novel ecd
30	681	41.0	2126	6	BD224646	Novel ecd
31	681	41.0	2126	6	AR274109	Sequence
32	673.4	40.5	6083	3	AY485269	Sequence
33	660.4	39.7	1934	6	A59201	Sequence
34	660.4	39.7	1934	6	AR207904	Sequence
35	660.4	39.7	1934	6	AR383195	Sequence
36	660.4	39.7	1934	6	AR383244	Sequence
37	660.4	39.7	2464	6	A59202	Sequence
38	660.4	39.7	2464	6	AR207905	Sequence
39	660.4	39.7	2464	6	AR383196	Sequence
40	660.4	39.7	2464	6	AR383245	Sequence
41	660.4	39.7	2745	3	HVECR	H.virescens
42	660.4	39.7	2745	6	A59203	Sequence
43	660.4	39.7	2745	6	AR207906	Sequence
44	660.4	39.7	2745	6	AR383197	Sequence
45	657.6	39.6	2463	6	AR207910	Sequence

ALIGNMENTS

RESULT 1
AX555352
LOCUS AX555352 3972 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 104 from Patent WO02061102.
ACCESSION AX555352
VERSION AX555352.1 GI:25898871
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 104 08-AUG-2002;
Syngenta Participations AG (CH)
FEATURES
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CDS 2007..3668
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ORIGIN

Query Match 100.0%; Score 1662; DB 6; Length 3972; Best Local Similarity 100.0%; Pred. No. 0; Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	2007	ATGAAGCTACTGTTCTTCTATCGAACAGCATGCCGATATTTCCGACCTTAAAGACTCAAG	2066						
QY	61	TGCTCCAAAGAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGCCTAC	120						
DB	2067	TGCTCCAAAGAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGCCTAC	2126						
QY	121	TCTCCAAACCAAAAGTCTCGGTGACTAGGGCACAATCTGACAGAAGTGGATCAAGG	180						
DB	2127	TCTCCAAACCAAAAGTCTCGGTGACTAGGGCACAATCTGACAGAAGTGGATCAAGG	2186						
QY	181	CTAGAAGACTGGACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT	240						
DB	2187	CTAGAAGACTGGACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT	2246						
QY	241	TTGAAAATGGATTCTTTACAGGATATAAAGCATTTGTTAACAGGATTTTGTACAAGAT	300						
DB	2247	TTGAAAATGGATTCTTTACAGGATATAAAGCATTTGTTAACAGGATTTTGTACAAGAT	2306						
QY	301	AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGCTGATATGCTCTTA	360						
DB	2307	AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGCTGATATGCTCTTA	2366						
QY	361	ACATTTGAGACACATAGATAAGTGGACATCATCTCGGAAGAGAGTAGTAACAAGGT	420						
DB	2367	ACATTTGAGACACATAGATAAGTGGACATCATCTCGGAAGAGAGTAGTAACAAGGT	2426						
QY	421	CAAAGA CAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTCTGCCAGAGTCCACG	480						
DB	2427	CAAAGA CAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTCTGCCAGAGTCCACG	2486						
QY	481	TGCAGAA CAAAGAGAGAAAGAGACAGACAGAGAGAGAAACAACTGCCAGTCAGT	540						
DB	2487	TGCAGAA CAAAGAGAGAAAGAGACAGACAGAGAGAGAAACAACTGCCAGTCAGT	2546						
QY	541	ACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCACAG	600						
DB	2547	ACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCACAG	2606						
QY	601	GCGGCAAGGATTCA CGAAGTGTGCCGAGGTTCTTAA CGGAGAGACTAATGAGCAGAAC	660						
DB	2607	GCGGCAAGGATTCA CGAAGTGTGCCGAGGTTCTTAA CGGAGAGACTAATGAGCAGAAC	2666						
QY	661	AGACTCAAGATGTGACGCGCTGTGCGGAAACCGAAGTCCCTGATCCGAGGCTCGTG	720						
DB	2667	AGACTCAAGATGTGACGCGCTGTGCGGAAACCGAAGTCCCTGATCCGAGGCTCGTG	2726						
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DB	2727	TGTTACCAAGAGGGGTACGAGCAGCCGTCCGAGGAAGATCTCAAGAGAGTTACAGACA	2786						
QY	781	TGCGAGTTAGAACAGAGAGAGAGAACTGACATGCCCTTCGTCAGATCAACAG	840						
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QY	901	AAGATATCTCAGTCCGATCAAAATTA CATTATTAAGGGGTCTCAAGCGAAGTGTATG	960						
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QY	961	CTGGAGTGGCGGACGGTACGACGGCGGACGAGCGGTGCTGTTCCGAAACACACAG	1020						
DB	2967	CTGGAGTGGCGGACGGTACGACGGCGGACGAGCGGTGCTGTTCCGAAACACACAG	3026						
QY	1021	CGGTACACGCGGACAACTACCGCAAGCGGGGCGATGTCTTACGTATCAGGACCTGGCTG	1080						

Db	3027	GGGTACACGGCGGACAACTACCGAAGCGGCGATGTCTCTACGTCACTCAGGACCTGCTG	3086						
QY	1081	CACCTCTGCGGTGTATGTACTCCATGACATGGACAATGTGCATACCGGCTGCTCACC	1140						
Db	3087	CACCTCTGCGGTGTATGTACTCCATGACATGGACAATGTGCATACCGGCTGCTCACC	3146						
QY	1141	GCATCGTTATATTTCTCAGACCGGCGGAGCCCTCGAGCAACCCCTTTTAGTGAGGAAATC	1200						
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Db	3207	CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCACAGCGGCTGCCT	3266						
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QY	1381	CTCAGAGAGATCTGGGACGCTGGCCAGTGTGACGACGAGCTTGGCCCCCGACCGAT	1440						
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QY	1441	GTACGCTGGGGACGAGCTCCACTTAGACGGCGAGACGCTGGCGCATGGCGCATGCCGAC	1500						
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QY	1501	GGCTAGACCATTTCCGATCTGGACATGTTGGGGGACGGGGATTTCCCGGGTCCGGGATTT	1560						
Db	3507	GGCTAGACCATTTCCGATCTGGACATGTTGGGGGACGGGGATTTCCCGGGTCCGGGATTT	3566						
QY	1561	ACCCCCACAGCTCCGCCCCCTACGGGCTCTGGATATGGCGACTTCCGATTTGACGAG	1620						
Db	3567	ACCCCCACAGCTCCGCCCCCTACGGGCTCTGGATATGGCGACTTCCGATTTGACGAG	3626						
QY	1621	ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGGTAG	1662						
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RESULT 2	AX555370	Sequence 122 from Patent WO02061102.	1767 bp	DNA	linear	PAT 27-NOV-2002
LOCUS	AX555370	Sequence 122 from Patent WO02061102.				
DEFINITION	AX555370					
ACCESSION	AX555370					
VERSION	AX555370.1	GI:25898889				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE	1	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.				
AUTHORS		Control of gene expression in plants				
TITLE		Patent: WO 02061102-A 122 08-AUG-2002;				
JOURNAL		Syngenta Participations AG (CH)				
FEATURES		Location/Qualifiers				
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ORIGIN

Query Match 97.0%; Score 1612.8; DB 6; Length 1767;
 Best Local Similarity 98.8%; Pred No. 0;
 Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;

QY 1 ATGAAGCTACTGTCTTCTTATCGAACAGCATGCGATATTTCCGACTTTAAAAAGCTCAAG 60
 DB 124 ATGAAGCTACTGTCTTCTTATCGAACAGCATGCGATATTTCCGACTTTAAAAAGCTCAAG 183

QY 61 TGCTCCAAAGAAAACCGAAGTGCAGGCTGCTGAAGAACTGCGAGTGCCTAC 120
 DB 184 TGCTCCAAAGAAAACCGAAGTGCAGGCTGCTGAAGAACTGCGAGTGCCTAC 243

QY 121 TCTCCAAAACCAAAAGGTCCTCGTACTAGGCGACATCTGACAGAAAGTGAATCAAGG 180
 DB 244 TCTCCAAAACCAAAAGGTCCTCGTACTAGGCGACATCTGACAGAAAGTGAATCAAGG 303

QY 181 CTGAAAAGACTGGAACAGCTATTTCTACTGATTTTTCTCGAAGAACCTTGACATGATT 240
 DB 304 CTGAAAAGACTGGAACAGCTATTTCTACTGATTTTTCTCGAAGAACCTTGACATGATT 363

QY 241 TTGAAAATGGAATCTTTACAGATATAAAGCAATTTGTTAAACAGGATTTTGTACAAAT 300
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QY 301 ATGTGTAATAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
 DB 424 ATGTGTAATAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483

QY 361 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAGAGAGTAGTAACAAAGGT 420
 DB 484 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAGAGAGTAGTAACAAAGGT 543

QY 421 CAAAGACAGTTGATGATGCGGCTATGAGCCCGAGTGGTGTCCACAGTCCAGC 480
 DB 544 CAAAGACAGTTGATGATGCGGCTATGAGCCCGAGTGGTGTCCACAGTCCAGC 603

QY 481 TGCAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAACTGCGAGTCAGT 540
 DB 604 TGCAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAGAAAGACAACTGCGAGTCAGT 663

QY 541 ACGACAGATGACAGCATATGCTGCGCATAATGCAATGTGACCTCCGCCCCCAGAG 600
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QY 601 GCGGCAAGGATTCAGAAAGTGTCCGAGGTTCTTAACCGGAGAGCTTAATGAGAGCAGAC 660
 DB 724 GCGGCAAGGATTCAGAAAGTGTCCGAGGTTCTTAACCGGAGAGCTTAATGAGAGCAGAC 783

QY 661 AGACTGAAGATGTGACCGCTGTCGCGCAGAACCAAGTCCCTGATCGCGAGGTCG 720
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DB 964 ATGACGATCTTAAACAGTGCAGCTTATTTGTAGAAATTCGAAAGGAGCTACCGGGATTTCTCC 1023

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DB 1024 AAGATATCTCAGTCCGATCAAAATTTACATATTTAAAGCGCTCATCAAGCGAAGTGTATGATG 1083

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DB 1204 CACTTCTGTCGCTGATGTACTCCATGAGCATGAGCAATGTGCACTACGCGCTGCTCAACC 1263

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DB 1264 GCCATCGTTATATTTCTCAGACCGCGCGAGCTTCGAGCAACCCCTTTTATGTGAGGAAATC 1323

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DB 1324 CAGAGATATACTTTGAAGACGCTCGGGGTTTACATTTTAAATCAGACAGCGCTGCGCT 1383

QY 1261 CGCTCGCGCGGCTGTTCCGCAAGATCTCGCGCTGCTGACGGAACCTCGCACGCTCGGC 1320

DB 1384 CGCTCGCGCGGCTGTTCCGCAAGATCTCGCGCTGCTGACGGAACCTCGCACGCTCGGC 1443

QY 1321 ACGCAGAACTCCAAACATGTGCTATCTGCTGAAGCTGAAGAAACAGGAAATTTCCGCAATC 1380

DB 1444 ACGCAGAACTCCAAACATGTGCTATCTGCTGAAGCTGAAGAAACAGGAAATTTCCGCAATC 1503

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DB 1504 CTCGAGGAGATCTCGGACGCTGCGGCAAGTGTGACGAGCAAGCTTGCCTCCCGGACCGAT 1545

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QY 1501 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGACGCGGATTTCCCGGGTCCGGGATTT 1560

DB 1606 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGACGCGGATTTCCCGGGTCCGGGATTT 1665

QY 1561 ACCCGCCACGACTCGCGCCCTTACGCGCTCTGAGATGCGCGACTTCGAGTTTTCGAGCAG 1620

DB 1666 ACCCGCCACGACTCGCGCCCTTACGCGCTCTGAGATGCGCGACTTCGAGTTTTCGAGCAG 1725

QY 1621 ATGTTTACGATGCGCTTGGAAATTCACGAGTACGCTGGGTAG 1662

DB 1726 ATGTTTACGATGCGCTTGGAAATTCACGAGTACGCTGGGTAG 1767

RESULT 3

AX555374 LOCUS 1800 bp DNA linear PAT 27-NOV-2002
 DEFINITION Sequence 126 from Patent WO02061102.
 ACCESSION AX555374
 VERSION AX555374.1 GI:25898893
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.
 TITLE Control of gene expression in plants
 JOURNAL Patent: WO 02061102-A 126 08-AUG-2002;
 Syngenta Participations AG (CH)
 FEATURES Location/Qualifiers

VERSION	AX555366.1	GI:25898885	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 118 08-AUG-2002;		
	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
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ORIGIN	Query Match 86.7%; Score 1441.6; DB 6; Length 1776;		
	Best Local Similarity 92.6%; Pred. No. 3.7e-297;		
	Matches 1539; Conservative 0; Mismatches 114; Indels 9; Gaps 2;		
QY	1	ATGAAGCTACTGTCTTCTATCGAACAAGCATGCGATATTTCGCGACTTAAAGAGCTCAAG	60
DB	124	ATGAAGCTACTGTCTTCTATCGAACAAGCATGCGATATTTCGCGACTTAAAGAGCTCAAG	183
QY	61	TGCTCCAAAGAAAACCGAAGTCGCGAAGTGTCTCGAAGAACAACTGGGAGTGTCCCTAC	120
DB	184	TGCTCCAAAGAAAACCGAAGTCGCGAAGTGTCTCGAAGAACAACTGGGAGTGTCCCTAC	243
QY	121	TCCTCCAAAGAAAACCGAAGTGTCTCGAAGTGTCTCGAAGAACAACTGGGAGTGTCCCTAC	180
DB	244	TCCTCCAAAGAAAACCGAAGTGTCTCGAAGTGTCTCGAAGAACAACTGGGAGTGTCCCTAC	303
QY	181	CTAGAAGAGTGGAAACAGCTATTCTTACTGATTTTCTCGAAGAACCTTGAATGATTT	240
DB	304	CTAGAAGAGTGGAAACAGCTATTCTTACTGATTTTCTCGAAGAACCTTGAATGATTT	363
QY	241	TTGAAAATGATTTCTTACAGGATATAAAGCATTTGTTAAACAGATATTGTTACAGAT	300
DB	364	TTGAAAATGATTTCTTACAGGATATAAAGCATTTGTTAAACAGATATTGTTACAGAT	423
QY	301	AATGTGAATAAGATCGCGTACAGATAGATTGCGTTTCAGTGGAGACTGATATGCGCTCTA	360
DB	424	AATGTGAATAAGATCGCGTACAGATAGATTGCGTTTCAGTGGAGACTGATATGCGCTCTA	483
QY	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAAACAAGGT	420
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DB	544	CAAAGACAGTTGATGTATCGACCGTATGAGGCCCGAGTGCCTGCCAGAGTCCACG	603
QY	481	TGCAGNACAAAGAGAAAAGGAGACAGAGAGAAAAGACAAACTGCCAGTCAGT	540

DB	604	TGCAAGAACAAAAGAGAAAAGAACGACACAGAGAGAAAAGACAAACTGCGAGTCAAGT	663
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DB	664	ACGACGACAGTGGACGATCATATGCTGCTCCATATATGCAATGTGACCTCCGCCCCCAGAG	723
QY	601	CGCGCAAGGATTACAGAAAGTGTGTCGAGGTTCTTAACGGAGAAAGCTAATGAGAGAGAAC	660
DB	724	CGCGCAAGGATTACAGAAAGTGTGTCGAGGTTCTTAACGGAGAAAGCTAATGAGAGAGAAC	783
QY	661	AGACTGAAGAATGTGACCGCTGTGCGGACCAAGAGTCCCTGATCGCGAGGCTCGTG	720
DB	784	AGACTGAAGAATGTGACCGCTGTGCGGACCAAGAGTCCCTGATCGCGAGGCTCGTG	843
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QY	781	TGGCAGTTAGAAAGAAAGAGAGAGGAAACTGACATGCCCTTCCGTGAGATCAACAGAG	840
DB	904	TGGCAGTTAGAAAGAAAGAGAGGAGGAG--TCAGATATGCCGTTCCGCCAGATCAACGAG	960
QY	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGAAATTCGCAAGGAGTACCGGGATCTTCC	900
DB	961	ATGACGATCTTAAACAGTGCAGCTTATTGTAGAAATTCGCAAGGAGTACCGGGATCTTCC	1020
QY	901	RAGATATCTCAGTCCGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	960
DB	1021	AAAGTCTCGAGTCCGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1080
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QY	1021	GGGTACACGCGGCAAACTACCGCAAGGCGGCGATGTCTAGTCTATCGAGGACCTGCTG	1080
DB	1141	GGGTACTCCGCGCAAACTACCGCAAGGCGGCGATGTCTAGTCTATCGAGGACCTGCTG	1200
QY	1081	CACTTCTGCGGTGTATGTACTTCCATGAGCATGGAACAATGTGCACTACGCGTGTCTCACC	1140
DB	1201	CACTTCTGCGGTGTATGTACTTCCATGAGCATGGAACAATGTGCACTACGCGTGTCTCACC	1260
QY	1141	GCCATCTGTATATTTCTCAGACCGCGGCGGCTCGAGCAACCCCTTTTCTAGTGGAGGAAATC	1200
DB	1261	GCCATCTGTATATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTCTAGTGGAGGAAATC	1320
QY	1201	CAGAGATACCTTGAAGACGCTGCGGTTTACATTTTAATTCAGACACAGCGGCTGCGCT	1260
DB	1321	CAGCGGTATTACCTGAACACGCTGCGGTTTACATTTTAATTCAGACACAGCGGCTGCGCT	1380
QY	1261	CGCTGGCGGTCTGTGCGCAAGATCTCGCGGCTCGACGGAATCGCGACGCTCGGC	1320
DB	1381	CGCTGGCGGTCTGTGCGCAAGATCTCGCGGCTCGACGGAATCGCGACGCTCGGC	1440
QY	1321	ACGCGAAGTCCAAACATGTGATCTCGCTGAAGAGTGAAGAACAGGAAACTTCGCGCAATTC	1380
DB	1441	ATGCGAAGTCCAAACATGTGATCTCGCTGAAGAGTGAAGAACAGGAAACTTCGCGCAATTC	1500
QY	1381	CTCGAGGAGATCTGGGACGCTGCGCGGATTCGACGACGAAAGCTTCCGCGCGGATTC	1440
DB	1501	CTCGAGGAGATCTGGGACGCTGCGCGGATTCGACGACGAAAGCTTCCGCGCGGATTC	1554
QY	1441	GTGCGCTGGGAGACGAGTCCACTTAGACGCGGAGGAGTGGCGATGCGGATGCGGAC	1500
DB	1555	GTGCGCTGGGAGACGAGTCCACTTAGACGCGGAGGAGTGGCGATGCGGATGCGGAC	1614
QY	1501	GGCTAGACGATTTCCATCTGACACATGTTGGGGAGCGGGATTTCCCGCGGATTCGCGGATTT	1560
DB	1615	GGCTAGACGATTTCCATCTGACACATGTTGGGGAGCGGGATTTCCCGCGGATTCGCGGATTT	1674
QY	1561	ACCCCCACGACTCCCGCGCTTACCGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG	1620

Db	1675	ACCCCCACGACTCGCGCCCTACGGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG	1734
Qy	1621	ATGTTTACCGATGCCCTTTGGAATTGACGAGTACGGTGGGTAG	1662
Db	1735	ATGTTTACCGATGCCCTTTGGAATTGACGAGTACGGTGGGTAG	1776
RESULT 5			
AX555384			
LOCUS	AX555384	1863 bp	DNA linear PAT 27-NOV-2002
DEFINITION	Sequence 136 from Patent WO02061102.		
ACCESSION	AX555384		
VERSION	AX555384.1	GI:25898903	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 136 08-AUG-2002;		
	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
source	1..1863		
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	/db_xref="taxon:32630"		
CDS	1..1863		
	/note="unnamed protein product; Ecdysone receptor chimera G(M)MD"		
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	/db_xref="GI:25898904"		
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ORIGIN			
Query Match	86.1%; Score 1431.6; DB 6; Length 1863;		
Best Local Similarity	99.2%; Pred. No. 4.6e-295;		
Matches 1439; Conservative	0; Mismatches 12; Indels 0; Gaps 0;		
Qy	1	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTTGGCGACTTAAAGCTCAAG	60
Db	124	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTTGGCGACTTAAAGCTCAAG	183
Qy	61	TGCTCCAAAGAAAACCGAAGTCCGCAAGTGCTGGAACAACACTGGGAGTGCCTAC	120
Db	184	TGCTCCAAAGAAAACCGAAGTCCGCAAGTGCTGGAACAACACTGGGAGTGCCTAC	243
Qy	121	TCCTCCAAACCAAAAGGCTCCGCTGACTAGGGCACAATCTGACAGAAGTGGAAATCAAGG	180
Db	244	TCCTCCAAACCAAAAGGCTCCGCTGACTAGGGCACAATCTGACAGAAGTGGAAATCAAGG	303
Qy	181	CTAGAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTGCATGATT	240
Db	304	CTAGAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTGCATGATT	363
Qy	241	TTGAAAATGGATTTCTTTACAGGATATAAAGCATTGTTAAACAGGATTTTGTGACAGAT	300
Db	364	TTGAAAATGGATTTCTTTACAGGATATAAAGCATTGTTAAACAGGATTTTGTGACAGAT	423
Qy	301	AATGTGAATAAGATGCGCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCTCTA	360

Db	1504	CTCAGGAGATCTTGGGAGCTGGCGGAGTTCGACGAGGAGCTT-----CCCAAGGCC	1557
Qy	1441	GTCAGCCTGGGGAGACAGCTCCACTTAGACGGCGAGGAGCTGGCGCATGCCGAC	1500
Db	1558	GTGCGGTCCACGGGGGAGCTCTCTCTTCACCGGACACGACGCGCGGCGGCGGC	1617
Qy	1501	GCG 1503	
Db	1618	GAG 1620	
RESULT 7			
AX555376		1428 bp	DNA
LOCUS		Sequence 128 from Patent WO02061102.	linear
DEFINITION		AX555376	PAT 27-NOV-2002
ACCESSION		AX555376	
VERSION		AX555376.1	GI:25898895
KEYWORDS			
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE			
AUTHORS		1	
TITLE		Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and	
JOURNAL		Johnson, B.D.	
FEATURES		Control of gene expression in plants	
source		Patent: WO 02061102-A 128 08-AUG-2002;	
		Syngenta Participations AG (CH)	
		Location/Qualifiers	
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		Domain fused to the Manduca Ecr Hinge and Ligand Binding	
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		NKDAVDRLASVETDMPDLRHRISATSSSESSNKGOROLTVSTRMRPCVPEST	
		CKNKRREKAQREKDLPSVTYVDHMPALWQCDPPPEARLHVVPRELTKEKME	
		QNRKLVTPLSANQSLRLARLVWYQEGFEQSEEDLKVYQTWQLEEESEETDMPR	
		QITEMTILTVQIVFAGLPGFSKISQSDQITLLKSSSEVMMLRVARRIDAAITDV	
		LFANQAVTRDNRKAGMSYVIEDLLHFRCRMYSMDNVHYALLTAIVIFSDRPLG	
		QPLLVEEIORYLKLRLVYILNQHSAPRCVLFGLKILGLVLTFLTLGTONSNMCISL	
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ORIGIN			
Query Match		85.7%; Score 1425; DB 6; Length 1428;	
Best Local Similarity		100.0%; Pred. No. 1.3e-293;	
Matches 1425; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGAAGCTACTGCTCTCTATCGAACAGCATCGATATTTGCGGACTTAAAAAGCTCAAG	60
Db	1	ATGAAGCTACTGCTCTCTATCGAACAGCATCGATATTTGCGGACTTAAAAAGCTCAAG	60
Qy	61	TGCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC	120
Db	61	TGCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC	120
Qy	121	TCTCCAAACCAAAAGGCTCGCTGACTAGGGCAGCATCTGACAGAGTGAANTCAAGG	180
Db	121	TCTCCAAACCAAAAGGCTCGCTGACTAGGGCAGCATCTGACAGAGTGAANTCAAGG	180
Qy	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTCGACATGATT	240
Db	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTCGACATGATT	240
Qy	241	TTGAAATGGATCTTTTACAGGATATAAAAGCATTTGTTAAAGGATTTTGTACAGAT	300

Db	241	TTGAAATGGATCTTTTACAGGATATAAAAGCATTTGTTAAAGGATTTTGTACAGAT	300
Qy	301	AATGTGAATAAAGATCCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA	360
Db	301	AATGTGAATAAAGATCCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA	360
Qy	361	ACATTCGAGACAGCATAGAATAAGTGGGACATCATCATATCGGAAGAGAGTAGTAAACAAAGGT	420
Db	361	ACATTCGAGACAGCATAGAATAAGTGGGACATCATCATCGGAAGAGAGTAGTAAACAAAGGT	420
Qy	421	CAAAAGACAGTTGACTGTATCGACGCGGTATGAGGCCCGAGTGCCTGCCAGAGTCCACG	480
Db	421	CAAAAGACAGTTGACTGTATCGACGCGGTATGAGGCCCGAGTGCCTGCCAGAGTCCACG	480
Qy	481	TGCAAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAACACAAAACCTGCCAGTCAGT	540
Db	481	TGCAAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAACACAAAACCTGCCAGTCAGT	540
Qy	541	ACGACGACAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACCCCTCGCCCCCAGAG	600
Db	541	ACGACGACAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACCCCTCGCCCCCAGAG	600
Qy	601	CGCGCAAGGATTCAAGAGTGTCTCGAGGTTCTTAACGAGAGAGCTTAATGGAGCAGAAC	660
Db	601	CGCGCAAGGATTCAAGAGTGTCTCGAGGTTCTTAACGAGAGAGCTTAATGGAGCAGAAC	660
Qy	661	AGACTGAAGATCTGACGCGCTGTCGGGGAACACAGAGTCCCTGATCGGAGGCTCGTG	720
Db	661	AGACTGAAGATCTGACGCGCTGTCGGGGAACACAGAGTCCCTGATCGGAGGCTCGTG	720
Qy	721	TGGTACCAGGAGGGTACGAGCAGCCGTTCGAGAGAAAGATCTCAAGAGAGTTACACAGACA	780
Db	721	TGGTACCAGGAGGGTACGAGCAGCCGTTCGAGAGAAAGATCTCAAGAGAGTTACACAGACA	780
Qy	781	TGGCAGTTAGAAGAGAGAGAGGAGGAACTGCACATGCCCTCCGTTCAGATCAGACAGAG	840
Db	781	TGGCAGTTAGAAGAGAGAGAGGAGGAACTGCACATGCCCTCCGTTCAGATCAGACAGAG	840
Qy	841	ATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGAAAAGGAGCTACCGGGATCTCC	900
Db	841	ATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGAAAAGGAGCTACCGGGATCTCC	900
Qy	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAATAAGCGCTCATCAAGCGAAGTGATGATG	960
Db	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAATAAGCGCTCATCAAGCGAAGTGATGATG	960
Qy	961	CTGCGAGTGGCGGACGGTACGAGCGCGGACGAGCAGCTGCTGTTTCGCGAACCAACAG	1020
Db	961	CTGCGAGTGGCGGACGGTACGAGCGCGGACGAGCAGCTGCTGTTTCGCGAACCAACAG	1020
Qy	1021	GCGTACACGCGCGACAACTACCGCAAGCGCGGATGCTCTACGTCATCGAGGACCTGCTG	1080
Db	1021	GCGTACACGCGCGACAACTACCGCAAGCGCGGATGCTCTACGTCATCGAGGACCTGCTG	1080
Qy	1081	CACCTTCTGCGGTGATGTACTCCATGAGCATGAGCAATGTGCACTACGCGCTCTCACC	1140
Db	1081	CACCTTCTGCGGTGATGTACTCCATGAGCATGAGCAATGTGCACTACGCGCTCTCACC	1140
Qy	1141	GCCATCGTTATTTCTCAGACCGGCGCTCAGCAACCCCTTTTGTAGTGGAGGAAATC	1200
Db	1141	GCCATCGTTATTTCTCAGACCGGCGCTCAGCAACCCCTTTTGTAGTGGAGGAAATC	1200
Qy	1201	CAGAGATACTACTTTGAAGACGCTCGCGGTTTACATTTTAAATCAGCAGCGCGCTCGCT	1260
Db	1201	CAGAGATACTACTTTGAAGACGCTCGCGGTTTACATTTTAAATCAGCAGCGCGCTCGCT	1260
Qy	1261	CGCTGCGCGGTGCTGTTGCGCAAGATCCTCGGCGCTGTCGCGGAACTCGCACCGCTCGGC	1320
Db	1261	CGCTGCGCGGTGCTGTTGCGCAAGATCCTCGGCGCTGTCGCGGAACTCGCACCGCTCGGC	1320
Qy	1321	ACGAGAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGGAAACTTCCGCCATTC	1380
Db	1321	ACGAGAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGGAAACTTCCGCCATTC	1380

QY	1381	CTCGAGGAGTCTGGAGCTGGCCGAGCTGTCGACGAGAGCTT	1425	Db	424	AATGTGAATAAAGATGCCGTCCAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA	483
Db	1381	CTCGAGGAGTCTGGAGCTGGCCGAGCTGTCGACGAGAGCTT	1425	QY	361	ACATTGAGACAGCATAGATAAAGTCCGACATCATCATCGGAAGAGAGTAGTAACAAGGT	420
				Db	484	ACATTGAGACAGCATAGATAAAGTCCGACATCATCATCGGAAGAGAGTAGTAACAAGGT	543
RESULT 8				QY	421	CAAAAGACAGTTGACTGTATTCGACCGGTATGAGGCCCGAGTCCGTCTCCAGAGTCCACG	480
AX555368				Db	544	CAAAAGACAGTTGACTGTATTCGACCGGTATGAGGCCCGAGTCCGTCTCCAGAGTCCACG	603
LOCUS	AX555368	1767 bp	DNA	QY	481	TGCAAGAACAAAG	540
DEFINITION	Sequence 120 from Patent WO02061102.			Db	604	TGCAAGAACAAAG	663
ACCESSION	AX555368			QY	541	ACGACGACAGTGGACGATCATATGCTGCCATATGCAATATGCAATATGCAATATGCAAT	600
VERSION	AX555368.1	GI:25898887		Db	664	ACGACGACAGTGGACGATCATATGCTGCCATATGCAATATGCAATATGCAATATGCAAT	723
KEYWORDS				QY	601	CGGCAAGGATTCACGAAGTGGTCCGAGGTTCCTAACGAGAGAGAGAGAGAGAGAGAGAG	660
SOURCE	synthetic construct			Db	724	CGGCAAGGATTCACGAAGTGGTCCGAGGTTCCTAACGAGAGAGAGAGAGAGAGAGAGAG	783
ORGANISM	synthetic construct			QY	661	AGACTGAAGATGTGACCGCTGTCCGCGAACCAGAAAGTCCCTGATCCGAGGCTCGTG	720
REFERENCE	1			Db	784	AGACTGAAGATGTGACCGCTGTCCGCGAACCAGAAAGTCCCTGATCCGAGGCTCGTG	843
AUTHORS	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.			QY	721	TGTTACCAAGGAGGTACGACGCGCTCGGAGGAGAGATCTCAAGAGAGAGTTCACAGACA	780
TITLE	Control of gene expression in plants			Db	844	TGTTACCAAGGAGGTACGACGCGCTTCGGAAGAGAGTTCCTCAAGAGGAGTTCACAGACA	903
JOURNAL	Patent: WO 02061102-A 120 08-AUG-2002;			QY	781	TGTTACCAAGGAGGTACGACGCGCTTCGGAAGAGAGTTCCTCAAGAGGAGTTCACAGACA	840
	Syngenta Participations AG (CH)			Db	904	TGTTACCAAGGAGGTACGACGCGCTTCGGAAGAGAGTTCCTCAAGAGGAGTTCACAGACA	963
FEATURES	Location/Qualifiers			QY	841	ATGACGATCTTAAACAGTCCGCTTATTTGAGATTTTCGAAAGAGGACTACCGGATTTCTCC	900
source	1..1767	/organism="synthetic construct"		Db	964	ATGACGATCTTAAACAGTCCGCTTATTTGAGATTTTCGAAAGAGGACTACCGGATTTCTCC	1023
	1..1767	/mol_type="unassigned DNA"		QY	901	AAGATATCTCAGTCCGATCAATATTAATTAAGAGGCTCATCAAGCGAAGTATGATG	960
	G(M)EV	/db_xref="taxon:32630"		Db	1024	AAGATATCTCAGTCCGATCAATATTAATTAAGAGGCTCATCAAGCGAAGTATGATG	1083
CDS		/note="unnamed protein product; Ecdysone receptor chimera"		QY	961	CTCGAGTGGCGGACGCTACGACGCGGTGTCCGAGTGGAGTTCCTGTTCCGAAACACCAAG	1020
		/codon_start=1		Db	1084	CTCGAGTGGCGGACGCTACGACGCGGTGTCCGAGTGGAGTTCCTGTTCCGAAACACCAAG	1143
		/transl_table=1		QY	1021	GGGTACACGCGGACAACTACCGCAAGGCGGCGATGCTCAGTGCATCGAGGACCTGCTG	1080
		/protein_id="CAD58255.1"		Db	1144	GGGTACACGCGGACAACTACCGCAAGGCGGCGATGCTCAGTGCATCGAGGACCTGCTG	1203
		/db_xref="GI:25898888"		QY	1081	CACCTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCATCTACGCGTGTCTCACC	1140
		/translation="MQOLYVDFSPAFIRYLPFWYFCRCRCPCLVLLQSSATMKL		Db	1204	CACCTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCATCTACGCGTGTCTCACC	1263
		LSISQACDICKLKKSKPKKAKLKNWECRYSPKTRSLPTRAHLEVESRL		QY	1141	GGCATCGTTTATTTCTCAGACCGGCGGCTTCGAGCAACCCCTTTTATGTTAGTGAGGAATC	1200
		ERLEOLFLLIPREDLMLKMSLDQIKALLTGFLVQDNVKNKDAVTRIASVEVDM		Db	1264	GGCATCGTTTATTTCTCAGACCGGCGGCTTCGAGCAACCCCTTTTATGTTAGTGAGGAATC	1323
		LTLRHRISATSSSNKQORLTIVSRMEPCVPESTCKNKRKEAOREKQSL		QY	1201	CAGAGATCTACTTGAAGACGCTGGCGGTTTACNTTTTAAATCAGCACGCGGCTCGCCT	1260
		PVSTTVDHMPAQCDPPPEARAHIEVPRFTEKLEMEQNRKLVNTPLSANQSL		Db	1324	CAGCGTATTTACCTGAACACGCTGGCGGTTTACNTTTTAAATCAGCACGCGGCTCGCCT	1383
		IARLVYODGYQPSSEDLKRVTTQWSADEDESDMPFRQITENTILTVQLIYEP		QY	1261	CGTGGCGGCTGTCTGTCGGCAAGATCTCTCGGCGTCTCGACCGAACTGCGCAACGCTCGGC	1320
		KGLPFSKISQPDQITLLKACSEVMMLRVARRYDAVSDVFLFANNQATYRDNRRAG		Db	1384	CGTGGCGGCTGTCTGTCGGCAAGATCTCTCGGCGTCTCGACCGAACTGCGCAACGCTCGGC	1443
		MAYVEDLILHFCRKMYSMSMDNVHALLTAIVIFSDRPGLEQFQVEETQRYLLNLR		QY	1321	ACGCGAAGTCCAAACATGTGCATCTCGTGAAGCTGAAAGAGAGAGAGAGAGAGAGAGAG	1380
		VYIMQHSAPCAVYAKILSVLTRELRLGMSNMCI SLKLRKRLPPFLEEIWDV		Db	1444	ATGCGAAGTCCAAACATGTGCATCTCGTGAAGCTCAAGAGAGAGAGAGAGAGAGAGAG	1503
		KLAPDFVSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSPGPFTHDSAPYAL		QY	1381	CTCGAGGAGATCTGGGACGTTGGCCGAGAGTGTGCAGCACGAGAGTTCGCCCGCCCGCCGAT	1440
		DWAEFEQMFDTDLGIDIEYGG"		Db	1504	CTCGAGGAGATCTGGGACGTTGGCCGAGAGTGTGCAGCACGAGAGTTCGCCCGCCCGCCGAT	1545
ORIGIN							
Query Match	85.7%	Score 1424;	DB 6;	Length 1767;			
Best Local Similarity	91.7%	Pred. No. 2.1e-293;					
Matches 1524;	Conservative	0;	Mismatches 120;	Indels 18;	Gaps 1;		
QY	1	ATGAAGCTACTGCTTTCTATCGAACAAAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	60				
Db	124	ATGAAGCTACTGCTTTCTATCGAACAAAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	183				
QY	61	TGCTCCAAAGAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGGAGTGTCCCTAC	120				
Db	184	TGCTCCAAAGAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGGAGTGTCCCTAC	243				
QY	121	TCTCCCAAAACCAAAAGGCTCTCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCAAGG	180				
Db	244	TCTCCCAAAACCAAAAGGCTCTCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCAAGG	303				
QY	181	CTAGAAAGACTGGAACAGCTATTCTACTATTTTCTCGAAGACCTTGCATGATGAT	240				
Db	304	CTAGAAAGACTGGAACAGCTATTCTACTATTTTCTCGAAGACCTTGCATGATGAT	363				
QY	241	TTGAAAATGATCTTTTACAGGATATAAAGCATTGTTACAGGATTTATTGTACAGAT	300				
Db	364	TTGAAAATGATCTTTTACAGGATATAAAGCATTGTTTAAACAGATTTATTGTACAGAT	423				
QY	301	AATGTGAATAAAGTCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA	360				

QY	1441	GTCAAGCTGGGGACGAGCTCCACTTAGACGGGAGGACGTGGCGATGGCGCATGCCGAC	1500
Db	1546	GTCAAGCTGGGGACGAGCTCCACTTAGACGGGAGGACGTGGCGATGGCGCATGCCGAC	1605
QY	1501	CGGCTAGACGATTTTCGATCTGGACATGTTGGGACCGGGATTCGCCGGGTCCGGGATTT	1560
Db	1606	CGGCTAGACGATTTTCGATCTGGACATGTTGGGACCGGGATTCGCCGGGTCCGGGATTT	1665
QY	1561	ACCCGCCACGACTCCGCCCCCTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACAG	1620
Db	1666	ACCCGCCACGACTCCGCCCCCTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACAG	1725
QY	1621	ATGTTTACCGATGCCCTTGGAAATGACGAGTACGGTGGGTAG	1662
Db	1726	ATGTTTACCGATGCCCTTGGAAATGACGAGTACGGTGGGTAG	1767
RESULT 9			
AX555390		1809 bp	DNA
LOCUS		linear	PAT 27-NOV-2002
DEFINITION		Sequence 142 from Patent WO02061102.	
ACCESSION		AX555390	
VERSION		AX555390.1	GI:25898909
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE		1	
AUTHORS		Pascal, E. J., Valentine, S. A., Brown, J. A., Cockrell, J. A. S. and Johnson, B. D.	
TITLE		Control of gene expression in plants	
JOURNAL		Patent: WO 02061102-A 142 08-AUG-2002;	
SYNGENTA PARTICIPATIONS AG (CH)		Location/Qualifiers	
FEATURES		1..1809	
source		/organism="synthetic construct"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:32630"	
CDS		1..1809	
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ORIGIN			
Query Match		85.6%;	Score 1422; DB 6; Length 1809;
Best Local Similarity		100.0%;	Pred. No. 5.7e-293;
Matches 1422;		Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	4	AGCTACTGTCTTCTATCGAACAGCATCGGATATTTGCCGACTTAAAGAGCTCAAGTGC	63
Db	385	AAAGTACTGTCTTCTATCGAACAGCATCGGATATTTGCCGACTTAAAGAGCTCAAGTGC	444
QY	64	TCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTACTCT	123
Db	445	TCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTACTCT	504
QY	124	CCCAAAACCAAAGGTCTCCGTGTACTAGGGACATCTCTGACAGAGTGGAAATCAAGGCTA	183

Oy	1264	TGCGCGTGTCTTGGCAAGATCTCGCGTGTCTGACGGAAGTGGCGACGCTGGGACG	1323
Db	1645	TGCGCGTGTCTTGGCAAGATCTCGCGTGTCTGACGGAAGTGGCGACGCTGGGACG	1704
Oy	1324	CAGAACTCCAACATGCTGCTGCTGAAGCTGAAGAACAGAACTTCCGCCATTCCTC	1383
Db	1705	CAGAACTCCAACATGCTGCTGCTGAAGCTGAAGAACAGAACTTCCGCCATTCCTC	1764
Oy	1384	GAGGAGATCTGGGACGTGGCGAAGTGTGCGACGACGAAAGCTT	1425
Db	1765	GAGGAGATCTGGGACGTGGCGAAGTGTGCGACGACGAAAGCTT	1806
RESULT 10			
AX555372			
LOCUS	AX555372	1782 bp	DNA linear PAT 27-NOV-2002
DEFINITION	Sequence 124 from Patent WO02061102.		
ACCESSION	AX555372		
VERSION	AX555372.1	GI:25898891	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 124 08-AUG-2002;		
SYNGENTA PARTICIPATIONS AG (CH)	Location/Qualifiers		
FEATURES	1..1782		
source	/organism="synthetic construct"		
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CDS	1..1782		
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ORIGIN			
Query Match	79.1%;	Score 1314.2;	DB 6; Length 1782;
Best Local Similarity	87.7%;	Pred. No. 6e-270;	
Matches 1471;	Conservative	0; Mismatches 173;	Indels 33; Gaps 2;
Oy	1	ATCAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	60
Db	124	ATGAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	183
Oy	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCTGCTAC	120
Db	184	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCTGCTAC	243
Oy	121	TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGCAGAGAGTGGAAATCAAG	180
Db	244	TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGCAGAGAGTGGAAATCAAG	303
Oy	181	CTAGAAGACTGGACAGCTATTCTTACTGATTTTCTCGAGAAAGACCTTGCATCATGATT	240

QY	1306	CTGGCGAGCTCGGACGACAGAACTCCAAACATGTCATCTCGTGAAGCTGAAGAACAGG	1365
Db	1444	TTGGCGAGCTGGGATGACAGAAATTCGAACATGTGATCTCGTGAAGCTCAAGAACAGG	1503
QY	1366	AAATCTCGGCATTTCTCGAGAGATCTGGACATCTGGACATGGCCGAAAGTGTGACGACGAAGCTT	1425
Db	1504	AAGCTGCGCGCTTCTGAGGAGATCTGGACGT-----GAAAGCTT	1545
QY	1426	GCCCCCGGACCGATGTGAGCTGCGGACAGAGCTCCACCTTAGACGCGGAGAGCTGGCG	1485
Db	1546	GCCCCCGGACCGATGTGAGCTGCGGACAGAGCTCCACCTTAGACGCGGAGAGCTGGCG	1605
QY	1486	ATGGCGCATCGGACGCGCTAGACGATTTGATCTGGACATGTTGGGAGCGGGATTC	1545
Db	1606	ATGGCGCATCGGACGCGCTAGACGATTTGATCTGGACATGTTGGGAGCGGGATTC	1665
QY	1546	CGGGTCTGGGATTTACCCCCACGACTCCGCCCTACGGCGCTCTGGATATGCCGAC	1605
Db	1666	CGGGTCTGGGATTTACCCCCACGACTCCGCCCTACGGCGCTCTGGATATGCCGAC	1725
QY	1606	TTGAGATTTGAGCAGATGTTTACCGATGCCCTTGGAAATGACGATCGGTGGGTAG	1662
Db	1726	TTGAGATTTGAGCAGATGTTTACCGATGCCCTTGGAAATGACGATCGGTGGGTAG	1782
RESULT 11			
AX555341		1518 bp DNA linear	PAT 27-NOV-2002
LOCUS		Sequence 93 from Patent WO02061102.	
DEFINITION		AX555341	
ACCESSION		AX555341.1	GI:25898860
VERSION			
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE			
AUTHORS		Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.	
TITLE		Control of gene expression in plants	
JOURNAL		Patent: WO 02061102-A 93 08-AUG-2002;	
SYNGENTA PARTICIPATIONS AG (CH)			
FEATURES		Location/Qualifiers	
source		1..1518	/organism="synthetic construct"
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CDS		1..1518	/note="unnamed protein product; Ecdysone Receptor chimera MNV"
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ORIGIN			
Query Match		73.2%;	Score 1216.6; DB 6; Length 1518;
Best Local Similarity		99.7%;	Pred. No. 4.1e-249;
Matches 1219; Conservative		0; Mismatches	4; Indels 0; Gaps 0;
QY	440	CGACGCGTATGAGCGCGGAGTGGTCTGCCAGATCCACGATGCAAGAACAAAGAGAG	499
Db	296	CGGTGGGCGATGAGGCGCGGAGTGGTCTGCCAGATCCACGATGCAAGAACAAAGAGAG	355

Db 1436 CCTACGGGCTCTGATATGCGGACTTCGAGTTTGACAGATGTTTACCGATGCCCTTG 1495
Qy 1640 GAATTGACAGTACCGTGGGTAG 1662
Db 1496 GAATTGACAGTACCGTGGGTAG 1518
RESULT 12
AX555317 1500 bp DNA linear PAT 27-NOV-2002
LOCUS Sequence 69 from Patent WO02061102.
DEFINITION AX555317
ACCESSION AX555317
VERSION AX555317.1 GI:25898836
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pascal,B.J., Valentin,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 69 08-AUG-2002;
Syngenta Participations AG (CH)
FEATURES
source 1..1500
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/db_xref="taxon:32630"
CDS 1..1500
/note="unnamed protein product; Ecdysone Receptor chimera
MRV"
/codon_start=1
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/translation="WGRELSPASSINGSTDEPRROKKGPAPQBELCLIVCGDRA
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BEEDTMRPQITVEMTILTVLQVIFAGKLPFGSKISQSDQITLLKSSSEVMULRVA
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VTFSPRGLQPLVVEEIOYLYLKLTVYILNOYSASPRCAVLFGKILGLTELRLTG
TONSMNCSLKLNRKLPELFEIWDVKLAPPTDVLGLDELHLDGEDVAMAHADALDD
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Query Match 70.2%; Score 1167.4; DB 6; Length 1500;
Best Local Similarity 98.0%; Pred. No. 1.3e-238;
Matches 1199; Conservative 0; Mismatches 6; Indels 18; Gaps 1;
Qy 440 CGACGGTATGAGCCCGGAGTGCCTCCAGAGTCCACGTGCAAGAACAAAGAGAG 499
Db 296 CGGTGGCATGAGCCCGGAGTGCCTCCAGAGTCCACGTGCAAGAACAAAGAGAG 355
Qy 500 AAAGAGACGACAG 559
Db 356 AAAGAGAGACAG 415
Qy 560 ATATGCTGCTGCAATATGACCTCCGCCCCCAGAGCGGCGGCAAGGATTCACGAAG 619
Db 416 ATATGCTGCTGCAATATGACCTCCGCCCCCAGAGCGGCGGCAAGGATTCACGAAG 475
Qy 620 TGGTCCCGAGGTTCTTAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 679
Db 476 TGGTCCCGAGGTTCTTAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
Qy 680 CGCTGTCGGGACACAG 739
Db 536 CGCTGTCGGGACACAG 595
Qy 740 AGCAGCGCTCGGAGGAGAGATCTCAAGAGAGATTCACAGAGATTCACAGAGATTC 799

Db 596 AGCAGCGCTCGAGAGAGATCTCAAGAGAGTTACACAGACATGCGAGTTAGAGAGAGAG 655
Qy 800 AAGAGGAGAGAACTGACATGCCCTTTCGTCAGATCAGAGATGACGATCTTAAACAGTGC 859
Db 656 AAGAGGAGAGAACTGACATGCCCTTTCGTCAGATCAGAGATGACGATCTTAAACAGTGC 715
Qy 860 AGCTTATTGTAGAAATTCGCAAGGAGACTACCGGATTCCTCAAGATATCTCAGTCCGATC 919
Db 716 AGCTTATTGTAGAAATTCGCAAGGAGACTACCGGATTCCTCAAGATATCTCAGTCCGATC 775
Qy 920 AAATACATTTAAGGCGTCATCAAGCGAGTGTATGATGCTGCGAGTGGCGGCGGCGT 979
Db 776 AAATACATTTAAGGCGTCATCAAGCGAGTGTATGATGCTGCGAGTGGCGGCGGCGT 835
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Db 836 ACAGCGCGGCGACGAGACGAGCGTGTCTGTCGCGAAACCAACGAGCGGTACACGCGCGCAACT 895
Qy 1040 ACCGCAAGCGCGGCGATGTCCTACGTCATCGAGGACCTGCTGTCGATCTGCTGCTGATGT 1099
Db 896 ACCGCAAGCGCGGCGATGTCCTACGTCATCGAGGACCTGCTGTCGATCTGCTGCTGATGT 955
Qy 1100 ACTCATGAGATGAGACATGTCACATGACGCGCTGCTCACCGCCATCGTTATTTCTCAG 1159
Db 956 ACTCATGAGATGAGACATGTCACATGACGCGCTGCTCACCGCCATCGTTATTTCTCAG 1015
Qy 1160 ACCGCGGCGGCTCGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATCTACTTTGAAGA 1219
Db 1016 ACCGCGGCGGCTCGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATCTACTTTGAAGA 1075
Qy 1220 CGCTGCGGCTTTACATTTTAAATCAGCACAGCGGCTGCTGCTGCGCGCTGCTGCTGCTG 1279
Db 1076 CGCTGCGGCTTTACATTTTAAATCAGCACAGCGGCTGCTGCTGCGCGCTGCTGCTGCTG 1135
Qy 1280 GCAAGATCTCGGCGTGTGACGAACTGCGGACGCTGCGGACGAGAACTCCAAACATGT 1339
Db 1136 GCAAGATCTCGGCGTGTGACGAACTGCGGACGCTGCGGACGAGAACTCCAAACATGT 1195
Qy 1340 GCATCTCGCTGAAGCTGAAGAACAGAGAACTTCCGCCATCTCTCGAGGAGATCTGGGAG 1399
Db 1196 GCATCTCGCTGAAGCTGAAGAACAGAGAACTTCCGCCATCTCTCGAGGAGATCTGGGAG 1255
Qy 1400 TGGCGCAAGTGTTCGACGAGAGCTTGGCCCCCCCCCGAGCTGTCAGCTTGGGGGAGCAGC 1459
Db 1256 T-----GAGCTTGGCCCCCCCCCGAGCTGTCAGCTTGGGGGAGCAGC 1297
Qy 1460 TCACCTTAGACGCGGACGCTGCGGACGCTGCGGACGCTGCGGACGCTGCGGACGCTTTCGATC 1519
Db 1298 TCACCTTAGACGCGGACGCTGCGGACGCTGCGGACGCTGCGGACGCTTTCGATC 1357
Qy 1520 TGGACATGTTGGGGGACGCGGATTCGCCGGGTCCGGGATTTACCCGCCACGACTCCGCCCC 1579
Db 1358 TGGACATGTTGGGGGACGCGGATTCGCCGGGTCCGGGATTTACCCGCCACGACTCCGCCCC 1417
Qy 1580 CCTACGCGGCTCTGGATATGGCCGACTTTCGAGTTTTCGAGCAGATGTTTACCGATGCCCTTG 1639
Db 1418 CCTACGCGGCTCTGGATATGGCCGACTTTCGAGTTTTCGAGCAGATGTTTACCGATGCCCTTG 1477
Qy 1640 GAATTGACAGTACCGTGGGTAG 1662
Db 1478 GAATTGACAGTACCGTGGGTAG 1500

RESULT 13
AX555395 1800 bp DNA linear PAT 27-NOV-2002
LOCUS Sequence 147 from Patent WO02061102.
DEFINITION AX555395
ACCESSION AX555395
VERSION AX555395.1 GI:25898914
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE	1	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.	Db	664	GACGTGGCGATGGCGCATGCCGACGCGGTAGACGATTTTCGATCTGACATGTTGGGGAC	723
AUTHORS			Qy	477	-----	476
TITLE		Control of gene expression in plants	Db	724	GGGGATTCCCGGTCGGGATTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGAT	793
JOURNAL		Patent: WO 02061102-A 147 08-AUG-2002;				
		Syngenta Participations AG (CH)	Qy	477	-----	476
FEATURES		Location/Qualifiers				
source		1..1800				
		/organism="synthetic construct"	Db	784	ATGGCCGACTTCGAGTTTGACGAGATGTTTACCAGTCCCTTGGAAATTGACGAGTAGCGT	843
		/mol_type="unassigned DNA"	Qy	477	-----CACTGCAAGAACAAAAAGAGAAAGCAAGAGAAAAAGCAAGAGAAAAAGCAAACTG	531
		/db_xref="taxon:32630"	Db	844	GGGAACACGTCGCAAGAACAAAAAGAGAAAGCAAGAGAAAAAGCAAGAGAAAAAGCAAACTG	903
		1..1800				
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		/transl_table=1	Qy	592	CCCCCAGAGCGGCAAGGATTCAACGAAGTGGTCCGAGGTTCTTAACGGAGAAAGCTAATG	651
		/protein_id="CAD58263.1"	Db	964	CCCCCAGAGCGGCAAGGATTCAACGAAGTGGTCCGAGGTTCTTAACGGAGAAAGCTAATG	1023
		/db_xref="GI:25898915"	Qy	652	GAGCAGACAGACTGAAGAAATGTGACCGCTGTCCGCGAACCAAGAGTCCCTGATCGCG	711
		/translation="MQQLYVDFPSPAFIRYLFAWYCFRCSPCLVLLVQGSATMKL	Db	1024	GAGCAGACAGACTGAAGAAATGTGACCGCTGTCCGCGAACCAAGAGTCCCTGATCGCG	1083
		LSSIEQACDI CRLLKKJCSKEPKKCAKCLKNWECRYSPTKRSPLTRAHLTAVESRL	Qy	712	AGGCTCGTGTGGTACCAGGAGGGGTACGAGCAGCGCTCGGAGGAAAGATCTCAAGAGAGTT	771
		ERLQQLFLIIPREDLMILKMDLQIDIKALLTGLFVDNNKNDADVTLRAVESVETMP	Db	1084	AGGCTCGTGTGGTACCAGGAGGGGTACGAGCAGCGCTCGGAGGAAAGATCTCAAGAGAGTT	1143
		LTLQHRISATSSSESNKQRLTVSTRMPECVVPSTCKLAPDPTVSLGDELHL	Qy	772	ACACAGACATGGCAGTTAGAAAGAAAGAGAGAGAGAACTGACATGCCCTTCCGTCAG	831
		DGEVMAHADALDDFDMLGDSGPGPTPHDSAPYGALDMADPEFPAARILHEVPR	Db	1144	ACACAGACATGGCAGTTAGAAAGAAAGAGAGAGAGAACTGACATGCCCTTCCGTCAG	1203
		IDEXGNTCKNRKEAKREKDKLPVSTTVDDHMPAIMOCDDPPPEAAARILHEVPR	Qy	832	ATCACAGAGATGACGATCTTAAACAGTGCAGCTTATTGTGAAATTCGCAAGGGAGCTACCG	891
		FLTEKLMQNRKLVNTPLSANOKSLIARLAWYQSEYQPSSEDLKRVTTQWOLEEVEE	Db	1204	ATCACAGAGATGACGATCTTAAACAGTGCAGCTTATTGTGAAATTCGCAAGGGAGCTACCG	1263
		BETDMPFRQITMILITVLIVFAKGLPGESKISQSDQITLLKASSEVMVLRVARR	Qy	892	GGATTCTCCAAAGATATCTCAGTCCGATCAAAATACATTTAAAGGGCTCATCAAGCGAA	951
		YDAATDSVLFANNOAYTRDNRKAGMSYVIEDLHFCRCMTYSMDNVDNHYALLTAIVI	Db	1264	GGATTCTCCAAAGATATCTCAGTCCGATCAAAATACATTTAAAGGGCTCATCAAGCGAA	1323
		FSDRPLQPLVBEIQRYLKLTRVILNQHSPRCVAVLFGKILGVLTLRLTGTQ	Qy	952	GTGATGATGTGCGAGTGGCGCGACGGTAACGCGCGGACGGACAGCGTGTCTGTCGCG	1011
		NSNMCSLSLKNRKLPPLEIBIWDVAEVSSTKL"	Db	1324	GTGATGATGTGCGAGTGGCGCGACGGTAACGCGCGGACGGACAGCGTGTCTGTCGCG	1383
ORIGIN			Qy	1012	AACAAACGAGCGGTACACGCGCGACACTACCGCAAGCGGCGCATGTCTCCTAGCTCATCGAG	1071
Query Match		70.2%; Score 1166; DB 6; Length 1800;	Db	1384	AACAAACGAGCGGTACACGCGCGACACTACCGCAAGCGGCGCATGTCTCCTAGCTCATCGAG	1443
Best Local Similarity		85.1%; Pred. No. 2,7e-238;	Qy	1072	GACCTGCTGCACATTTCTGTCGCTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCG	1131
Matches 1425; Conservative		0; Mismatches 0; Indels 249; Gaps 1;	Db	1444	GACCTGCTGCACATTTCTGTCGCTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCG	1503
Qy	1	ATGAAGCTACTGCTCTTATGAAACAGATGCGATATTTGCGGACTTAAAAAGCTCAAG	Qy	1132	CTGCTCAACGCGCATTCCTCAGACCGGCGCGCTCGAGCAACCCCTTTTAGTG	1191
Db	124	ATGAAGCTACTGCTCTTATGAAACAGATGCGATATTTGCGGACTTAAAAAGCTCAAG	Db	1504	CTGCTCAACGCGCATTCCTCAGACCGGCGCGCTCGAGCAACCCCTTTTAGTG	1563
Qy	61	TGCTCCAAAGAAAAACCGAAGTGCAGGAGTGTCTGAAGAAACAACTGGAGGTGCGCTAC	Qy	1192	GAGGAATCCAGAGATACCTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGACG	1251
Db	184	TGCTCCAAAGAAAAACCGAAGTGCAGGAGTGTCTGAAGAAACAACTGGAGGTGCGCTAC	Db	1564	GAGGAATCCAGAGATACCTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGACG	1623
Qy	121	TCTCCAAACAAAAAGGTCCTGCTAGTGGGACATCTGACAGAGTGAATCAAGG	Qy	1252	GCCTGCGCTCGCTCGCGCGTCTGTTCCGCAAGATCTCCGCGTGTGACGGAACCTGCC	1311
Db	244	TCTCCAAACAAAAAGGTCCTGCTAGTGGGACATCTGACAGAGTGAATCAAGG	Db	1624	GCCTGCGCTCGCTCGCGCGTCTGTTCCGCAAGATCTCCGCGTGTGACGGAACCTGCC	1683
Qy	181	CTGAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAAGACCTTGACATGAT	Qy	1312	ACGCTCGGCAAGAACTCCAAATGTGATCTCGCTGAGAGCTGAGAGACAGGAACTT	1371
Db	304	CTGAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAAGACCTTGACATGAT	Db	1684	ACGCTCGGCAAGAACTCCAAATGTGATCTCGCTGAGAGCTGAGAGACAGGAACTT	1743
Qy	241	TTGAAAATGGATTTCTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAGAT	Qy	1372	CCGCAATTTCTCGAGGAGATCTGGAAGTGTGCGCCGAAGTGTGAGAGCGAAAGCTT	1425
Db	364	TTGAAAATGGATTTCTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAGAT	Db	1744	CCGCAATTTCTCGAGGAGATCTGGAAGTGTGCGCCGAAGTGTGAGAGCGAAAGCTT	1797
Qy	301	AATGTGAATAAGATGCGCTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA				
Db	424	AATGTGAATAAGATGCGCTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA				
Qy	361	ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAAGT				
Db	484	ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAAGT				
Qy	421	CAAAAGACAGTTGATGACCGGTATGAGCGCCGAGTGGTCCGAGAGTC----				
Db	544	CAAAAGACAGTTGATGACCGGTATGAGCGCCGAGTGGTCCGAGAGTC----				
Qy	477	-----				
Db	604	TGCAAGCTTGCCCCCGACCGATGTACGCTGGGGGACGAGCTCCACTTAGACGGCGAG				
Qy	477	-----				

RESULT 14
AX555327
LOCUS AX555327 1533 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 79 from Patent WO20061102.
ACCESSION AX555327
VERSION AX555327.1 GI:25898846
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 79 08-AUG-2002;
SYNTEGA Participations AG (CH)
FEATURES
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EMV"

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MLURVRYDAATDSVLFANNOAYTRDNYRKAGMSYVIDLLHFCRCMTSMNDNVHYA
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LRTGTQNSMCMISLKLKNRKLPPLEIWDVAEYSTTKLAPPTDVSGLDELHLDGED
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GG"

ORIGIN
Query Match 66.8%; Score 1109.8; DB 6; Length 1533;
Best Local Similarity 92.8%; Pred. No. 2.7e-226;
Matches 1181; Conservative 0; Mismatches 77; Indels 15; Gaps 1;
QY 405 GAGTAGTAAAGGTCAGAGACAGTTGACTGTATCGACGCGTATGAGCCGCGAGTGCCT 464
DB 261 GAATGTCAAGAAATGCCGGTGAAGAGTGTAGCGGTGGGCATGAGGCCGAGTGCCT 320
QY 465 CGTCCAGAGTCCA CTGCAAGAAACAAAGAGAGAGAAAGAGAGACAGAGAGAAAGCA 524
DB 321 GGTGCCAGAAACGACAGTGTGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 525 CAAACTGCCAGTACAGACAGTGCAGCATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584
DB 381 CAAACTACCACTGAGCAGACAGTGCAGCATCATATGCTGCTGCTGCTGCTGCTGCTGCTG 440
QY 585 CCTCTCGCCCGCCAGAGCGGCGAGGATT-----CACGAAAGTGTGCTCCCGAG 629
DB 441 TCACACACCCCGAGGAGCGAGGATTCTGGAATGTTTCAGCATGAAGTGTGCTCCCGG 500
QY 630 GTTCTTAACGGAGAAGCTAATGAGCAGACAGACTGAAGAAATGTGACGCGCGTGTCCGC 689
DB 501 GTTCTCTCGAGAGCTGATGAGCAGAGATCGCTGAAGAAACATACCCCGCTCACCGC 560
QY 690 GAACCAAGTCCCTGATCCGAGGCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 749
DB 561 CAACCAAGTCTCTGATCCGAGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
QY 750 GGAGGAGAGTCTCAAGAGAGTTACACAGACATGCGCAGTTAGAGAGAGAGAGAGAGAGGA 809
DB 621 GGAGGAGAGTCTCAAGAGAGTTACACAGACATGCGCAGTTAGAGAGAGAGAGAGAGAGGA 680

QY 810 AACTGACATGCCCTTCGGTCAGATCACAGAGATGACGATCTTAAACAGTGCAGCTTATGT 869
DB 681 AACTGACATGCCCTTCGGTCAGATCACAGAGATGACGATCTTAAACAGTGCAGCTTATGT 740
QY 870 AGAATTCGAAAGGAGTACCGGATTTCTCAAGATATCTCAGTCCGATCAATTACATTT 929
DB 741 AGAATTCGAAAGGAGTACCGGATTTCTCAAGATATCTCAGTCCGATCAATTACATTT 800
QY 930 ATTAAGCGCTCATCAAGCGAAGTATGATCTCGAGTGGCGAGCGTACGAGCGCGC 989
DB 801 ATTAAGCGCTCATCAAGCGAAGTATGATCTCGAGTGGCGAGCGTACGAGCGCGC 860
QY 990 GACGACAGCGTGTCTTTCGCGAAACAAACGAGCGGTACACGCGCGCAACTACCGAAGC 1049
DB 861 GACGACAGCGTGTCTTTCGCGAAACAAACGAGCGGTACACGCGCGCAACTACCGAAGC 920
QY 1050 GGGCATGTCTTACGTCATCGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1109
DB 921 GGGCATGTCTTACGTCATCGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
QY 1110 CATGACAAATGTGACACTACGCGCTGCTCACCGCCATCGTTATATCTCAGACCGCGCAGG 1169
DB 981 CATGACAAATGTGACACTACGCGCTGCTCACCGCCATCGTTATATCTCAGACCGCGCAGG 1040
QY 1170 CCTGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTACTTTGAAGACGCTCGGGT 1229
DB 1041 CCTGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTACTTTGAAGACGCTCGGGT 1100
QY 1230 TTACATTTAAATCAGACAGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1289
DB 1101 TTACATTTAAATCAGACAGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1160
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QY 1350 GAAGCTGAAGAACAGGAAACTTCCGCCATTTCTCGAGGAGATCTGGGAGCTGCGCGAAGT 1409
DB 1221 GAAGCTGAAGAACAGGAAACTTCCGCCATTTCTCGAGGAGATCTGGGAGCTGCGCGAAGT 1280
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QY 1470 CGGCGAGACGCTGGCGATGGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1529
DB 1341 CGGCGAGACGCTGGCGATGGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1400
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DB 1401 GGGGACCGGGATTTCCCGGGTCCGGGATTTACCCCCCAGACTCGCCCCCTTACGGCGC 1460
QY 1590 TCTGATATGCGCGACTTCCGAGTTTTCAGAGATGTTTACCGATGCGCTTGGATTCACGA 1649
DB 1461 TCTGATATGCGCGACTTCCGAGTTTTCAGAGATGTTTACCGATGCGCTTGGATTCACGA 1520
QY 1650 GTACCGTGGGTAG 1662
DB 1521 GTACCGTGGGTAG 1533

RESULT 15
AX555313
LOCUS AX555313 1509 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 65 from Patent WO20061102.
ACCESSION AX555313
VERSION AX555313.1 GI:25898832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1

AUTHORS

TITLE

JOURNAL

FEATURES

source

Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.

Control of gene expression in plants

Patent: WO 02061102-A 65 08-AUG-2002;

Syngenta Participations AG (CH)

Location/Qualifiers

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/db_xref="GI:25898833"

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EESDMPFRQITETILTQVLIQVFAKGLPGFAKISQSDQITLLKACSEVMMLRVAR
RYDAATDSVLFANNOAVSRDNYRKAGSVYIEDLLHFCRCWYMMNDVHYALTAV
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LDDFDLMLGDSFGPGFTPHDSAPYCALMDADFEPEQMETDALGIDEYGG"

ORIGIN

Query Match 59.9%; Score 996.2; DB 6; Length 1509;
Best Local Similarity 89.6%; Pred. No. 4.9e-202;
Matches 1096; Conservative 0; Mismatches 110; Indels 9; Gaps 2;

QY

440

CGACCGGTATGAGGCCGAGTGCCTCGTCGACGATCCACGTGCAGAGCAAAAGAGAG

499

DB

296

CGGTGGCATGAGGCCGAGTGCCTGCCAGAGTCCACGTGCAAGAACAAAGAGAG

355

QY

500

AAAGGAGGACAGAGAGAAAGACAACTGCCAGTCAGTACGACGACAGTGCAGCATC

559

DB

356

AAAGGAGGACAGAGAGAAAGACAACTGCCAGTCAGTACGACGACAGTGCAGCATC

415

QY

560

ATATGCTGCTCCATAATGTACCTTCGCCCCCAGAGCGGCAAGGATTCACGAAG

619

DB

416

ATATGCTGCTCCATAATGTACCTTCGCCCCCAGAGCGGCAAGGATTCACGAAG

475

QY

620

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679

DB

476

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535

QY

680

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739

DB

536

CGCTGTGCGGAAACAGAAAGTCCCTGATCGCAGGCTCGTGTGTACAGGAGGGTATG

595

QY

740

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799

DB

596

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655

QY

800

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859

DB

656

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712

QY

860

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DB

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QY

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1039

DB

833

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892

QY

1040

ACCGCAAGGCGGCGATGTCTCACTCATCGATCATCGAGGACCTGTCTGTCTGTGTATGT

1099

Db

893

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952

QY

1100

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1159

DB

953

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1012

QY

1160

ACCGCCAGCGCTCGAGCAACCCCTTTTATGTGGAGAAATCCAGAGATCTACTTGAAGA

1219

DB

1013

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1072

QY

1220

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DB

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1192

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DB

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QY

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CCTACGCGCTCTGGATATGCGCGACTTTCAGATTGAGCAGATGTTTACCGATGCCCTTG

1639

DB

1427

CCTACGCGCTCTGGATATGCGCGACTTTCAGATTGAGCAGATGTTTACCGATGCCCTTG

1486

QY

1640

GAATTGACGAGTACGGTGGGTAG

1662

DB

1487

GAATTGACGAGTACGGTGGGTAG

1509

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Job time : 7234.52 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 08:10:36 ; Search time 914.987 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: geneseqn2003ds:*
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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	100.0	3972	6	ABT07353 Ecdysone
2	1662	100.0	3972	10	ADF49176 Ecdysone
3	1612.8	97.0	1767	6	ABT07368 Chimeric
4	1612.8	97.0	1767	10	ADF49194 Ecdysone
5	1552.2	93.4	1800	6	ABT07370 Chimeric
6	1552.2	93.4	1800	10	ADF49198 Ecdysone
7	1441.6	86.7	1776	6	ABT07366 Chimeric
8	1441.6	86.7	1776	10	ADF49190 Ecdysone
9	1431.8	86.1	1863	6	ABT07377 Chimeric
10	1431.8	86.1	1863	10	ADF49208 Ecdysone
11	1426.6	85.8	1848	6	ABT07376 Chimeric
12	1426.6	85.8	1848	10	ADF49206 Ecdysone
13	1425	85.7	1428	6	ABT07371 Chimeric
14	1425	85.7	1428	10	ADF49200 Ecdysone
15	1424	85.7	1767	6	ABT07367 Chimeric
16	1424	85.7	1767	10	ADF49192 Ecdysone
17	1422	85.6	1809	6	ABT07382 Chimeric
18	1422	85.6	1809	10	ADF49214 Ecdysone
19	1314.2	79.1	1782	6	ABT07369 Chimeric
20	1314.2	79.1	1782	10	ADF49196 Ecdysone

21	1216.6	73.2	1518	6	ABT07344 Chimeric
22	1216.6	73.2	1518	10	ADF49165 Ecdysone
23	1167.4	70.2	1500	6	ABT07332 Chimeric
24	1167.4	70.2	1500	10	ADF49141 Ecdysone
25	1166	70.2	1800	6	ABT07386 Chimeric
26	1166	70.2	1800	10	ADF49219 Ecdysone
27	1109.8	66.8	1533	6	ABT07337 Chimeric
28	1109.8	66.8	1533	10	ADF49151 Ecdysone
29	996.2	59.9	1509	6	ABT07330 Chimeric
30	996.2	59.9	1509	10	ADF49137 Ecdysone
31	978.6	58.9	1500	6	ABT07331 Chimeric
32	978.6	58.9	1500	10	ADF49139 Ecdysone
33	976.6	58.8	2840	6	ABT07274 Manduca s
34	976.6	58.8	2840	10	ADF49073 Manduca s
35	976.6	58.8	2840	12	ADI33132 Tobacco h
36	954.6	57.4	1551	6	ABT07333 Chimeric
37	954.6	57.4	1551	10	ADF49143 Ecdysone
38	954.6	57.4	1566	6	ABT07342 Chimeric
39	954.6	57.4	1566	10	ADF49161 Ecdysone
40	951.8	57.3	1464	6	ABT07339 Chimeric
41	951.8	57.3	1464	10	ADF49155 Ecdysone
42	889.4	53.5	1524	6	ABT07336 Chimeric
43	889.4	53.5	1524	10	ADF49149 Ecdysone
44	871.8	52.5	1515	6	ABT07335 Chimeric
45	871.8	52.5	1515	10	ADF49147 Ecdysone

ALIGNMENTS

RESULT 1

ABT07353

ID ABT07353 standard; DNA; 3972 BP.

XX AC ABT07353;

XX DT 07-NOV-2002 (first entry)

XX DE Ecdysone receptor containing vector pCGS202 DNA SEQ ID NO: 104.

XX KW Plant; gene expression control; insect; hormone receptor; fertility;

XX OS ecdysone receptor; gene; ds.

XX PN Synthetic.

XX PD WO200261102-A2.

XX PF 08-AUG-2002.

XX PR 24-OCT-2001; 2001WO-US051417.

XX PR 24-OCT-2000; 2000US-0242969P.

XX PR (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX DR WPI; 2002-619259/66.

XX PT P-PSDB; ABJ05371.

XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

XX PS Claim 28; Page 255-258; 319pp; English.

XX CC The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (ECR) of an insect, a ligand binding domain of an insect ECR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of

CC	appropriate ligands that may be used in controlling plant fertility. The	
CC	method is useful for decreasing or increasing plant gene expression. The	
CC	present sequence is a coding sequence described in the exemplification of	
CC	the invention	
XX		
SQ	Sequence 3972 BP; 1027 A; 895 C; 929 G; 1121 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1662; DB 6; Length 3972;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGAAGCTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG 60	
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QY	61 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGCTAC 120	
DB	2067 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGCTAC 2126	
QY	121 TCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGCTAC 180	
DB	2127 TCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGCTAC 2186	
QY	181 CTGAAGACATGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT 240	
DB	2187 CTGAAGACATGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT 2246	
QY	241 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300	
DB	2247 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 2306	
QY	301 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360	
DB	2307 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 2366	
QY	361 ACATTGAGACACATAGATAAGTGGACATCATCGGAAGAGAGTAGTAACAAGAGT 420	
DB	2367 ACATTGAGACACATAGATAAGTGGACATCATCGGAAGAGAGTAGTAACAAGAGT 2426	
QY	421 CAAAGACAGTTGACTGTATGCGACGGTATGAGGCCGAGTGGTCTGCTCCAGAGTCCACG 480	
DB	2427 CAAAGACAGTTGACTGTATGCGACGGTATGAGGCCGAGTGGTCTGCTCCAGAGTCCACG 2486	
QY	481 TCGAAGAACAAAGAGAGAAAGAGACACAGAGAGAAAGACAAACTGCCAGTCACT 540	
DB	2487 TCGAAGAACAAAGAGAGAAAGAGACACAGAGAGAAAGACAAACTGCCAGTCACT 2546	
QY	541 ACGACACAGTGGACGATCATATGCTGCGATAATGCAATGTGACCTCCGCCCCCAGAG 600	
DB	2547 ACGACACAGTGGACGATCATATGCTGCGATAATGCAATGTGACCTCCGCCCCCAGAG 2606	
QY	601 GCGGCAAGGATTACAGAAAGTGTCCGAGGTTCTTAAACGGAAGACTTAATGGAGCAGAAC 660	
DB	2607 GCGGCAAGGATTACAGAAAGTGTCCGAGGTTCTTAAACGGAAGACTTAATGGAGCAGAAC 2666	
QY	661 AGACTGAAGAAATGACGCGCTGTGCGGAAACAGAGAGTCCCTGATCGCAGGCTCGTG 720	
DB	2667 AGACTGAAGAAATGACGCGCTGTGCGGAAACAGAGAGTCCCTGATCGCAGGCTCGTG 2726	
QY	721 TGTGTACAGAGGGGTACAGAGAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACA 780	
DB	2727 TGTGTACAGAGGGGTACAGAGAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACA 2786	
QY	781 TGGCAGTTAGAGAAAGAGAGAGAGAACTGACATGCCCTTCCTCGATAGATTCACAGAG 840	
DB	2787 TGGCAGTTAGAGAAAGAGAGAGAGAACTGACATGCCCTTCCTCGATAGATTCACAGAG 2846	
QY	841 ATGACCATCTTACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCGGATTTCTCC 900	
DB	2847 ATGACCATCTTACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCGGATTTCTCC 2906	
QY	901 AAGATATCTCAGTCCCATCAAAATTACATTTATTAAGGCGCTCATCAAGCGAAGTGTATG 960	

DB	2907 AAGATATCTCAGTCCGATCAAAATTATTAAGGCGCTCATCAAGCGAAGTGATGATG 2966	
QY	961 CTGCGAGTGGCGGACGGTACGACCGGCGAGCGGACAGCGTGTGTTCCGAAACACACAG 1020	
DB	2967 CTGCGAGTGGCGGACGGTACGACCGGCGAGCGGACAGCGTGTGTTCCGAAACACACAG 3026	
QY	1021 GGTACACGCGGACAACTACCGCAAGGCGGCGCATGTCTCTAGTCTACGAGGACCTGCTG 1080	
DB	3027 GGTACACGCGGACAACTACCGCAAGGCGGCGCATGTCTCTAGTCTACGAGGACCTGCTG 3086	
QY	1081 CACTTCTGCGGTATGATCTCATATGAGATGGAACAATGTGCACTACGCGCTGCTCACC 1140	
DB	3087 CACTTCTGCGGTATGATCTCATATGAGATGGAACAATGTGCACTACGCGCTGCTCACC 3146	
QY	1141 GGCATCGTTATATTTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTGAGGAAATC 1200	
DB	3147 GGCATCGTTATATTTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTGAGGAAATC 3206	
QY	1201 CAGAGATACCTACTTGAAGACGCTGCGGTTTACATTTTAAATCAGACACGCGCTGCGCT 1260	
DB	3207 CAGAGATACCTACTTGAAGACGCTGCGGTTTACATTTTAAATCAGACACGCGCTGCGCT 3266	
QY	1261 CGCTGCGCGTGTCTGTTCCGCAAGATCTCGGCGTGTGACGAACTGCGCACGCTCGGC 1320	
DB	3267 CGCTGCGCGTGTCTGTTCCGCAAGATCTCGGCGTGTGACGAACTGCGCACGCTCGGC 3326	
QY	1321 ACCGAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAAACAGGAAACTTCCGCCATT 1380	
DB	3327 ACCGAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAAACAGGAAACTTCCGCCATT 3386	
QY	1381 CTCGAGGAGATCTGGGACGTGGCCGAAGTGTGACGACGAAGCTTGCCCCCGGACCGAT 1440	
DB	3387 CTCGAGGAGATCTGGGACGTGGCCGAAGTGTGACGACGAAGCTTGCCCCCGGACCGAT 3446	
QY	1441 GTGAGCTGGGGACGAGCTCCACTTAGACGGCGAGAGCTGGCGATGGCGCATGCCGAC 1500	
DB	3447 GTGAGCTGGGGACGAGCTCCACTTAGACGGCGAGAGCTGGCGATGGCGCATGCCGAC 3506	
QY	1501 GCGCTAGACATTTCCGATCTGGAACATGTTGGGGGACGGGATTTCCCGGGTCCGGGATTT 1560	
DB	3507 GCGCTAGACATTTCCGATCTGGAACATGTTGGGGGACGGGATTTCCCGGGTCCGGGATTT 3566	
QY	1561 ACCCCCCACAGCTCCGCCCCCTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1620	
DB	3567 ACCCCCCACAGCTCCGCCCCCTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 3626	
QY	1621 ATGTTTACCATGCCCTTGAATTTGACGAGTACGTTGGGTAG 1662	
DB	3627 ATGTTTACCATGCCCTTGAATTTGACGAGTACGTTGGGTAG 3668	
RESULT 2		
ID	ADF49176 standard; DNA; 3972 BP.	
XX	ADF49176;	
AC	AC	
XX	XX	
DT	12-FEB-2004 (first entry)	
XX	Ecdysone receptor/VP16 transactivation domain DNA seq id 104.	
DE	receptor cassette; chimeric receptor polypeptide; DNA binding domain;	
XX	hinge domain; ecdysone receptor; Ecr; ligand binding domain;	
KW	activation domain; transgenic seed; transgenic plant; plant line;	
KW	herbicide; pesticide; chimeric ecdysone receptor; Ecr;	
KW	yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.	
XX	Synthetic.	
OS	Manduca sexta.	
OS	Ascomycota.	
OS	Herpes simplex virus unknown type.	
XX	US2003154509-A1.	
FN		

Db	3567	ACCCCCACGACTCGGCCCTACGGGCTCTGGATATGGCCGACTTCGAGTTTGAGCAG	3626
Qy	1621	ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGTTGGGTAG	1662
Db	3627	ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGTTGGGTAG	3668
RESULT 3			
ID	ABT07368		
XX	ABT07368	standard; DNA; 1767 BP.	
AC	ABT07368;		
XX	29-AUG-2003 (revised)		
DT	07-NOV-2002 (first entry)		
XX	Chimeric ecdysone receptor coding sequence SEQ ID NO: 122.		
XX	Plant; gene expression control; insect; hormone receptor; fertility;		
KW	ecdysone receptor; gene; ds.		
XX	Manduca sexta.		
OS	Spodoptera frugiperda.		
OS	Chimeric.		
XX	WO200261102-A2.		
XX	08-AUG-2002.		
XX	24-OCT-2001; 2001WO-US051417.		
XX	24-OCT-2000; 2000US-0242969P.		
PR	(SYGN) SYNGENTA PARTICIPATIONS AG.		
XX	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;		
PI	WPI; 2002-619259/66.		
DR	P-PSDB; ABJ05374.		
XX	New receptor cassette encoding a chimeric receptor polypeptide, useful in		
PT	regulating expression of target polypeptides in plants in the presence of		
PT	appropriate ligands that may be used in controlling plant fertility.		
XX	Example 23; Page 275-278; 319pp; English.		
PS	The present invention relates to a receptor cassette encoding a chimeric		
XX	receptor polypeptide comprising at least one DNA binding domain, a hinge		
CC	domain of an ecdysone receptor (EcR) of an insect, a ligand binding		
CC	domain of an insect EcR, where the ligand binding domain is heterologous		
CC	with respect to the hinge domain and an activation domain. The chimeric		
CC	insect hormone receptors and receptor cassettes are useful in regulating		
CC	expression of target polypeptides in plants in the presence of		
CC	appropriate ligands that may be used in controlling plant fertility. The		
CC	method is useful for decreasing or increasing plant gene expression. The		
CC	present sequence is a coding sequence described in the exemplification of		
CC	the invention. (Updated on 29-AUG-2003 to standardise OS field)		
XX	Sequence 1767 BP; 476 A; 431 C; 477 G; 383 T; 0 U; 0 Other;		
SQ	Query Match		
	Best Local Similarity 98.8%; Pred. No. 0;		
	Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;		
Qy	1 ATGAAGCTACTGCTTCTATCGAACAAAGCATGGGATATTTGGCGACTTAAAAGCTCAAG	60	
Db	124 ATGAAGCTACTGCTTCTATCGAACAAAGCATGGGATATTTGGCGACTTAAAAGCTCAAG	183	
Qy	61 TGCCTCAAGAAACCGAGTGCCTCAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC	120	
Db	184 TGTCTCAAGAAACCGAGTGCCTCAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC	243	

Qy	121	TCCTCCAAAACCAAAGGTCTCGCTGACTAGGGACATCTGACAGAAGTGAATCAAGG	180
Db	244	TCCTCCAAAACCAAAGGTCTCGCTGACTAGGGACATCTGACAGAAGTGAATCAAGG	303
Qy	181	CTAGAAAGACTGGAAACAGCTATTTCTGACTGATTTTCTCGAGAACCTTGACATGAT	240
Db	304	CTAGAAAGACTGGAAACAGCTATTTCTGACTGATTTTCTCGAGAACCTTGACATGAT	363
Qy	241	TTGAAAATGGATTTCTTACAGGATATAAAGCAATGTTAAACAGGATTTATTGTACAAGAT	300
Db	364	TTGAAAATGGATTTCTTACAGGATATAAAGCAATGTTAAACAGGATTTATTGTACAAGAT	423
Qy	301	AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCCTCTA	360
Db	424	AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCCTCTA	483
Qy	361	ACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAAACAAGGT	420
Db	484	ACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAAACAAGGT	543
Qy	421	CAAAGACAGTTGACTGTATCGACCGCTATGAGGCCGAGTGCCTGCTCCAGAGTCCACG	480
Db	544	CAAAGACAGTTGACTGTATCGACCGCTATGAGGCCGAGTGCCTGCTCCAGAGTCCACG	603
Qy	481	TGCAAGAAACAAAAGAGAGAAAAGAGCAACAGAGAGAAAAGCAAAACTGCCAGTCAGT	540
Db	604	TGCAAGAAACAAAAGAGAGAAAAGAGCAACAGAGAGAAAAGCAAAACTGCCAGTCAGT	663
Qy	541	ACGACGACAGTGGACGATCATATGCTGCTGCATATGCMATGTGACCTCCGCCCCAGAG	600
Db	664	ACGACGACAGTGGACGATCATATGCTGCTGCATATGCMATGTGACCTCCGCCCCAGAG	723
Qy	601	GCAGCAAGGATTCCAGAAAGTGGTCCCGAGGTTCCTAAACGGAGAGCTTAATGGAGCAAG	660
Db	724	GCAGCAAGGATTCCAGAAAGTGGTCCCGAGGTTCCTAAACGGAGAGCTTAATGGAGCAAG	783
Qy	661	AGACTGAAGAAATGTGACCGCGCTGTGCGCGAATGCTGATCGGAGGCTCGTG	720
Db	784	AGACTGAAGAAATGTGACCGCGCTGTGCGCGAATGCTGATCGGAGGCTCGTG	843
Qy	721	TGTTACAGAGAGGTTACGAGCAGCGCTCGGAGAGAGATCTCAAGAGAGTTTACACAGCA	780
Db	844	TGTTACAGAGAGGTTACGAGCAGCGCTCGGAGAGAGATCTCAAGAGAGTTTACACAGCA	903
Qy	781	TGGCAGTTTGAAGAAAGAGAGAGGAGAACTGACATGCCCTTCCGTTCAGATCAGAG	840
Db	904	TGGCAGTTTGAAGAAAGAGAGAGGAGAACTGACATGCCCTTCCGTTCAGATCAGAG	963
Qy	841	ATGACGATCTTAAACAGTGGACGCTTATTTGTAAGATTTCGAAAGGAGCTACCGGATTTCTCC	900
Db	964	ATGACGATCTTAAACAGTGGACGCTTATTTGTAAGATTTCGAAAGGAGCTACCGGATTTCTCC	1023
Qy	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGCGTTCATCAAGCGAAGTATGATG	960
Db	1024	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGCGTTCATCAAGCGAAGTATGATG	1083
Qy	961	CTGCGAGTGGCGGACGCGTACGACGCGGCGAGCAGAGCGTGTGTTTCGCGAACCAACG	1020
Db	1084	CTGCGAGTGGCGGACGCGTACGACGCGGCGAGCAGAGCGTGTGTTTCGCGAACCAACG	1143
Qy	1021	CGGTACAGCGCGCAACACTACCGCGGCGATGCTTACGTCATCGAGGAGCTGCTG	1080
Db	1144	CGGTACAGCGCGCAACACTACCGCGGCGATGCTTACGTCATCGAGGAGCTGCTG	1203
Qy	1081	CACCTTCTGTCGCTGTATGCTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTACC	1140
Db	1204	CACCTTCTGTCGCTGTATGCTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTACC	1263
Qy	1141	GCCATCGTATATTTCTGACAGCGCGCGCTCGAGCAACCCCTTTTAGTCGAGGAAATC	1200
Db	1264	GCCATCGTATATTTCTGACAGCGCGCGCTCGAGCAACCCCTTTTAGTCGAGGAAATC	1323
Qy	1201	CAGAGATACTACTTGAAGACGCTCGGGGTTTACATTTTAAATCAGACAGCGCGCTCGCT	1260

Db 1324 CAGAGATCTACTTGAAGACGCTGGGTTTACATTTTAAATCAGTACAGCGCTCGCT 1383
 QY 1261 CGCTGGCGCTGCTGTTGGCAAGATCTCTGGCGTCTGACGGAACCTGGCGACGCTCGC 1320
 Db 1384 CGCTGGCGCTGCTGTTGGCAAGATCTCTGGCGTCTGACGGAACCTGGCGACGCTCGC 1443
 QY 1321 AGCGAGAACTCAACATGTCATCTCGCTGAAGCTGMAAGACAGGAACCTCCGCCATTTC 1380
 Db 1444 AGCGAGAACTCAACATGTCATCTCGCTGAAGCTGMAAGACAGGAACCTCCGCCATTTC 1503
 QY 1381 CTCGAGGAGATCTGGAGCATGTCGCGAAGTGTCCAGACGAAGCTTGGCCCCCGACCGAT 1440
 Db 1504 CTCGAGGAGATCTGGAGCATGTCGCGAAGTGTCCAGACGAAGCTTGGCCCCCGACCGAT 1545
 QY 1441 GTGAGCTGGGAGACGAGCTCACTTAGACGCGGAGACGTCGGGATGCGGATGCGGAC 1500
 Db 1546 GTGAGCTGGGAGACGAGCTCACTTAGACGCGGAGACGTCGGGATGCGGATGCGGAC 1605
 QY 1501 GCGTAGACGATTCGATCTGACATGTTGGGGAGCGGGATTCGCCGGTCCGGGATTT 1560
 Db 1606 GCGTAGACGATTCGATCTGACATGTTGGGGAGCGGGATTCGCCGGTCCGGGATTT 1665
 QY 1561 ACCCCACGACTCCGCCCTTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1620
 Db 1666 ACCCCACGACTCCGCCCTTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1725
 QY 1621 ATGTTTACGATGCCCTTGGAAATGACGAGTACGAGTACGGTGGGTAG 1662
 Db 1726 ATGTTTACGATGCCCTTGGAAATGACGAGTACGAGTACGGTGGGTAG 1767

RESULT 4

ADP49194

ID ADF49194 standard; DNA; 1767 BP.

AC ADF49194;

XX ADF49194;

DT 12-FEB-2004 (first entry)

XX Ecdysone receptor/VP16 transactivation domain DNA seq id 122.

DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.

XX Synthetic.

OS Manduca sexta.

OS Ascomycota.

OS Spodoptera frugiperda.

OS Herpes simplex virus unknown type.

XX US2003154509-A1.

PN 14-AUG-2003.

XX 24-OCT-2001; 2001US-00087167.

XX 24-OCT-2001; 2001US-00087167.

XX (PASC/) PASCAL E J.

XX (VALE/) VALENTINE S A.

XX (BROW/) BROWN J A.

XX (COCK/) COCKRELL A S.

XX (JOHN/) JOHNSON B D.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2003-897756/82.

XX P-PSDB; ADF49195.

XX

PT New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX Example 23; SEQ ID NO 122; 186pp; English.
 XX
 CC The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.,
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-VP16
 CC transactivation domain fusion protein.
 XX
 SQ Sequence 1767 BP; 476 A; 431 C; 477 G; 383 T; 0 U; 0 Other;

Query Match 97.0%; Score 1612.8; DB 10; Length 1767;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;
 QY 1 ATGAAGCTACTGTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGTCAAG 60
 Db 124 ATGAAGCTACTGTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGTCAAG 183
 QY 61 TGCTCCAAAGAAAAACCGAAGTGCCTCAAGTGTCTGMAAGAACACTGGGAGTGCCTAC 120
 Db 184 TGCTCCAAAGAAAAACCGAAGTGCCTCAAGTGTCTGMAAGAACACTGGGAGTGCCTAC 243
 QY 121 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTCACAGAACTGGAATCAAGG 180
 Db 244 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTCACAGAACTGGAATCAAGG 303
 QY 181 CTGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGACATGATT 240
 Db 304 CTGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGACATGATT 363
 QY 241 TTGAAATGGATCTTTACAGGATATAAAGCATTTTAAAGGATTTTAAAGGATTTTAAAGAT 300
 Db 364 TTGAAATGGATCTTTACAGGATATAAAGCATTTTAAAGGATTTTAAAGGATTTTAAAGAT 423
 QY 301 AATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
 Db 424 AATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483
 QY 361 ACATTTGAGACAGCATAGAAATAAGTGGACATCATCATATCGGAGAGAGTAGTAACAAGGT 420
 Db 484 ACATTTGAGACAGCATAGAAATAAGTGGACATCATCATATCGGAGAGAGTAGTAACAAGGT 543
 QY 421 CAAAGACAGTTGACTGTATTCGACGGTATGAGCCCGAGTGCCTCCCGAGAGTCCACG 480
 Db 544 CAAAGACAGTTGACTGTATTCGACGGTATGAGCCCGAGTGCCTCCCGAGAGTCCACG 603
 QY 481 TCGCAAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAAACATGCGCAGTCAGT 540
 Db 604 TCGCAAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAAACATGCGCAGTCAGT 663
 QY 541 ACGACGACAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACCTCCGCCCCAGAG 600
 Db 664 ACGACGACAGTGGACGATCATATGCTGCGCATTAATGCAATGTGACCTCCGCCCCAGAG 723
 QY 601 GCGGCAAGGATTCAGAAAGTGGTCCGAGTTCCTAACCGGAGAGAGCTTAATGGAGCAGAAC 660
 Db 724 GCGGCAAGGATTCAGAAAGTGGTCCGAGTTCCTAACCGGAGAGAGCTTAATGGAGCAGAAC 783
 QY 661 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGATCCCTGATCGGAGGCTCGTG 720
 Db 784 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGATCCCTGATCGGAGGCTCGTG 843
 QY 721 TGTATCAGGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGATTACACAGACA 780

XX	Sequence	1800 BP; 482 A; 444 C; 485 G; 389 T; 0 U; 0 Other;
SQ		
	Query Match	93.4%; Score 1552.2; DB 10; Length 1800;
	Best Local Similarity	95.9%; Pred. No. 0;
	Matches 1609; Conservative	0; Mismatches 53; Indels 15; Gaps 1;
Qy	1	ATGAAGCTACTGTTCTTCTATCGAACAAAGCATGGATATTGGCCGACCTTAAAGCTCAAG 60
Db	124	ATGAAGCTACTGTTCTTCTATCGAACAAAGCATGGATATTGGCCGATTTAAAAAGCTCAAG 183
Qy	61	TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTCGGAGTGTGCCTAC 120
Db	184	TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGNAGAACAACTGGGAGTGTGCCTAC 243
Qy	121	TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGACAGAAGTGGNATCAAGG 180
Db	244	TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCAAGG 303
Qy	181	CTAGAAGACTGGAACAGCTATTCTACTCATTTTTCTCTCGAGAAGACCTTGACATGATT 240
Db	304	CTAGAAGACTGGAACAGCTATTCTTACTGATTTTTCTCTCGAGAAGACCTTGACATGATT 363
Qy	241	TTGAAATGGATTCTTTACAGGATATAAAGCATTTGTAA CAGGATTATTGTGACAAGAT 300
Db	364	TTGAAATGGATTCTTTACAGGATATAAAGCATTTGTAA CAGGATTATTGTGACAAGAT 423
Qy	301	AATGTGAATAAAGATGCGGTCA CAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTCA 360
Db	424	AATGTGAATAAAGATGCGGTCA CAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTCA 483
Qy	361	ACATTGAGACAGCATAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTATAACAAGGT 420
Db	484	ACATTGAGACAGCATAGNAATAGTGCACATCATCATCGGAAGAGAGTAGTATAACAAGGT 543
Qy	421	CAAGA CAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCCTGCCAGAGTCCACG 480
Db	544	CAAGA CAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCCTGCCAGAAAACG CAG 603
Qy	481	TGCAAGAACAAAGAGAGAAAGAGACAGAGAGAAAAAGACAAATGCCAGTCAGT 540
Db	604	TGTGCGCAAAAGAGAAAGAGAAAGAGACAGAGAGAAAAGACAAACTTACCAAGTGAGC 663
Qy	541	ACGACGACAGTGGACGATCATATGCCTGCCATAATGCAATGTGACCTCGCCCCCAGAG 600
Db	664	ACACGACAGTAGCAGTATATGCCCCCAATCATGCAAGTGTGATCCACCAACCCCGGAG 723
Qy	601	CGCGCAAGGATTT-----CACGAAGTGTCCCGAGTTCTCTAAACGGAGAAG 645
Db	724	CGAGCGAGGATTTGTGGAATGTTTG CAGCATGAAGTGTGCCCGGGTTCTCTCGAGAGAG 783
Qy	646	CTAATGGAGACGAAACAGACTGAAGAAATGTGACGCCGTGTGGCGGAACACAGAAATCCCTG 705
Db	784	CTGATGGAGCAGATCGGCTGAAGAACATACCCCCCTCACCGGCCAACACGACAGTTCCCTG 843
Qy	706	ATCGCGAGGCTGTTGTGTATCCAGAGGGGTACGACAGCCGTCGGAGGAGATCTCAAG 765
Db	844	ATCGCGAGGCTGTTGTGTATCCAGAGGGGTACGACAGCCGTCGGAGGAGATCTCAAG 903
Qy	766	AGAGTTACACACACATGCGAGTTAGAGAAGAAAGAGAGGAGGAAAACCTGACATGCCCTTC 825
Db	904	AGAGTTACACACACATGCGATTTAGAGAAGAGAGAGAGGAGGAAAACCTGACATGCCCTTC 963
Qy	826	CCTCAGATCACAGAGATGACGATCTTAA CAGTGCAGCTTATTGTAGAAATTCGCAAGGGA 885
Db	964	CCTCAGATCACAGAGATGACGATCTTAA CAGTGCAGCTTATTGTAGAAATTCGCAAGGGA 1023
Qy	886	CTACCGGGATTCTCCAAGATATCTCAGTCCGATCAAAATTA CATTTATAAAGCGCTCATCA 945
Db	1024	CTACCGGGATTCTCCAAGATATCTCAGTCCGATCAAAATTA CATTTATAAAGCGCTCATCA 1083
Qy	946	AGCGAAGTGATGATGCTCGAGTGGCGGACGGTACGACGCGGCGGACGAGCAGCGTCTG 1005

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX P-PSDB; ABJ05372.
 DR WPI; 2002-619259/66.
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX Example 23; Page 265-267; 319pp; English.
 XX The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC domain of an insect ECR, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a coding sequence described in the exemplification of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX Sequence 1776 BP; 466 A; 444 C; 481 G; 385 T; 0 U; 0 Other;
 SQ
 Query Match 86.7%; Score 1441.6; DB 6; Length 1776;
 Best Local Similarity 92.6%; Pred. No. 0;
 Matches 1539; Conservative 0; Mismatches 114; Indels 9; Gaps 2;
 QY 1 ATGAAGCTACTGCTCTTATCGAAGAGCATGGATATTCGCGATTTAAAGAGCTCAAG 60
 DB 124 ATGAAGCTACTGCTCTTATCGAAGAGCATGGATATTCGCGATTTAAAGAGCTCAAG 183
 QY 61 TGTCTCAAG 120
 DB 184 TGTCTCAAG 243
 QY 121 TCTCTCAAG 180
 DB 244 TCTCTCAAG 303
 QY 181 CTAG 240
 DB 304 CTAG 363
 QY 241 TTGAAG 300
 DB 364 TTGAAG 423
 QY 301 AATGTGAAG 360
 DB 424 AATGTGAAG 483
 QY 361 ACATTGAG 420
 DB 484 ACATTGAG 543
 QY 421 CAAAG 480
 DB 544 CAAAG 603
 QY 481 TGCAAG 540
 DB 604 TGCAAG 663
 QY 541 ACAG 600
 DB 664 ACAG 723
 QY 601 GCGCAG 660

DB 724 GCGCAAG 783
 QY 661 AGACTGAAG 720
 DB 784 AGACTGAAG 843
 QY 721 TGGTACCAG 780
 DB 844 TGGTACCAG 903
 QY 781 TGGCAGTGTAG 840
 DB 904 TGGCAGTGTAG 960
 QY 841 ATGACAGTCTTAAACAG 900
 DB 961 ATGACAGTCTTAAACAG 1020
 QY 901 AAGATATCTCAGTCCGATCAAAATTAACATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 1021 AAGATATCTCAGTCCGATCAAAATTAACATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 961 CTGCGAGTGGCGGAG 1020
 DB 1081 CTGCGAGTGGCGGAG 1140
 QY 1021 GCGTACAGCGGAG 1080
 DB 1141 GCGTACAGCGGAG 1200
 QY 1081 CACTTCTGCGGTGTATGTCTCATATGAGCATATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1140
 DB 1201 CACTTCTGCGGTGTATGTCTCATATGAGCATATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1260
 QY 1141 GCGTACAGCGGAG 1200
 DB 1261 GCGTACAGCGGAG 1320
 QY 1201 CAGAGATATCTTCAAG 1260
 DB 1321 CAGCGGTATTTACCTGAG 1380
 QY 1261 GCGTACAGCGGAG 1320
 DB 1381 GCGTACAGCGGAG 1440
 QY 1321 ACAG 1380
 DB 1441 ATGCAG 1500
 QY 1381 CTCGAGGAG 1440
 DB 1501 CTCGAGGAG 1554
 QY 1441 GTGAG 1500
 DB 1554 GTGAG 1614
 QY 1501 GCGGTAG 1560
 DB 1614 GCGGTAG 1674
 QY 1561 ACCCGGAG 1620
 DB 1674 ACCCGGAG 1734
 QY 1621 ATGTTTACGAG 1682
 DB 1735 ATGTTTACGAG 1776

ADP49190 standard; DNA; 1776 BP.
ADP49190;
12-FEB-2004 (first entry)
Ecdysone receptor/VP16 transactivation domain DNA seq id 118.
receptor cassette; chimeric receptor polypeptide; DNA binding domain;
hinge domain; ecdysone receptor; ECR; ligand binding domain;
activation domain; transgenic seed; transgenic plant; plant line;
herbicide; pesticide; chimeric ecdysone receptor; ECR;
yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.
Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Agrotis ipsilon.
OS Herpes simplex virus unknown type.
XX PN US2003154509-A1.
XX XX 14-AUG-2003.
XX XX 24-OCT-2001; 2001US-00087167.
XX XX 24-OCT-2001; 2001US-00087167.
XX PA (PASC/) PASCAL E J.
XX PA (VALE/) VALENTINE S A.
XX PA (BROW/) BROWN J A.
XX PA (COCK/) COCKRELL A S.
XX PA (JOHN/) JOHNSON B D.
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX WPI: 2003-897756/82.
XX DR P-PSDB; ADP49191.
XX XX
XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful
XX PT for regulating the expression of target polypeptides in plants in the
XX PT presence of appropriate chemical ligands.
XX XX
XX XX Example 23; SEQ ID NO 118; 186pp; English.
XX CC The invention describes a receptor cassette encoding a chimeric receptor
XX CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
XX CC (E) domain that is heterologous with respect to the D domain, and an
XX CC activation domain. The receptor cassette and method are useful in
XX CC regulating the expression of target polypeptides in plants in the
XX CC presence of appropriate chemical ligands. The transgenic seeds and plants
XX CC can be used for the breeding of improved plant lines that, for e.g.
XX CC increase the effectiveness of conventional methods such as herbicide or
XX CC pesticide treatment. This sequence encodes an ecdysone receptor-VP16
XX CC transactivation domain fusion protein.
XX XX
XX SQ Sequence 1776 BP; 466 A; 444 C; 481 G; 385 T; 0 U; 0 Other;
Query Match 86.7%; Score 1441.6; DB 10; Length 1776;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1539; Conservative 0; Mismatches 114; Indels 9; Gaps 2;
QY 1 ATGAAGCTACTGCTCTATCGAACAGCATCGGATATTCGCGACTTAAAGAGCTCAAG 60
Db 124 ATGAAGCTACTGCTCTATCGAACAGCATCGGATATTCGCGACTTAAAGAGCTCAAG 183
QY 61 TCGTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 120
Db 184 TGCCTCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 243
QY 121 TCTCCCAAAACCAAAGGTCTCGGTGACTAGGGCACATCTTCACAGAAAGTGAATCAAG 180

Db 244 TCTCCCAAAACCAAAGGTCTCGGTGACTAGGGCACATCTGACAGAAAGTGAATCAAG 303
QY 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCTCGAGAGACCTTGACATGATT 240
Db 304 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCTCGAGAGACCTTGACATGATT 363
QY 241 TTGAAAATGGATTCTTTTACAGGATATAAAAGCATTTTAAACAGGATTTATTTGTACAAGAT 300
Db 364 TTGAAAATGGATTCTTTTACAGGATATAAAAGCATTTTAAACAGGATTTATTTGTACAAGAT 423
QY 301 AATGTCAATAAAGATCCGCTCAAGATAGATTGGCTTTCAGTGAGAGACTGATATGCTCTTA 360
Db 424 AATGTCAATAAAGATCCGCTCAAGATAGATTGGCTTTCAGTGAGAGACTGATATGCTCTTA 483
QY 361 ACATTGAGACAGCATAGAAATAGTGGGACATCATCATCGAAGAGAGTAGTAACAAAGGT 420
Db 484 ACATTGAGACAGCATAGAAATAGTGGGACATCATCATCGAAGAGAGTAGTAACAAAGGT 543
QY 421 CAAAAGACAGTTGACTCTGATCGACCGCTATGAGGCCGAGTGGCTGTCCTCAGAGTCCACG 480
Db 544 CAAAAGACAGTTGACTCTGATCGACCGCTATGAGGCCGAGTGGCTGTCCTCAGAGTCCACG 603
QY 481 TGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAGAAAAGACAACTGCCAGTCAGT 540
Db 604 TGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAGAAAAGACAACTGCCAGTCAGT 663
QY 541 ACCACACAGTGGACGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 664 ACCACACAGTGGACGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
QY 601 GCGGCAAGGATTCACGAAGTGGTCCGAGTTCCTAACGAGAGAACTAATGGAGAGAAC 660
Db 724 GCGGCAAGGATTCACGAAGTGGTCCGAGTTCCTAACGAGAGAACTAATGGAGAGAAC 783
QY 661 AGACTGAAGATGTGACCGCGCTGTCGCGCAACAGAGTCCCTGATCGGAGGCTCGTG 720
Db 784 AGACTGAAGATGTGACCGCGCTGTCGCGCAACAGAGTCCCTGATCGGAGGCTCGTG 843
QY 721 TGGTACCAGAGGGGTACGAGCAGCGCTCGGAGAGAGATCTCAAGAGAGTTTACACAGACA 780
Db 844 TGGTACCAGAGGGGTATGAACTTCAAGAGAGAGATCTCAAGAGAGTTTACACAGACC 903
QY 781 TGGCAGTTAGAAAGAAAGAGAGAGAGAACTGACATGCCCTTCGCTCAGATCAGAGAG 840
Db 904 TGGCAGTTAGAAAGAAAG 960
QY 841 ATGACGATCTTAACAGTGCAGCTTATTTGTAGAAATTCGAAAGAGACTACCGGATTTCTCC 900
Db 961 ATGACGATCTTAACAGTGCAGCTTATTTGTAGAAATTCGAAAGAGACTACCGGATTTCTCC 1020
QY 901 AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGCGGTCTCAAGCGAAGTGAATG 960
Db 1021 AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGCGGTCTCAAGCGAAGTGAATG 1080
QY 961 CTGCGAGTGGCGGACGCTGACGAGCGCGGACCGAGAGCGGTGCTGTCGCGAACAAACAG 1020
Db 1081 CTGCGAGTGGCGGCGGTGACGAGCGCGGACCGAGAGCGGTGCTGTCGCGAACAAACAG 1140
QY 1021 GCGTACACGCGGACAACTACCGCAAGCGGGATGTCCTACGTCATCGAGGACCTGCTG 1080
Db 1141 GCGTACCTCCGCGAACAATACCGCAAGCGGGATGTCCTACGTCATCGAGGATCTCTTG 1200
QY 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGCAATGTGCACTACGCGCTGCTCACC 1140
Db 1201 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGCAATGTGCACTACGCGCTGCTTACG 1260
QY 1141 GCGATCGTTATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTAAAGTGGAGAGAAATC 1200
Db 1261 GCGATCGTTATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTAAAGTGGAGAGAAATC 1320
QY 1201 CAGAGATACTACTTGAAGAGCGCTCGGGGTTTACATTTTAAATCAGACAGCGCGCTCGCT 1260
Db 1321 CAGCGGATATTACCTGAAACAGCTGCGGGGTGTACATCTTGAACCAAAACAGTGGCTGCGCG 1380

Qy 901 AAGATATCTAGTCGGATCAAAATTACATTATTAAGGGGTCTATCAAGCGAAGTCAATG 960
 Db 1024 AAGATATCTAGTCGGATCAAAATTACATTATTAAGGGGTCTATCAAGCGAAGTCAATG 1083
 Qy 961 CTGGAGTGGCGGACGGTACGCGCGGACGACAGCGTGTTCGGGAAACAACGAG 1020
 Db 1084 CTGGAGTGGCGGACGGTACGCGCGGACGACAGCGTGTTCGGGAAACAACGAG 1143
 Qy 1021 GCGTACAGCGCGGACAACTACCGAAGCGGCGATGCTTCAAGTCATCGAGGACCTGCTG 1080
 Db 1144 GCGTACAGCGCGGACAACTACCGAAGCGGCGATGCTTCAAGTCATCGAGGACCTGCTG 1203
 Qy 1081 CACTTCTGCGGTGTATGTTCTCCATGAGCATGACAAATGTGCACTAGCGGCTGCTCACC 1140
 Db 1204 CACTTCTGCGGTGTATGTTCTCCATGAGCATGACAAATGTGCACTAGCGGCTGCTCACC 1263
 Qy 1141 GCCATCGTTATTTCTCAGACGGCGGCGCTCGAGCAACCCCTTTTAGTGGAGGAATC 1200
 Db 1264 GCCATCGTTATTTCTCAGACGGCGGCGCTCGAGCAACCCCTTTTAGTGGAGGAATC 1323
 Qy 1201 CAGAGATACTACTTGAAGACGCTCGGCTTTTACATTTTAAATCAGCAAGCGCTCGCCT 1260
 Db 1324 CAGAGATACTACTTGAAGACGCTCGGCTTTTACATTTTAAATCAGCAAGCGCTCGCCT 1383
 Qy 1261 CGCTCGCGCTGCTGTTTCGGCAAGATCCTCGGCGTCTGACGGAACCTCGCACGCTCGGC 1320
 Db 1384 CGCTCGCGCTGCTGTTTCGGCAAGATCCTCGGCGTCTGACGGAACCTCGCACGCTCGGC 1443
 Qy 1321 ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGAAAGACAGGAACTTCCGCCATTC 1380
 Db 1444 ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGAAAGACAGGAACTTCCGCCATTC 1503
 Qy 1381 CTCGAGGAGATCTGGGAGTGCGGCGGAAAGTGTGACGACGAAAGCTTGGCCCCCAGCCGAT 1440
 Db 1504 CTCGAGGAGATCTGGGAGTGCGGCGGAAAGTGTGACGACGAAAGCTTGGAGCTCGCCACCGCG 1563
 Qy 1441 CTCAGCCTGGG 1451
 Db 1564 GCCGACCCAGG 1574
 RESULT 10
 ADF49208
 ID ADF49208 standard; DNA; 1863 BP.
 XX AC ADF49208;
 DT
 XX 12-FEB-2004 (first entry)
 DE Ecdysone receptor/Dof1 transactivation domain DNA seq id 136.
 XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
 KW yeast GAL4 DNA binding domain; Dof1 transactivation domain; ds; gene.
 XX
 OS Synthetic.
 OS Manduca sexta.
 OS Ascomycota.
 OS Zea mays.
 XX
 PN US2003154509-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 24-OCT-2001; 2001US-00087167.
 XX
 PR 24-OCT-2001; 2001US-00087167.
 XX
 PA (PASC/) PASCAL E J.
 PA (VALE/) VALENTINE S A.

PA (BROW/) BROWN J A.
 PA (COCK/) COCKRELL A S.
 XX (JOHN/) JOHNSON B D.
 PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX WPI; 2003-897756/82.
 XX
 PT New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX
 PS Example 25; SEQ ID NO 136; 186pp; English.
 XX
 CC The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.,
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-Dof1
 CC transactivation domain fusion protein.
 XX
 SQ Sequence 1863 BP; 487 A; 489 C; 510 G; 377 T; 0 U; 0 Other;
 Query Match 86.1%; Score 1431.8; DB 10; Length 1863;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 ATGAGCTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
 Db 124 ATGAGCTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
 Qy 61 TGTCTCCAAAGAAAAACCGAAGTGGCGGAGTGTCTGAAGAACAACTGGGAGTGTGCGTAC 120
 Db 184 TGTCTCCAAAGAAAAACCGAAGTGGCGGAGTGTCTGAAGAACAACTGGGAGTGTGCGTAC 243
 Qy 121 TCTCCCAAAACCAAAAGGTCTCGCTAGTGGGACATCTGACAGAAAGTGGAAATCAAG 180
 Db 244 TCTCCCAAAACCAAAAGGTCTCGCTAGTGGGACATCTGACAGAAAGTGGAAATCAAG 303
 Qy 181 CTAGAAAGACTGGAAACAGCTATTTTCTACTGATTTTCTCTCGAGAAAGCTTGAACATGATT 240
 Db 304 CTAGAAAGACTGGAAACAGCTATTTTCTACTGATTTTCTCTCGAGAAAGCTTGAACATGATT 363
 Qy 241 TTGAAAATGGATTTCTTACAGGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAAGAT 300
 Db 364 TTGAAAATGGATTTCTTACAGGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAAGAT 423
 Qy 301 AATGTGAAATGAAGATCGCGTCACAGATAGATTGCTTTCAGTGGAGACTGTATATGCTCTTA 360
 Db 424 AATGTGAAATGAAGATCGCGTCACAGATAGATTGCTTTCAGTGGAGACTGTATATGCTCTTA 483
 Qy 361 ACATTGAGACAGCATAGAATAAGTGGACATCATCATCTCGGAAGAGAGTAGTAAACAAAGGT 420
 Db 484 ACATTGAGACAGCATAGAATAAGTGGACATCATCATCTCGGAAGAGAGTAGTAAACAAAGGT 543
 Qy 421 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGGCTGCTCCAGAGTCCACG 480
 Db 544 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGGCTGCTCCAGAGTCCACG 603
 Qy 481 TGCAAGAACAAAAGAGAGAAAAGAGAACAGACAGAGAGAAAAAGACAAACTGCCAGTCAAGT 540
 Db 604 TGCAGAAACAAAAGAGAGAAAAGAGAACAGACAGAGAGAAAAGACAAACTGCCAGTCAAGT 663
 Qy 541 ACAGACAGTGGACGATCATATGCTGCGCATATTAATGCAATGTGACCTCCGCCCCACGAG 600
 Db 664 ACAGACAGTGGACGATCATATGCTGCGCATATTAATGCAATGTGACCTCCGCCCCACGAG 723
 Qy 601 CGGCAAGGATTACAGAAAGTGGTCCCGAGGTTCTTCTACGGAGAGAGCTAAATGGAGACAGAAC 660

Db 724 GCGGCAAGATTACGAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATCGAGCAGAAC 783
Qy 661 AGACTGAAGAAATGTGACCGCGTGTGCGCGAACAACGAAAGTCCCTGATCGCGAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTGACCGCGTGTGCGCGAACAACGAAAGTCCCTGATCGCGAGGCTCGTG 843
Qy 721 TGGTACCAAGAGGGGTACGACAGCCGTCGGAGGAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAAGAGGGGTACGACAGCCGTCGGAGGAGATCTCAAGAGAGTTACACAGACA 903
Qy 781 TGGCAGTTAGAGAAAGAGAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCACAGAG 840
Db 904 TGGCAGTTAGAGAAAGAGAGAGGAGGAACTGACATGCCCTTCCGTCAGATCACAGAG 963
Qy 841 ATGACGATCTTAAAGTGCAGCTTATTTGTAAGATTCGCAAAAGGAGTACCCGGATTCTCC 900
Db 964 ATGACGATCTTAAAGTGCAGCTTATTTGTAAGATTCGCAAAAGGAGTACCCGGATTCTCC 1023
Qy 901 AAGATATCTAGTCCGATCAATTAATACATTTAAAGGCGTCAATCAAGCGAAGTATGATG 960
Db 1024 AAGATATCTAGTCCGATCAATTAATTAAGGCGTCAATCAAGCGAAGTATGATG 1083
Qy 961 CTGCGAGTGGCGCGAGTACGACGCGCGACGAGCAGCGTGTCTTCCGCAACCAACAG 1020
Db 1084 CTGCGAGTGGCGCGAGTACGACGCGCGCGACGAGCAGCGTGTCTTCCGCAACCAACAG 1143
Qy 1021 GCGTACACGCGCGAACAATACCGCAAGCGGCGATGCTTACGTCATCGAGGACCTGCTG 1080
Db 1144 GCGTACACGCGCGAACAATACCGCAAGCGGCGATGCTTACGTCATCGAGGACCTGCTG 1203
Qy 1081 CACTTCTGTCGCTGTATGCTACTCCATGACATGGAATGTGCATACGCGTGTCTCACC 1140
Db 1204 CACTTCTGTCGCTGTATGCTACTCCATGACATGGAATGTGCATACGCGTGTCTCACC 1263
Qy 1141 GCGTCTGTTATATCTCAGACGCGCGCAGGCTCGAGCAACCCCTTTTGTGAGGAAATC 1200
Db 1264 GCGTCTGTTATATCTCAGACGCGCGCAGGCTCGAGCAACCCCTTTTGTGAGGAAATC 1323
Qy 1201 CAGAGATACCTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1260
Db 1324 CAGAGATACCTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1383
Qy 1261 CGCTGCGCGCTGCTTCCGCAAGATCTCCTGCGGTCGACGGAACCTGCGACGCTCGGC 1320
Db 1384 CGCTGCGCGCTGCTTCCGCAAGATCTCCTGCGGTCGACGGAACCTGCGACGCTCGGC 1443
Qy 1321 ACGCAGAACTCCAACATGTGCACTCTCGCTGAAGCTGAAGAAACAGGAACTTCCGCAATC 1380
Db 1444 ACGCAGAACTCCAACATGTGCACTCTCGCTGAAGCTGAAGAAACAGGAACTTCCGCAATC 1503
Qy 1381 CTCGAGGAGATCTGGGACGTCGCGAAGTGTGCAAGCAAGCTTGGCCCCCGGACCGAT 1440
Db 1504 CTCGAGGAGATCTGGGACGTCGCGAAGTGTGCAAGCAAGCTTGGCCCCCGGACCGG 1563
Qy 1441 CTCAGCCTGGG 1451
Db 1564 GCCGACCCAGG 1574

RESULT 11
ABT07376
ID ABT07376 standard; DNA; 1848 BP.
XX
AC
XX
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
XX
KW Chimeric ecdysone receptor coding sequence SEQ ID NO: 134.
KW plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.

XX Manduca sexta.
OS Manduca sexta.
OS Chimeric.
FN WO200261102-A2.
XX
PD 08-AUG-2002.
XX
PF 24-OCT-2001; 2001WO-US051417.
XX
PR 24-OCT-2000; 2000US-0242969P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI; 2002-619259/66.
XX
PS P-PSDB; ABJ05378.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX
PS Example 25; Page 296-298; 319pp; English.
XX
CC The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
CC domain of an insect EcR, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
Query Match 85.8%; Score 1426.6; DB 6; Length 1848;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
Qy 1 ATGAGCTACTGTCTTCTATCGAACAAGCTGCGATATTTGCGGACTTAAAAAGCTCAAG 60
Db 124 ATGAGCTACTGTCTTCTATCGAACAAGCTGCGATATTTGCGGACTTAAAAAGCTCAAG 183
Qy 61 TGCTCCAAAGAAAAA CCGAAGTGCAGTGTCTGAAAGAACAACTGGGAGTGTGCTAC 120
Db 184 TGCTCCAAAGAAAAA CCGAAGTGCAGTGTCTGAAAGAACAACTGGGAGTGTGCTAC 243
Qy 121 TCTCCAAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTCAGAGAGAGCTTGCATGATT 180
Db 244 TCTCCAAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTCAGAGAGAGCTTGCATGATT 303
Qy 181 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTCGAAGAGACCTTGCATGATT 240
Db 304 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTCGAAGAGAGCTTGCATGATT 363
Qy 241 TTGAAAATGGATTCTTTTACAGGATATAAAGCAATTTTAAACAGGATTTTGTGTACAGAT 300
Db 364 TTGAAAATGGATTCTTTTACAGGATATAAAGCAATTTTAAACAGGATTTTGTGTACAGAT 423
Qy 301 AATGTGAATAAAGATCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
Db 424 AATGTGAATAAAGATCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483
Qy 361 ACATTTGAGACACATAGATAAGTGCACATCATCTCGAAGAGAGAGTAGTAACAAGGT 420
Db 484 ACATTTGAGACACATAGATAAGTGCACATCATCTCGAAGAGAGAGTAGTAACAAGGT 543
Qy 421 CAAAGACAGTTGACTGTATTCGACGGGTATGAGGCCCGAGTGTGCTGCCAGAGTCCAG 480

544	DB	CAAAGACAGTTGACTGTGATCGACGCGCTATGAGGCCGAGTGCGTCTGCTCCAGAGTCCACG	603
481	QY	TGCAAGNACAAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAAATGCCAGGTCACT	540
604	DB	TGCAAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAAATGCCAGGTCACT	663
541	QY	ACGACGACGTGGACGACATATATGCTCTGCCATTAATGCAATGTGACCCCTCGCCCCCAGAG	600
664	DB	ACGACGACGTGGACGACATATATGCTCTGCCATTAATGCAATGTGACCCCTCGCCCCCAGAG	723
601	QY	CGCGCAAGGATTCACGGAAGTGGTCCGAGGTTCTTAACGAGAGAGTAAATGGAGCAGAAC	660
724	DB	CGCGCAAGGATTCACGGAAGTGGTCCGAGGTTCTTAACGAGAGAGTAAATGGAGCAGAAC	783
661	QY	AGACTGAAGAAATGTGACCGCCGCTGTCCGCGAAACGAGAGTCCCTGATCCGAGGCTCGTG	720
784	DB	AGACTGAAGAAATGTGACCGCCGCTGTCCGCGAAACGAGAGTCCCTGATCCGAGGCTCGTG	843
721	QY	TGGTACCAGAGGGGTACGAGCAGCCGTCCGAGGAGATCTCAAGAGAGTTACACAGACA	780
844	DB	TGGTACCAGAGGGGTACGAGCAGCCGTCCGAGGAGATCTCAAGAGAGTTACACAGACA	903
781	QY	TGGCAGTTAGAGAAGAGAGAGGAGGAAACTGACATGCCCTTCGTTCAGATCAACAGAG	840
904	DB	TGGCAGTTAGAGAAGAGAGAGGAGGAAACTGACATGCCCTTCGTTCAGATCAACAGAG	963
841	QY	ATGACGATCTTAACAGTGCAGCTTATTTGTAGAAATTCGCAAGGGACTACCGGATCTTCC	900
964	DB	ATGACGATCTTAACAGTGCAGCTTATTTGTAGAAATTCGCAAGGGACTACCGGATCTTCC	1023
901	QY	AAGATATCTCAGTCCGATCAAAATFACATATTTAAAGCGCTCATCAAGCGAAGTGATGATG	960
1024	DB	AAGATATCTCAGTCCGATCAAAATFACATATTTAAAGCGCTCATCAAGCGAAGTGATGATG	1083
961	QY	CTCGGAGTGGCGCAGCGGTACGACGCGGCGCACGAGCAGCGTGTGTTTCGCGAAACACCAG	1020
1084	DB	CTCGGAGTGGCGCAGCGGTACGACGCGGCGCACGAGCAGCGTGTGTTTCGCGAAACACCAG	1143
1021	QY	GGGTACAGCGCGCAAACTACCGCAAGCGGGGATGTCTTACGTCACTAGGAGACCTGCTG	1080
1144	DB	GGGTACAGCGCGCAAACTACCGCAAGCGGGGATGTCTTACGTCACTAGGAGACCTGCTG	1203
1081	QY	CACCTTCTGTCGGTGTATGTACTCCATGAGCATGGAACAATGTGCACTACGCGCTGCTCACC	1140
1204	DB	CACCTTCTGTCGGTGTATGTACTCCATGAGCATGGAACAATGTGCACTACGCGCTGCTCACC	1263
1141	QY	GCCATCGTTATATTTCTCAGACCGGCCAGGCTCGAGCAACCCCTTTTGTGGAGGAAATC	1200
1264	DB	GCCATCGTTATATTTCTCAGACCGGCCAGGCTCGAGCAACCCCTTTTGTGGAGGAAATC	1323
1201	QY	CAGAGATACTACTTGAAGACGCTCGGGTTTACATTTTAAATCAGCACAGCGGTCGCTT	1260
1324	DB	CAGAGATACTACTTGAAGACGCTCGGGTTTACATTTTAAATCAGCACAGCGGTCGCTT	1383
1261	QY	CGCTCGCCGCTGTTTCGGCAAGATCTCGGCGTGTGACGGAATCTGCGCAGCTCGCTCGGC	1320
1384	DB	CGCTCGCCGCTGTTTCGGCAAGATCTCGGCGTGTGACGGAATCTGCGCAGCTCGCTCGGC	1443
1321	QY	ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGAAGAACAGGAAATTCGCGCAATTC	1380
1444	DB	ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGAAGAACAGGAAATTCGCGCAATTC	1503
1381	QY	CTCAGAGAGATCTGGGACGTGGCGAAGTGTGACGAGCAAGCTTGTCCCGCCCGACCGAT	1440
1504	DB	CTCAGAGAGATCTGGGACGTGGCGAAGTGTGACGAGCAAGCTTGTCCCGCCCGACCGAT	1567
1441	QY	GTACGCTGGGGGACGAGCTCCACTTAGACGCGGAGGACGTGGCGATGGCGCATGCCGAC	1500
1558	DB	GTGCGGTGCACGGGCGGACTCTTCTTCTTCCACCGGAGACGACGCGGCGACCGCGGC	1617
1501	QY	GGC	1503

Db	1618	GAG 1620
RESULT 12		
ADF49206		
ID	ADF49206	standard; DNA; 1848 BP.
XX	AC	ADF49206;
XX	AC	ADF49206;
XX	AC	ADF49206;
XX	AC	ADF49206;
DT	12-FEB-2004	(first entry)
XX	XX	
DE	XX	Ecdysone receptor/C1 transactivation domain DNA seq id 134.
XX	XX	
KW	XX	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW	XX	hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW	XX	activation domain; transgenic seed; transgenic plant; plant line;
KW	XX	herbicide; pesticide; chimeric ecdysone receptor; ECR;
KW	XX	yeast GAL4 DNA binding domain; C1 transactivation domain; ds; gene.
XX	XX	
XX	OS	Synthetic.
OS	OS	Manduca sexta.
OS	OS	Ascomycota.
OS	OS	Zea mays.
XX	XX	
XX	XX	US2003154509-A1.
XX	XX	
XX	XX	14-AUG-2003.
XX	XX	
XX	XX	24-OCT-2001; 2001US-00087167.
XX	XX	
XX	XX	24-OCT-2001; 2001US-00087167.
XX	XX	
XX	XX	(PASCAL/ PASCAL E J.
PA	PA	(VALE/ VALENTINE S A.
PA	PA	(BROW/ BROWN J A. A.
PA	PA	(COCK/ COCKRELL A. S.
PA	PA	(JOHN/ JOHNSON B D.
XX	XX	
XX	XX	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
PI	PI	
XX	XX	WPT, 2003-897756/82.
XX	XX	
XX	XX	New receptor cassette encoding a chimeric receptor polypeptide, useful
PT	PT	for regulating the expression of target polypeptides in plants in the
PT	PT	presence of appropriate chemical ligands.
XX	XX	
XX	XX	Example 25; SEQ ID NO 134; 186pp; English.
PS	PS	
XX	XX	The invention describes a receptor cassette encoding a chimeric receptor
CC	CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC	CC	(D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
CC	CC	(E) domain that is heterologous with respect to the D domain, and an
CC	CC	activation domain. The receptor cassette and method are useful in
CC	CC	regulating the expression of target polypeptides in plants in the
CC	CC	presence of appropriate chemical ligands. The transgenic seeds and plants
CC	CC	can be used for the breeding of improved plant lines that, for e.g.
CC	CC	increase the effectiveness of conventional methods such as herbicide or
CC	CC	pesticide treatment. This sequence encodes an ecdysone receptor-C1
CC	CC	transactivation domain fusion protein.
XX	XX	
XX	XX	Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
SQ	SQ	
	Query Match	85.8%; Score 1426.6; DB 10; Length 1848;
	Best Local Similarity	97.3%; Pred. No. 0;
	Matches 1463; Conservative	0; Mismatches 34; Indels 6; Gaps 1;
QY	1	ATGAAGCTACTGTTCTTCTATCGAACACGATCGCGATATTTGCCGACTTAAAAGCTCAAG 60
Db	124	ATGAAGCTACTGTTCTTCTATCGAACACGATCGCGATATTTGCCGACTTAAAAGCTCAAG 183
QY	61	TGCTCCAAAGAAAAACCGAAGTGCCCAAGTGTCGAAAGAACAACTGGGAGTGTGCTAC 120
Db	184	TGCTCCAAAGAAAAACCGAAGTGCCCAAGTGTCGAAAGAACAACTGGGAGTGTGCTAC 243

QY 121 TCTCCAAACCAAAAGGTCTCCGTGACTAGGCGACATCTGACAGAGAGTGGAAATCAAGG 180
Db 244 TCTCCAAACCAAAAGGTCTCCGTGACTAGGCGCAATCTGACAGAGAGTGGAAATCAAGG 303
QY 181 CTAGAAAGACTGGAACAGACTATTTCTACTGATTTTTCTCGAGAGAGACTTTGACATGATT 240
Db 304 CTAGAAAGACTGGAACAGACTATTTCTACTGATTTTTCTCGAGAGAGACTTTGACATGATT 363
QY 241 TTGAAATGGATTTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
Db 364 TTGAAATGGATTTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 423
QY 301 AATGTGAATAAAGATGCGGTTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
Db 424 AATGTGAATAAAGATGCGGTTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 483
QY 361 ACATTGAGACAGCATAGATAAGTTCGACATCATCATCGAAGAGAGTAGTAACAAGGT 420
Db 484 ACATTGAGACAGCATAGATAAGTTCGACATCATCATCGAAGAGAGTAGTAACAAGGT 543
QY 421 CAAAGACAGTTGACTGTATCGACGGTATAGGCGCGAGTGGTCTGTCAGAGTCCACG 480
Db 544 CAAAGACAGTTGACTGTATCGACGGTATAGGCGCGAGTGGTCTGTCAGAGTCCACG 603
QY 481 TGCAGAACCAAGAGAGAAAGCAAGACACAGAGAGAGAAACAACTGCCAGTCAAGT 540
Db 604 TGCAGAACCAAGAGAGAAAGCAAGACACAGAGAGAGAAACAACTGCCAGTCAAGT 563
QY 541 AGCAGCAGATGAGCAGATCATATGCTTCGCTAATGCAATGTGACCCCTCCGCCCCCAGAG 600
Db 664 AGCAGCAGATGAGCAGATCATATGCTTCGCTAATGCAATGTGACCCCTCCGCCCCCAGAG 723
QY 601 GCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGAGCTTAATGAGCAGAAC 660
Db 724 GCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGAGCTTAATGAGCAGAAC 783
QY 661 AGACTGAAGAAATGTACGCGCTGTGCGGCAACCAAGAGTCCCTGATCGCAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTACGCGCTGTGCGGCAACCAAGAGTCCCTGATCGCAGGCTCGTG 843
QY 721 TGGTACACGAGGGGTACAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACACGAGGGGTACAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGACA 903
QY 781 TGGCAGTTAGAAAGAAAGAGAGAGGAGAAACCTGACATGCCCTTCGTCAGATCAAGAG 840
Db 904 TGGCAGTTAGAAAGAAAGAGAGAGGAGAAACCTGACATGCCCTTCGTCAGATCAAGAG 963
QY 841 ATGACGATCTTAAACAGTCAAGCTTATTTAGAAATTCGCAAGGGACTACCGGGATTCTCC 900
Db 964 ATGACGATCTTAAACAGTCAAGCTTATTTAGAAATTCGCAAGGGACTACCGGGATTCTCC 1023
QY 901 AAGATATCTCAGTCCGATCAAAATTTACATTTAAGGCGCTCATCAAGCGAAGTGTATG 960
Db 1024 AAGATATCTCAGTCCGATCAAAATTTACATTTAAGGCGCTCATCAAGCGAAGTGTATG 1083
QY 961 CTGCGAGTGGCGGACGCTACGACGCGGCGACGAGCAGCGTGTGTTCCGGAACAAACAG 1020
Db 1084 CTGCGAGTGGCGGACGCTACGACGCGGCGACGAGCAGCGTGTGTTCCGGAACAAACAG 1143
QY 1021 GCGTACACGCGGACAACTACCCGAGGCGGCGATCTCTACGTCATCGAGGACCTGCTG 1080
Db 1144 GCGTACACGCGGACAACTACCCGAGGCGGCGATCTCTACGTCATCGAGGACCTGCTG 1203
QY 1081 CACTTCTGCGGTATGTAATCTCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
Db 1204 CACTTCTGCGGTATGTAATCTCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1263
QY 1141 GCCATCGTTATATTTCTCAGACCGGCGGCTCGAGCAACCCCTTTTGTGGAGGAAATC 1200
Db 1264 GCCATCGTTATATTTCTCAGACCGGCGGCTCGAGCAACCCCTTTTGTGGAGGAAATC 1323

QY 1201 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1260
Db 1324 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1383
QY 1261 CGCTGCGCGTGTCTGTTGCGGCAAGATCCTCGCGTGTCTGACGGAACCTGCGCAGCTCGGC 1320
Db 1384 CGCTGCGCGTGTCTGTTGCGGCAAGATCCTCGCGTGTCTGACGGAACCTGCGCAGCTCGGC 1443
QY 1321 ACGCAGAACTCCAACTATGTGCTGCTGAAGCTGAAGAAACAGGAAACTTTCCGCCATTC 1380
Db 1444 ACGCAGAACTCCAACTATGTGCTGCTGAAGCTGAAGAAACAGGAAACTTTCCGCCATTC 1503
QY 1381 CTCAGAGAGATCTCGGACGCTGCGGCAAGTGTGACGAGAAAGCTTGCCTCCCGCCGAT 1440
Db 1504 CTCAGAGAGATCTCGGACGCTGCGGCAAGTGTGACGAGAAAGCTT-----CCCAAGGCC 1557
QY 1441 GTACGCTGCGGACGAGCTCCTAGACGCGGAGGACGTTGCGGATGCGGATGCGGCGAC 1500
Db 1558 GTGCGGTGACGCGGCGGACTCTTCTTTCCACCGGACAGCGCGGCGACGCGGCG 1617
QY 1501 GCG 1503
Db 1618 GAG 1620

RESULT 13
ABT07371
ID ABT07371 standard; DNA; 1428 BP.
XX AC ABT07371;
XX DT 07-NOV-2002 (first entry)
XX DE Chimeric ecdysone receptor coding sequence SEQ ID NO: 128.
XX KW Plant; gene expression control; Insect; hormone receptor; fertility;
XX KW ecdysone receptor; gene; ds.
XX OS Manduca sexta.
XX OS Unidentified.
XX OS Chimeric.
XX WO200261102-A2.
XX PN 08-AUG-2002.
XX PD 24-OCT-2001; 2001WO-US051417.
XX PF 24-OCT-2000; 2000US-0242969P.
XX PR (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX PI WPI; 2002-619259/66.
XX DR P-PSDB; ABJ05377.
XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX PT regulating expression of target polypeptides in plants in the presence of
XX PT appropriate ligands that may be used in controlling plant fertility.
XX PS Example 25; Page 291-293; 319pp; English.
XX CC The present invention relates to a receptor cassette encoding a chimeric
XX CC receptor polypeptide comprising at least one DNA binding domain, a hinge
XX CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX CC domain of an insect EcR, where the ligand binding domain is heterologous
XX CC with respect to the hinge domain and an activation domain. The chimeric
XX CC insect hormone receptors and receptor cassettes are useful in regulating
XX CC expression of target polypeptides in plants in the presence of
XX CC appropriate ligands that may be used in controlling plant fertility. The
XX CC method is useful for decreasing or increasing plant gene expression. The
XX CC present sequence is a coding sequence described in the exemplification of

CC the invention
XX
SQ Sequence 1428 BP; 423 A; 338 C; 379 G; 288 T; 0 U; 0 Other;
Query Match 85.7%; Score 1425; DB 6; Length 1428;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGCTACTGTTCTTCTATCGAACAAGCATGCGATATTTGCCGACCTTAAAGACTCAAG 60
DB 1 ATGAAGCTACTGTTCTTCTATCGAACAAGCATGCGATATTTGCCGACCTTAAAGACTCAAG 60
QY 61 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGACACTGCGAGTGTGCGTAC 120
DB 61 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGACACTGCGAGTGTGCGTAC 120
QY 121 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCAAGG 180
DB 121 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCAAGG 180
QY 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTGACATGATT 240
DB 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTTGACATGATT 240
QY 241 TTGAAATGGATTTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
DB 241 TTGAAATGGATTTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
QY 301 AATGTGAATAAAGATGCCGTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
DB 301 AATGTGAATAAAGATGCCGTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
QY 361 ACATTGAGACAGCATAGAAATAGTCCGACATCATCTCGAAGAGAGTAGTAAACAAGGT 420
DB 361 ACATTGAGACAGCATAGAAATAGTCCGACATCATCTCGAAGAGAGTAGTAAACAAGGT 420
QY 421 CAAACACAGTTGACTGTATCGACGGTATGAGGCCGAGTGGTCTGCCAGAGTCCACG 480
DB 421 CAAACACAGTTGACTGTATCGACGGTATGAGGCCGAGTGGTCTGCCAGAGTCCACG 480
QY 481 TGCAAGAACAAGAAGAAAGAAAGCAACAGAGAGAAAGAAACTGCCAGTCAGT 540
DB 481 TGCAAGAACAAGAAGAAAGAAAGCAACAGAGAGAAAGAAACTGCCAGTCAGT 540
QY 541 ACACACAGCTGACAGATCATATGCTGCCATAATGCAATGTCACCTCCGCCCCAGAG 600
DB 541 ACACACAGCTGACAGATCATATGCTGCCATAATGCAATGTCACCTCCGCCCCAGAG 600
QY 601 GCGGCAAGGATTACGAAGTGGTCCGAGGTTCTTAAAGGAGAGTAAATGGAGCAGAAC 660
DB 601 GCGGCAAGGATTACGAAGTGGTCCGAGGTTCTTAAAGGAGAGTAAATGGAGCAGAAC 660
QY 661 AGACTGAAGAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGAGGCTCGTG 720
DB 661 AGACTGAAGAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGAGGCTCGTG 720
QY 721 TGGTACCAGAGGGTACAGACAGCCGTCGAGGAGAGATCTCAAGAGAGTTACACAGACA 780
DB 721 TGGTACCAGAGGGTACAGACAGCCGTCGAGGAGAGATCTCAAGAGAGTTACACAGACA 780
QY 781 TGCGAGTTAGAAGAAAGAGAGGAGGAAACTGACATGCCCTTCCGTCAGATCAACAGAG 840
DB 781 TGCGAGTTAGAAGAAAGAGAGGAGGAAACTGACATGCCCTTCCGTCAGATCAACAGAG 840
QY 841 ATGACGATCTTAAAGTCAAGTCTTATTTAGAAATTTGCAAGGAGTACCCGGATTCTCC 900
DB 841 ATGACGATCTTAAAGTCAAGTCTTATTTAGAAATTTGCAAGGAGTACCCGGATTCTCC 900
QY 901 AAGATATCTCAGTCCGATCAAAATACATTTAAAGGCGTATCAAGCGAAGTGTATG 960
DB 901 AAGATATCTCAGTCCGATCAAAATACATTTAAAGGCGTATCAAGCGAAGTGTATG 960
QY 961 CTGCGAGTGGCGCAGCGGTACGACGCGCGACCGGACAGCGTGTGTTCCGGAACCAACGAG 1020

DB 961 CTGCGAGTGGCGCAGCGGTACGACGCGGACCGGACGAGCGGTGCTGTTCCGGAACACGAG 1020
QY 1021 GGTACACGCGGACAACTACCGAAGGCGGCGATGCTCTAGCTATCGAGGACCTGCTG 1080
DB 1021 GGTACACGCGGACAACTACCGAAGGCGGCGATGCTCTAGCTATCGAGGACCTGCTG 1080
QY 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
DB 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
QY 1141 GCCATGTTATATTTCTCAGACCGGCGCAGCCCTCGAGCAACCCCTTTTAGTGGAGAAATC 1200
DB 1141 GCCATGTTATATTTCTCAGACCGGCGCAGCCCTCGAGCAACCCCTTTTAGTGGAGAAATC 1200
QY 1201 CAGAGATACTACTTGAAGAGCGTGGGTTTACATTTTAAATCAGACACAGCGGCTCGCCT 1260
DB 1201 CAGAGATACTACTTGAAGAGCGTGGGTTTACATTTTAAATCAGACACAGCGGCTCGCCT 1260
QY 1261 CGCTGCGCGTGTGTTTCGCAAGATCTCGGCGTCTGACGGAACCTGCGCAGCTCGGC 1320
DB 1261 CGCTGCGCGTGTGTTTCGCAAGATCTCGGCGTCTGACGGAACCTGCGCAGCTCGGC 1320
QY 1321 ACCAGAACTCCAAATGTGCACTCTCGTGAAGCTGAAGAACAGGAAACTTCGCGCATTC 1380
DB 1321 ACCAGAACTCCAAATGTGCACTCTCGTGAAGCTGAAGAACAGGAAACTTCGCGCATTC 1380
QY 1381 CTCGAGGAGATCTGGGACGTTGGCGGAGTGTTCGACGACGAAGCTT 1425
DB 1381 CTCGAGGAGATCTGGGACGTTGGCGGAGTGTTCGACGACGAAGCTT 1425
RESULT 14
ADF49200
ID ADF49200 standard; DNA; 1428 BP.
XX
AC ADF49200;
XX AC
XX XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/VP16 transactivation domain DNA seq id 128.
XX
DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.
XX Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
XX
XX 14-AUG-2003.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX (PASC/) PASCAL E J.
PA (VALE/) VALENTINE S A.
PA (BROW/) BROWN J A.
PA (COCK/) COCKRELL A S.
PA (JOHN/) JOHNSON B D.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
DR P-PSDB; ADF49201.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
PI

for regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands.

Example 25; SEQ ID NO 128; 186pp; English.

The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding (E) domain that is heterologous with respect to the D domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants can be used for the breeding of improved plant lines that, for e.g., increase the effectiveness of conventional methods such as herbicide or pesticide treatment. This sequence encodes an ecdysone receptor-Vp16 transactivation domain fusion protein.

Sequence 1428 BP; 423 A; 338 C; 379 G; 288 T; 0 U; 0 Other;

Query Match 85.7%; Score 1425; DB 10; Length 1428;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAGCTACTCTCTTATCGAACAAGCATCGGATATTGCGACTTAAAGGCTCAAG	60
DB	1	ATGAAGCTACTCTCTTATCGAACAAGCATCGGATATTGCGACTTAAAGGCTCAAG	60
QY	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGGTAC	120
DB	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGGTAC	120
QY	121	TTCTCCAAAGAAAAGGTTCTCGCTAGTGGGACATCTCAGAGAGTGAATCAAGG	180
DB	121	TTCTCCAAAGAAAAGGTTCTCGCTAGTGGGACATCTCAGAGAGTGAATCAAGG	180
QY	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACCTTCACATGATT	240
DB	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACCTTCACATGATT	240
QY	241	TTGAAAATCGATTCTTTACAGATATAAAGCATTTTAAAGGATTTTGTACAGAT	300
DB	241	TTGAAAATCGATTCTTTACAGATATAAAGCATTTTAAAGGATTTTGTACAGAT	300
QY	301	AATGTGAATTAAGATGCGCTCAGATAGATTGGCTTCAGTGGAGACTATATGCTCTA	360
DB	301	AATGTGAATTAAGATGCGCTCAGATAGATTGGCTTCAGTGGAGACTATATGCTCTA	360
QY	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT	420
DB	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT	420
QY	421	CAAAGACAGTTGATGTATCGACGCTATGAGCCCGAGTGGCTGCTCCAGAGTCCAG	480
DB	421	CAAAGACAGTTGATGTATCGACGCTATGAGCCCGAGTGGCTGCTCCAGAGTCCAG	480
QY	481	TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAAAGACAACTGCCAGTCACT	540
DB	481	TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAAAGACAACTGCCAGTCACT	540
QY	541	ACGACGACAGTGGACCATCATATGCTTGCATATGCAATGTGACCTCCGCCCCAGAG	600
DB	541	ACGACGACAGTGGACCATCATATGCTTGCATATGCAATGTGACCTCCGCCCCAGAG	600
QY	601	CGGCAAGGATTACCAAGTGGTCCGAGGTTCTTAACCGAGAGAGTAAATGGAGCAGAC	660
DB	601	CGGCAAGGATTACCAAGTGGTCCGAGGTTCTTAACCGAGAGAGTAAATGGAGCAGAC	660
QY	661	AGACTGAAGATGTGACCGCTGTGGCGAACAGAGTCCCTGATCGGAGGCTCGTG	720
DB	661	AGACTGAAGATGTGACCGCTGTGGCGAACAGAGTCCCTGATCGGAGGCTCGTG	720
QY	721	TGCTACCAAGGGGTACGAGACCGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780

Db	721	TGTTACCAAGGGGTACGAGACCGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780
QY	781	TGGCAGTTTAGAAGAAAGAGAGAGGAAACTGACATGCCCTTCCGTGACATCACAGAG	840
Db	781	TGGCAGTTTAGAAGAAAGAGAGAGGAAACTGACATGCCCTTCCGTGACATCACAGAG	840
QY	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGATTTCGAAAGGGACTACCGGGATTCTCC	900
Db	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGATTTCGAAAGGGACTACCGGGATTCTCC	900
QY	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGGCTCATCAAGGCAAGTGTATG	960
Db	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGGCTCATCAAGGCAAGTGTATG	960
QY	961	CTGCGAGTGGCGCGACCGGTACGACGCGCGACGAGCGTGTTCGCGAAACAACGAG	1020
Db	961	CTGCGAGTGGCGCGACCGGTACGACGCGCGACGAGCGTGTTCGCGAAACAACGAG	1020
QY	1021	CGGTACACGCGCGACCAACTACCGAAGCGCGGCATGCTCTAGTTCATCGAGGACCTGCTG	1080
Db	1021	CGGTACACGCGCGACCAACTACCGAAGCGCGGCATGCTCTAGTTCATCGAGGACCTGCTG	1080
QY	1081	CACCTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGTGTCTACC	1140
Db	1081	CACCTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGTGTCTACC	1140
QY	1141	GCCATCGTTATATCTCAGACGCGCGCCCTCGAGCAACCCCTTTTGTAGTGAGGAATC	1200
Db	1141	GCCATCGTTATATCTCAGACGCGCGCCCTCGAGCAACCCCTTTTGTAGTGAGGAATC	1200
QY	1201	CAGAGATACTACTTGAAGACGCTGGGTTTACATTTTAAATCAGACAGCGCGTGGCT	1260
Db	1201	CAGAGATACTACTTGAAGACGCTGGGTTTACATTTTAAATCAGACAGCGCGTGGCT	1260
QY	1261	CGTCCGCGCTGCTGTTTGGCAAGATCCTCGCGTGTGACGGAATCGCGACGCTCGGC	1320
Db	1261	CGTCCGCGCTGCTGTTTGGCAAGATCCTCGCGTGTGACGGAATCGCGACGCTCGGC	1320
QY	1321	ACGAGAGAACTCCAAACATGTGCACTCTGCTGAGCTGAAGAAACAGGAAACTTCGCGCATTC	1380
Db	1321	ACGAGAGAACTCCAAACATGTGCACTCTGCTGAGCTGAAGAAACAGGAAACTTCGCGCATTC	1380
QY	1381	CTCAGGAGATCTGGAGCGTGGCCGAAAGTGTGACGACGAAAGCTT 1425	
Db	1381	CTCAGGAGATCTGGAGCGTGGCCGAAAGTGTGACGACGAAAGCTT 1425	

RESULT 15

ABT07367

ID ABT07367 standard; DNA; 1767 BP.

XX AC ABT07367;

XX XX 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 120.

XX KW Plant; gene expression control; insect; hormone receptor; fertility; ecdysone receptor; gene; ds.

XX OS Manduca sexta.

OS Ostrinia nubilalis.

OS Chimeric.

XX XX W0200261102-A2.

XX XX 08-AUG-2002.

XX XX 24-OCT-2001; 2001WO-US051417.

XX XX 24-OCT-2000; 2000US-0242969P.

XX XX

(SYGN) SYNGENTA PARTICIPATIONS AG.
Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
WPI; 2002-619259/66.
P-PSDB; ABJ05373.
New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.
Claim 13; Page 270-272; 319pp; English.
The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect EcR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a coding sequence described in the exemplification of the invention. (Updated on 29-AUG-2003 to standardise OS field)
SQ Sequence 1767 BP; 474 A; 438 C; 473 G; 382 T; 0 U; 0 Other;
Query Match 85.7%; Score 1424; DB 6; Length 1767;
Beat Local Similarity 91.7%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 120; Indels 18; Gaps 1;
QY 1 ATGAGCTACTCTCTCTATCGAACAGCATGCGATATTTCGCCACTTTAAAGACTCAAG 60
DB 124 ATGAGCTACTCTCTCTATCGAACAGCATGCGATATTTCGCCACTTTAAAGACTCAAG 183
QY 61 TGCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC 120
DB 184 TGCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC 243
QY 121 TCTCCAAACCAAAAGGTCTCCGTGACTAGGCGACATCTGACAGAAGTGGATCAAG 180
DB 244 TCTCCAAACCAAAAGGTCTCCGTGACTAGGCGACATCTGACAGAAGTGGATCAAG 303
QY 181 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACTTTGACATGATT 240
DB 304 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACTTTGACATGATT 363
QY 241 TTGAAATGGATTCTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300
DB 364 TTGAAATGGATTCTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 423
QY 301 AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA 360
DB 424 AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA 483
QY 361 ACATTGAGACAGCATAGATAAAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAGGT 420
DB 484 ACATTGAGACAGCATAGATAAAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAGGT 543
QY 421 CAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTCCGCTCCACAGTCCACG 480
DB 544 CAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTCCGCTCCACAGTCCACG 603
QY 481 TGCAAGAACAAAGAAAGAAAGAACGACAGAGAGAAAGAACAACTGCCAGTCAGT 540
DB 604 TGCAAGAACAAAGAAAGAAAGAACGACAGAGAGAAAGAACAACTGCCAGTCAGT 663
QY 541 ACGACGACAGTGGACGATCATATGCTGCTCAATGCAATGATGCAATGATGCAATGCAATG 600
DB 664 ACGACGACAGTGGACGATCATATGCTGCTCAATGCAATGATGCAATGATGCAATGCAATG 723
QY 601 GCGGCAAGATTACGAAGTGGTCCCGAGTTCTTAACGGAGAAAGCTTAATGGAGCAAGAAC 660

DB 724 GCGGCAAGGATTACGAAGTGGTCCGAGGTTCTTAACGGAGAAAGCTTAATGGAGCAAGAC 783
QY 661 AGACTGAAGAAATGTGACCGCGCTGTGCGGCAACAGAAAGTCCCTGTATCGGAGGCTCGTG 720
DB 784 AGACTGAAGAAATGTGACCGCGCTGTGCGGCAACAGAAAGTCCCTGTATCGGAGGCTCGTG 843
QY 721 TGGTACCAGAGGGGTACGAGCAGCCGTGCGAGGAAGATCTCAAGAGAGATTACACAGACA 780
DB 844 TGGTACCAGAGCGATACGAGCAGCCCTTCGGAAGAGGATCTCAAAAGGGTGACGAGACT 903
QY 781 TGGCAGTTAGAAAGAAAGAAAGAGGAGGAAACTGACATGCCCTTCCTGCTCAGATCAGAG 840
DB 904 TGGCAATCAGCAGATGAAGAAGACGAAGACTCAGACATGCCATTCGCCCCAGATCAGAGAA 963
QY 841 ATGACAGATCTTAACAGTGCAGCTTATTGTAGAATTGCAAAAGGACTACCGGATTTCTCC 900
DB 964 ATGACCATCTCAGTACAGTACAGCTTAATAGTCGAGTTTGCCAAAGGCTTACCTGGTTTCA 1023
QY 901 AAGATATCTCAGTCCGATCAAAATTAACATTAATAAGSCGTCAACGCAAGTGAATGATG 960
DB 1024 AAGATCTCAACACTGACACAGATCAATATTAAAGGCAATGCTCAAGCGAAGTGAATGATG 1083
QY 961 CTGCGAGTGGCGGACGCTGACGAGCGGCGGACGAGCAGCGCTGTGTTCCGCAACCAAG 1020
DB 1084 CTGCGAGTGGCGGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTTCGCAACCAAG 1143
QY 1021 GCGTACAGCGCGACAACTACCGAAGCGGCGATGCTCTACGTCATCGAGGAGCTGCTG 1080
DB 1144 GCGTACACTCGCAACAACTACCGAAGCGGCGATGCGCTTACGTCATCGAAGACTGCTG 1203
QY 1081 CACTTCTGCTGGTATGTACTCCATGAGCATGACAAATGTGACATACGCGCTGCTCAAC 1140
DB 1204 CACTTCTGCTGGTATGTACTCCATGAGCATGACAACTGATGACAACTGATGATGATG 1263
QY 1141 GCAATGTTATTTCTCAGACCGCGGCGCTCGAGCAACCCCTTTTGTAGTGGAGGAATC 1200
DB 1264 GCAATGTTATTTCTCAGACCGCGGCGCTCGAGCAACCCCTTTTGTAGTGGAGGAATC 1323
QY 1201 CAGAGATCTACTTGAAGACGCTGCGGCTTTTACATTTTAAATCAGACACAGCGCTCGCCT 1260
DB 1324 CAGCGGTATTTACCTGAACACGCTGCGGCTGTACATCATGAACACAGACAGCGCTCGCG 1383
QY 1261 CGCTGCGCGTGTGTTTCGGCAAGATCCTCGGCGGTGTGACGGAACCTGCGCACTGCGGC 1320
DB 1384 CGTTGCGCGCTCATCTACGCGAAGATTTCTGCTGCTGTCTTACCGAGTTGCGGACGCTGGGC 1443
QY 1321 ACGCAGAACTCCAAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1444 ATGCAAGAAATTCGAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1503
QY 1381 CTCAGGAGATCTGGGACGCTGGCGGAGTGTGACACGACGAAGCTTGGCCCCCGACCGAT 1440
DB 1504 CTGGAGAGATCTGGGACGT-----GAAGCTTTGCCCCCGACCGAT 1545
QY 1441 GTCAGCTCGGGGACGAGCTCCACTTATAGACGGGAGGACGCTGGCGATGGCGCATGCGGAC 1500
DB 1546 GTCAGCTCGGGGACGAGCTCCACTTATAGACGGGAGGACGCTGGCGATGGCGCATGCGGAC 1605
QY 1501 GCGCTAGACGATTTTCGATCTGGAATGCTGGGAGCGGGGATTTCCCGGGTCCGGGATTT 1560
DB 1606 GCGCTAGACGATTTTCGATCTGGAATGCTGGGAGCGGGGATTTCCCGGGTCCGGGATTT 1665
QY 1561 ACCCCCCACGACTCCGCCCCCTACGCGCTCTGATATGGCCGACTTCGAGTTTGAGCAG 1620
DB 1666 ACCCCCCACGACTCCGCCCCCTACGCGCTCTGATATGGCCGACTTCGAGTTTGAGCAG 1725
QY 1621 ATGTTTACGATGCCCTTTGGAAATTGACGAGTACGCTGGGTAG 1662
DB 1726 ATGTTTACGATGCCCTTTGGAAATTGACGAGTACGCTGGGTAG 1767

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:02:48 ; Search time 5669.37 Seconds
(without alignments)
11158.701 Million cell updates/sec

Title: US-10-087-167-104_COPY_2007_3668

Perfect score: 1662

Sequence: 1 atgagctactgtctctat.....ttgacgagtagtggtggtag 1662

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_g881:*
- 9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306.8	18.5	963	CNS0905M	BX067382 Single re
2	224	13.5	728	BM650826	BM650826 17006873
3	220.4	13.3	851	CNS011ME	AL100448 Drosophila
4	214.4	12.9	271	CG918549	CG918549 OIS0458-0
5	189	11.4	470	AA538642	AA538642 LD18219.5
6	183.6	11.0	607	AA664510	AA664510 ESTF192-
7	151.6	9.1	574	AI258616	AI258616 LP01848.5
8	144.8	8.7	197	CG706271	CG706271 OS20322.0
9	143.2	8.6	1050	CNS016YX	AL107379 Drosophila
10	135.6	8.2	1031	BQ058428	BQ058428 AGENCOURT
11	134.6	8.1	918	BQ214241	BQ214241 AGENCOURT
12	134.4	8.1	867	BQ222200	BQ222200 AGENCOURT
13	134.2	8.1	667	CD673041	CD673041 fs1905.y
14	134.2	8.1	1685	CR614375	CR614375 full-leng
15	134.2	8.1	1763	CR610600	CR610600 full-leng
16	134.2	8.1	1828	CR617823	CR617823 full-leng
17	134.2	8.1	1922	CR604070	CR604070 full-leng
18	134.2	8.1	1924	CR609885	CR609885 full-leng
19	134.2	8.1	1965	CR598124	CR598124 full-leng
20	134.2	8.1	1978	CR598123	CR598123 full-leng
21	134.2	8.1	2041	BC033500	BC033500 Homo sapi
22	133	8.0	842	CNS06JUC	AL401698 T7 end of
23	132.8	8.0	721	BE382387	BE382387 601298693
24	131.8	7.9	651	CN309352	CN309352 170005999

C 25	128.8	7.7	1088	5	BX463524	BX463524
C 26	123.4	7.4	1062	5	BX367164	BX367164
C 27	123.2	7.4	1963	3	AK077620	Mus muscu
28	122	7.3	866	4	BG675073	BG675073
29	121.2	7.3	649	6	CD304821	CD304821
30	121	7.3	622	5	BQ636916	BQ636916
31	121	7.3	1026	5	BQ052341	BQ052341
32	119.8	7.2	957	2	BE878950	BE878950
C 33	119.6	7.2	1003	5	BX344136	BX344136
C 34	119.6	7.2	1135	5	BX365740	BX365740
35	119.4	7.2	1138	5	BM912640	BM912640
C 36	119	7.2	965	1	AL582953	AL582953
37	118.4	7.1	618	6	CD309514	CD309514
38	117.8	7.1	986	5	BQ877581	BQ877581
39	117.8	7.1	2035	3	CR749648	CR749648
C 40	115.6	7.0	920	1	AL522738	AL522738
C 41	115	6.9	972	1	AL522399	AL522399
42	114	6.9	1158	4	BM554635	BM554635
C 43	113.6	6.8	444	9	AG215235	AG215235
C 44	113.2	6.8	919	4	BI654278	BI654278
C 45	113	6.8	1085	5	BX406790	BX406790

ALIGNMENTS

RESULT 1
CNS0905M
LOCUS
DEFINITION
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total females. 5-PRIME end of clone
FK0AAC51AC03 of strain 6-9 of Anopheles gambiae (African malaria mosquito).
ACCESSION
BX067382
VERSION
BX067382.1
GI:27640663
KEYWORDS
HTC.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE
1 (bases 1 to 963)
AUTHORS
Direct Submission
TITLE
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr

FEATURES
Location/Qualifiers
1..963
source
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AAC51AC03"
/plasmid="pME18S-FL"
/note="end : 5-PRIME"

ORIGIN
Query Match 18.5%; Score 306.8; DB 3; Length 963;
Best Local Similarity 70.8%; Pred. No. 2.8e-72;
Matches 436; Conservative 0; Mismatches 177; Indels 3; Gaps 2;

QY	814	GACATGCCCTTCGTCAGATCACAGATGACGATCTTAAACAGTCAGCTTATTGTAGAA	873
DB	9	GAATTCCTTCCTCCGGACATAACGGAATCACATCTCCACAGTACAATACTGTCGAG	68
QY	874	TTCCGCAAGGGACTACCGGATTCCTCAAGATATCTCAGTCCGATCAATATCATTTA	933
DB	69	TTTCGGAGGAGTCTCCAGCATTCACCAAGATCCCGCAG-AGGATCAGATACGTTACTA	127
QY	934	AAGCGCTCATCAAGGAAAGTATGATGTGTCGAGTGGCGGACGGTACGACGGCGGACG	993
DB	128	AAGGCTGTCTCCAGTGAGTGATGATTTTCCGATGGCCCGCCGCTACGACGCCGAAACC	187

Qy 994 GACAGCGTGTCTTTCGGAACAAACAGGCGTACACGCGCGAACAATACCGCAAGCGCGGC 1053
 Db 188 GACTCCATCTCTTTCGGAACAAACAGGCGTACACGCGCGAACAATACCGCAAGCGCGGC 247
 Qy 1054 ATGTCCTACGTCATCGAGGACCTCTGCACCTCTGTGCGTGTATGTACTCTCATGAGCATG 1113
 Db 248 ATGGCGGACACGATCGAGGACCTGTGCACCTTCTGCCGCGAGATGTACACGCTCACCGTG 307
 Qy 1114 GACAATGTGCACTACGCGCTCTCTACCGCCATCGTTATATTTCTCAGACCGCGCAGGCGTC 1173
 Db 308 GACAACGTCGATAGCGCTCTGACCGGATCGTCACTTCTCCGACCGCGCGCGCTC 367
 Qy 1174 GAGCAACCCCTTTTAGTGGAGAAATCCAGAGATACTACTTTGAAGAGCTCGCGGTTTAC 1233
 Db 368 GAGAAGCGGAGCTGTGTGGAACGATCCAGAGCTACTACATCGACACGCTCGCGGCTTAC 427
 Qy 1234 ATTTTAATACGACAGCGCTCGCTCGCTGCGCGGTGTTCGGCAAGATCCTCGGC 1293
 Db 428 ATCTTGAACCGGACCGGCGGACCGGAAGTGTAGC--GTACGTTTCGGAACTCTGTCTG 485
 Qy 1294 GTGCTGACGGAACTCGGACGCTCGGCGCGAGAACTCCAAATGTGCATCTCGCTGAAG 1353
 Db 486 ATCTGACCGAGCTCGGACGCTCGGCAACAGAACTCGGAGATGTGCTTCTCGCTCAAG 545
 Qy 1354 CTGAAGAACAGGAACTTCGCGCATCTCTCGAGGAGATCTGGAGCTGGCGCAAGTGTG 1413
 Db 546 CTGAAGAACCGTAAGCTCGCGCTTCTCGAGGAGATATGGGACGTGCGAGCATACCG 605
 Qy 1414 AGCAGAAAGCTTGCC 1429
 Db 606 CCGGTGGCTGCTC 621

RESULT 2
 BM650826
 LOCUS 1700687372602 A.Gam.ad.cdna1 Anopheles gambiae cDNA clone
 DEFINITION 19600449637314 5', mRNA sequence.

ACCESSION BM650826
 VERSION BM650826.1 GI:18950337
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 728)
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 240453151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AYT row: E column: 24
 Seq primer: M13 Reverse.

FEATURES
 source
 1..728
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449637314"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cdna1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.

ORIGIN

Query Match 13.5%; Score 224; DB 4; Length 728;
 Best Local Similarity 61.4%; Pred. No. 1.1e-49;
 Matches 403; Conservative 0; Mismatches 235; Indels 18; Gaps 2;
 Qy 428 AGTTGACTGTATCGACGCGTATGAGCCCGAGTGCCTGCTCCAGAGTCCACGTGCAAGA 487
 Db 79 AGAAGTGTCTCGCGTCCGCGCATCGCGCGAGTGCCTGCTCCGGAAGATCACTGGGCCA 138
 Qy 488 ACAAAGAGAGAAAAGGAAGCACAGAGAGAAAACAACTGCCAGTCAGTACGACGA 547
 Db 139 TCAAGCGGAGGAGAGAGAGGCGCAAGAGAGAGAAAGGTGCGCGCGGAAACCCGTCGA 198
 Qy 548 CAGTGACGATCATATGCTTGCCTATGCAATATGACCTCCCGCCCGCCAGAGCGGCA 607
 Db 199 CCACCACCGTGAGTACAACGACAGCAGCTACAAGTCGGAGCTCTGCCGCTGCTGA 258
 Qy 608 GGATTCACGAAAGTGTCCGAG-----GTTCTTAAACGAGAACTAATGAGC 655
 Db 259 TGAAGTGTGAATCACCGCCCGCGCGATACCGCTACTGCCGGAAGCTGTGTAACG 318
 Qy 656 AGAACGACTGAAGATGTGACCCGCTGTCCGCGAACAGAGTCCCTGATCCGAGGC 715
 Db 319 AAAAAACGACAAAGAAACATACCTCTGCTGACGGCGAACAGATGGCGCTCATCTACAAC 378
 Qy 716 TCGTGTGTACCAAGAGGGGTACGACGCGCTCGGAGGAAGATCTCAAGAGAGTTACAC 775
 Db 379 TGATCTGTTACCAAGATGGCTACGACGACCGTCCGAGGAAGATCTCAAGAGGATAATGA 438
 Qy 776 AGACATGGCAGTTAGAAGAGAGAGAGAGAACTGATGTCGCCCTCCGTCAGATCA 835
 Db 439 TTAATCACCAACGAGGAGGAAGATCCCCACGAA-----ATCCACTTCCGCGCACATA 492
 Qy 836 CAGAGATGACGATCTTAACAGTCGCGCTTATTGTAGAAATTCGCAAGGGGACTACCGGAT 895
 Db 493 CGGAATACCATCTCTCACAGTACAATACTGTCGAGTTCCGAGAGGACTGCGGACAT 552
 Qy 896 TCTCCAAGATATCTCAGTCCGATCAAAATTAATATTAAAGGCTCATCAAGCGAACTGA 955
 Db 553 TTACCAAGATCCCGCAGGAGGATCAGATAAGTTACTTAAAGGCTGTCTCCAGTGAGTGA 612
 Qy 956 TGATGTGCGAGTGGCGGACGCTGACGCGCGGACGAGCGAGTCTTTCGCGACA 1015
 Db 613 TGATGTGCGAATGGCGCGCGGTACGACCGCGGAAACCGGACTCCATCTCTTTGCCAACA 672
 Qy 1016 ACCAGGCGTACACGCGGCAACTACCGAAGCGGCGCATGTCTACGTATCGAG 1071
 Db 673 ACCGATCGTACACGCGGACTCGTACAGATGGGGGCGGACACCATCGAG 728

RESULT 3

CNS011ME 851 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
 DEFINITION BACN06K02 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL100448.1 GI:5612059
 VERSION AL100448
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 851)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.

FEATURES
source
Location/Qualifiers
1. .851
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC06K02"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"

ORIGIN

Query Match 13.3%; Score 220.4; DB 9; Length 851;
Best Local Similarity 64.7%; Pred. No. 1.1e-48;
Matches 343; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
QY 935 AGCGTCATCAACGAGTGTATGCTCGAGTGGCGGAGGTACGCGCGGACGG 994
Db 266 AGGCGTGTCTCGGAGGTGATGCTCGTATGGCAGCGCTATGACACAGCTCG 325
QY 995 ACAGCGTGTCTCGGAGAACACGCGGTACACGCGGACAACTACCCGAGGGGCA 1054
Db 326 ATCAATATCTTCGGCATATATAGATATATACGGGGATCTTACAAATGGCGAA 385
QY 1055 TGTCTTACGTATCGAGGACCTGCTGCACTTCTGTCGGTGTATGCTCATGAGCATGG 1114
Db 386 TGGCTGATAACATTGAAGACCTGCTGCACTTCTGCGCCAAATGTTCTCGATGAAGTGG 445
QY 1115 ACATGTGCACTACGCGTGTCTACCGCATGTTATATCTCAGACCGCGGCGCTCG 1174
Db 446 ACAACGTCAATACGCGCTTCTCACTGCCATTTGTGATCTTCTCGGCGCGGCGCTCG 505
QY 1175 AGCAACCCCTTTAGTGGAGGAATCCAGAGATCTACTTTGAAGACGCTGGGGTTTACA 1234
Db 506 AGAAGGCCCACTAGTTCGAAGCGATCGAGCTCTACTCATCGACGCTACGATTTATA 565
QY 1235 TTTTAAATCAGCAACGCGTCTCGCTCGTGGCCGCTGTGTTTGGCAAGATCTCGGG 1294
Db 566 TACTCAACGCCCACTGGCGACTCAATG-AGCCTCGTCTTCTACGCAAGCTGCTCTCGA 624
QY 1295 TGTGACGGAACTGGCGACGCTCGGACGCAAGCTCCACATGTGCTGCTGCAAGC 1354
Db 625 TCCTCACCGAGCTGCGTACGCTGGGCAACAGAACCGCCGAGATGTGTTTCTCACTAAGC 684
QY 1355 TGAAGACAGAACTTCGCGCACTTCTCGAGAGATCTGGGACGCTGGCGAAGTGTGCA 1414
Db 685 TCAAAACCCCAACTGCCCCAGTTCTCGAGAGATCTGGGAGCTTATGTCATCCCGC 744
QY 1415 CGACGAAGCTTGCCCCCGACCGATGTCTAGCTTGGGGAGCGAGCTCCAC 1464
Db 745 CATCGGTCAGTCGCACCTTCAGATTACCAGGAGGAGACGAGCGTCTC 794

RESULT 4
CG918549/c
LOCUS
DEFINITION
01S0458-03Ci-G10 UniformMu MuTAIL Library Zea mays genomic clone
01S0458-03Ci-G10, genomic survey sequence.
CG918549
CG918549
GSS.
CG918549.1 GI:39778232
SOURCE
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 271)
Lashaw,S., Tan B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
01S0458-03, Primer set: C
Class: transposon insertion site.
FEATURES
source
Location/Qualifiers
1. .271
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0458-03Ci-G10"
/clone_lib="UniformMu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 12.9%; Score 214.4; DB 9; Length 271;
Best Local Similarity 95.3%; Pred. No. 3.6e-47;
Matches 221; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1413 GACGACGAGCTTGGCCCCCGACCGATGTCTAGCTGGGGGACGAGCTCCACTTAGACGG 1472
Db 234 GAAGCGTAAAGTGGCCCCCGACCGATGTCTAGCTGGGGGACGAGCTCCACTTAGACGG 175
QY 1473 CGAGGACGCTGGCGATGGCGCATGCCGACGCGCTAGACGATTCGATCTCGACATGTTGGG 1532
Db 174 CGAGGACGCTGGCGATGGCGCATGCCGACGCGCTAGACGATTCGATCTCGACATGTTGGG 115
QY 1533 GAGCGGGGATTCGCCGGTCCGGGATTTACCCCCACGACTCGCCCCCTAGCGGCTCT 1592
Db 114 GGACGGGGATTCGCCGGTCCGGGATTTACCCCCACGACTCGCCCCCTAGCGGCTCT 55
QY 1593 GATATGGCGGACTTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAAAT 1644
Db 54 GGATATGGCGGACTTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAAAT 3

RESULT 5
AA538642
LOCUS

DEFINITION
AA538642 470 bp mRNA linear EST 19-APR-2001
LD18219.5prime LD Drosophila melanogaster embryo Bluescript
Drosophila melanogaster cDNA clone LD18219 5prime similar to
M74078: Drosophila melanogaster ecdysone receptor (ECR) mRNA,
complete cds, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA538642.1 GI:2285158
EST.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 470)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Teang,G.,
Lewis,S. and Rubin,G.M.

```

TITLE      BDGP/HMI Drosophila EST Project
JOURNAL    Unpublished (2001)
COMMENT    Contact: Stapleton, M.
           BDGP
           Lawrence Berkeley National Lab
           One Cyclotron Rd, Berkeley, CA 94720, USA
           Fax: 510 486 6796
           Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
           Plate: 182 row: B column: 7
           High quality sequence stop: 343.
FEATURES   Location/Qualifiers
            1..470
             /organism="Drosophila melanogaster"
             /mol_type="mRNA"
             /db_xref="BDGP EST:BDcln017358"
             /db_xref="taxon:7227"
             /clone="LD18219"
             /sex="male and female"
             /dev_stages="0 to 24 hours mixed stage embryonic"
             /lab_host="SOJR"
             /clone_lib="LD Drosophila melanogaster embryo BlueScript"
             /note="Organ: embryo; Vector: BlueScript SK; Site_1:
             EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA
             Synthesis kit. Oligo dT-primed and directionally cloned at
             EcoRI and XhoI in BlueScript SK(+/-)"
ORIGIN
Query Match      11.4%; Score 189; DB 1; Length 470;
Best Local Similarity 63.6%; Pred. No. 3.7e-40;
Matches 288; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
Qy 1012 AACACACGGGCTACACGGCGGACAACTACCGAGGGCGCATCTCTACGTCATCGAG 1071
Db 1 AATAATAGATCATATACGGCGGATTTCTACAAAATGGCCGGAATGGCTGATTAACATTTGAA 60
Qy 1072 GACCTGCTGCACCTTCTGTCGGTGATGTACTCCATGAGCATGGACAATGTGCACCTACGCG 1131
Db 61 GACCTGCTGCATTTCTGCGGCCAATGTTCTGATGAAGTGGACAAGTGCATACGCG 120
Qy 1132 CTGCTACCGGCATCGTTATATTTCTAGACCGCGCGGCTCGAGCAACCCCTTTTAGTG 1191
Db 121 CTCTCACTGCCATTTGTATCTTCTCGGACCGCGCGGCTCGAGAGGCGCTAACTAGTC 180
Qy 1192 GAGGAATCCAGAGATCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGACAGC 1251
Db 181 GAAGCGATCCAGAGCTACTACATCGACAGCTACGCATTTATATCTCAACCGCCACTGC 240
Qy 1252 GCGTCGCTCGTGGCGCGTGTGTTTCGGCAAGATCCTCGCGTGCTGACGGAATCGCG 1311
Db 241 GCGGACTCAATGAGCTCTGCTTTCTACGAAAGTCTCTCGATCTCACCGAGCTGGT 300
Qy 1312 AGCTTCGGGACGCAAGATCCCAATGTGCAATCTCGCTGAAGCTGAAGAACAGGAACCTT 1371
Db 301 AGCTTCGGGCAACAGAACCGCGAGATGTTTCTCACTAAAGCTCAAAAACCGCAAACTG 360
Qy 1372 CGGCCATTTCTCGAGGAGATCTGGGACGCTGGCGGAAGTGTGACGACCAAGCTTGCCTCC 1431
Db 361 CCCAAGTTCCTCGAGGAGATCTGGGACGTTCTATGCCATCCCGCCATCGTTCAGTCGCAC 420
Qy 1432 CCGACCGATGTGAGCTTCGGGACGAGCTCCAC 1464
Db 421 CTTTCAGATTACCAGGAGGAACAGCGCTCTC 453

RESULT 6
LOCUS      AA664510/c
DEFINITION ESTFrg2- Human Brain, Clontech Homo sapiens cDNA clone pUC19-Frg2
           3', mRNA sequence.
ACCESSION AA664510
VERSION   AA664510.1 GI:2619123
KEYWORDS EST.
SOURCE    Homo sapiens (human)

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ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 607)
            Ming, H. and Huang, B.R.
            TITLE      Research on mechanism of p75NTR induced apoptosis
            JOURNAL    Unpublished (1997)
            COMMENT    Other ESTs: ESTFrg2+
            Contact: Ming Hong
            National Laboratory of Medical Molecular Biology
            Chinese Academic of Medical Sciences & PUMC
            5 Dongdan Santiao, Beijing 100005, P.R.China
            Tel: 86-10-65296406
            Email: huangbr@dm.imicams.ac.cn
            Seq primer: M13 Reverse
            High quality sequence stop: 607.
FEATURES   Location/Qualifiers
            1..607
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="pUC19-Frg2"
             /sex="male"
             /tissue_type="brain"
             /dev_stage="embryonic"
             /lab_host="E.coli Y1090r-"
             /clone_lib="Human Brain, Clontech"
             /note="Organ: brain; Vector: lambda gt11; Site_1: EcoRI;
             Site_2: EcoRI"
ORIGIN
Query Match      11.0%; Score 183.6; DB 1; Length 607;
Best Local Similarity 87.1%; Pred. No. 1.2e-38;
Matches 243; Conservative 0; Mismatches 31; Indels 5; Gaps 4;
Qy 171 GGAATCAAGGCTAGAAAGACTGGAAAGAGCTATTTCTACTGATTTTCTCTCGAAGACCT 230
Db 566 GNGATCCAGGCTNGAAAGCCTCGGAAGCGCTTTTCNACGGATTTTCCCCCGAGGAAGCCCT 507
Qy 231 TGACATGATTTTG--AAATGGATTTCTTACAGATATAAAAGCATTT-GTTAACAGATT 287
Db 506 TGACGCGATTTTGGAAAANGGGATTTCTTTACNGGATTTAAACCAATTTGGTTAACAGATT 447
Qy 288 ATTTGTA-CAAGATAATGTGAATAAAGATCCCGTCACAGATAGATTGGCTT-CAGTGGAG 345
Db 446 ATTTGTACCAAGATAATGTGAATAAAGATCCCGTCACAGATAGATTGGCTTCCAGTGGAG 387
Qy 346 ACTGATATGCTCTTAACATTTGAGACAGCATAGATAAGTCGACATCATCATCGGAAGAG 405
Db 386 ACTGATATGCTCTTAACATTTGAGACAGCATAGATAAGTCGACATCATCATCGGAAGAG 327
Qy 406 AGTAGTAACCAAGGTCAAGACAGCTTGACGTGATCGACG 444
Db 326 AGTAGTAACCAAGGTCAAGACAGCTTGACGTGATCGCGC 288

RESULT 7
LOCUS      AI258616
DEFINITION LP01848:Sprime LP Drosophila melanogaster larval-early pupal pOT2
            Drosophila melanogaster cDNA clone LP01848 Sprime similar to
            M74078: Ecr FBgn0000546 FID:g157318 SWISS-PROT:P34021, mRNA
            sequence.
ACCESSION AI258616
VERSION   AI258616.1 GI:3866141
KEYWORDS EST.
SOURCE    Drosophila melanogaster (fruit fly)
ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
            1 (bases 1 to 574)
REFERENCE Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
AUTHORS

```


Lewis, S. and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 hit genomic sequence DS05325
 Plate: 18 row: D column: 12
 High quality sequence stop: 533.
 Location/Qualifiers
 1..574
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="LP01848"
 /sex="male and female"
 /dev_stage="larvae-pupae"
 /lab_host="DHS-alpha"
 /clone_lib="LP Drosophila melanogaster larval-early pupal
 pOT2"
 /note="Organ: whole body; Vector: pOT2; Site 1: EcoRI;
 site 2: XhoI; Sized fractionated cDNAs were directly
 ligated into pOT2. Plasmid cDNA library."
 "

TITLE
 JOURNAL
 COMMENT

KEYWORDS
 SOURCE
 ORGANISM

GSS.
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 197)
 Latschew, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 Sequence tagged transposon insertions from the UniformMu maize
 population
 Unpublished (2003)
 Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drm@ufl.edu
 Sequence flanking probable Mu insertion site in UniformMu line:
 02S2032-03, Primer set: C
 Class: transposon insertion site.
 Location/Qualifiers
 1..197
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="02S2032-03C1-D09"
 /clone_lib="UniformMu MutAIL Library"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."
 "

FEATURES
 source

ORIGIN
 Query Match 9.1%; Score 151.6; DB 1; Length 574;
 Best Local Similarity 60.0%; Pred. No. 6.7e-30;
 Matches 275; Conservative 0; Mismatches 174; Indels 9; Gaps 1;
 QY 630 GTTCTTAACCGAAGACTAATGAGCAGACAGACTGAAGATGTGACCCGCTGTCCGC 689
 Db 126 GCTACTACCTGATGAATATTGCCAAGTGTCAAGCGCGCAATATACCTTCTCTTAACTGA 185
 QY 690 GAACGAGAGTCCCTGATCGGAGGCTCGTGTGTACAGGAGGGGTACGACGCGTC 749
 Db 186 CAATCAGTTGGCGGTTTATATACAAAGTTAATTTGGTACCAAGGATGGCTATGACGAGCATC 245
 QY 750 GGAGGAAGATCTCAAGAGAGTTACACAGACATGGCAGTTAGAGAGAGAGAGAGAGGA 809
 Db 246 TGAAGAGGATCTCAGCGGTATAT- - - - -GAGTCAACCGATGAGAACGAGAGCCA 296
 QY 810 AACTGACATGCCCTTCGTCAGATCAGAGATGACGATCTTAAACAGTCAGCTTATGTT 869
 Db 297 AACGGACGTCAGCTTTCGGCATATACCGAGATAACCATATCTACCGTCCAGTTGATTGT 356
 QY 870 AGAATTCGCAAGGAGTACCGGATCTCCAGATATCTCAGTCCGATCAATATACATT 929
 Db 357 TGAGTTTGTCTAAAGGCTACACGCGTTTACAAAGATACCCAGGAGACAGATCACGTT 416
 QY 930 ATTAAGGGCTCATCAAGCGAAGTGTATGCTGCGAGTGGCGCGGATACGACGCGC 989
 Db 417 ACTAAGGCCCTGCTGTCGAGGTGATGATGCTGCGTATGCGACGAGCTATGACACAG 476
 QY 990 GACGGACAGCGTCTGTTCCGCAACACACAGCGGTACACGCGGACAACTACCGCAAGGC 1049
 Db 477 CTCGGACTCAATATCTTCGCGAATAATAGATCATATACGCGGATCTTTACAAATGGC 536
 QY 1050 GGGCATGCTCATGCTATCAGGACCTGCTGCACCTTCT 1087
 Db 537 CGGAATGGCTGATAACATTGAAGACCTGCTGCATTTCT 574

RESULT 8
 CG706271
 LOCUS
 DEFINITION
 02S2032-03C1-D09 UniformMu MutAIL Library Zea mays genomic clone
 02S2032-03C1-D09, genomic survey sequence.
 ACCESSION
 CG706271
 VERSION
 CG706271.1 GI:37696881

RESULT 9
 CNS016YX
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence Sp6 end of BAC
 BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL107379.1 GI:5627062
 GSS.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1050)
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

RESULT 10
 CNS016YX
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence Sp6 end of BAC
 BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL107379.1 GI:5627062
 GSS.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1050)
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (BDGP) -
 http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelO8AC11.

FEATURES
 source
 Location/Qualifiers
 1. 1050
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACN17G18"
 /clone_lib="DrosBAC"
 /plasmid="pBelO8AC11"
 /note="end : SP6"

ORIGIN
 Query Match 8.6%; Score 143.2; DB 9; Length 1050;
 Best Local Similarity 51.1%; Pred. No. 1.6e-27;
 Matches 246; Conservative 1; Mismatches 231; Indels 3; Gaps 2;

Qy 935 AGGCGTCATCAAGCAAGTATGATGCTGCGAGTGGCGGCGGATACGACGGCGGCGG 994
 Db 388 AGGCGTGTCTGCGGAGGTGNTGCTGCGTNTGGCAGCGCTATGCCACAGCTCGG 447
 Qy 995 ACAGCGTGTCTGCGGAACACCGGCGTACACGCGGAGCAACTACCGCAAGCGGGCA 1054
 Db 448 ACTCNNTTCTTCGCGNTATAGTCTNTNCGCGGNTTCTNCAANATGCGGAA 507
 Qy 1055 TGCTACGTATCGAGGACCTGTGCACTTCTGTCGGTGATGATCTCCATGAGCATGG 1114
 Db 508 TGGCTGNTAACTTGNAGACCTGTGCTTCTGCGCCNNNTGTTCTCGNTGNGGTGG 567
 Qy 1115 ACAATGTGCACTACCGGTGTCTACCGCGATGTTATATCTCAGACGGCGGCGCTCG 1174
 Db 568 NCCNCGTCGNATNCCGCTTCTCNCCTGCAATGNTCTTCTCGGNCGGCGGCGCTCG 627
 Qy 1175 AGCAACCCCTTTTGTGGAGGAAATCCAGAGATACTACTTGAAGACGCTGGGGTTTACA 1234
 Db 628 NGNNGCCNNNTGTCGNGCGTCCNGAGCTNCTNCAACGNTNNGNATTTTWA 687
 Qy 1235 TTTTAAATCAGCAGCGGCTGCGCTGCTGCGCGCTGCTGTTGCGGAAGATCTCGCGG 1294
 Db 688 TNCCTAACCGGCACTGCGGNGANTCAATGNGNCTGCTTCTTNNGNANNTGCTCTCGN 747
 Qy 1295 TGCTAGCGAACTGCGCAGCTGCGCAGCGAGAACTCCAAATGTCATCTCGCTGAAGC 1354
 Db 748 TCTTCCCGG-GCTGCGTNGCTGGGNGNCCNANGC--GNGTGTTTCTCACTAAGNT 804
 Qy 1355 TGAAGAACAGGAAACTTCCGCACTTCTCGAGAGATCTGGGACGTGGCGCGAAGTGTGCA 1414
 Db 805 NNNAGTCCGNNNCTGNCNNGTTCTCGGNGNNTTCTGGGNGNTTNNNNNNCCGN 864
 Qy 1415 C 1415
 Db 865 C 865

RESULT 10
 BQ058428
 LOCUS
 DEFINITION BQ058428 1031 bp mRNA linear EST 29-MAR-2002
 5', mRNA sequence.
 ACCESSION BQ058428
 VERSION BQ058428.1 GI:19817768
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 1031)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC2067 row: k column: 11
 High quality sequence stop: 634.

FEATURES
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 Location/Qualifiers
 1. 1031
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5814274"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 99"
 /notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN
 Query Match 8.2%; Score 135.6; DB 5; Length 1031;
 Best Local Similarity 55.6%; Pred. No. 1.9e-25;
 Matches 330; Conservative 0; Mismatches 249; Indels 15; Gaps 3;
 Qy 820 CCCTTCGTCAGATCAAGAGATGACATCTTAAACAGTGCAGCTTATTGTAGATTGCGCA 879
 Db 191 CGCTTTCCCACTTCCAGGAGTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT 250
 Qy 880 AAGGACTACCGGATTTCTCAAGATATCTCAGTCCGATCAAAATTAATTATTAAAGCG 939
 Db 251 AAGCAATGCTGTTTCTCTGAGTGGCGGAGGACCAGATCGCCCTCTGAAGGCA 310
 Qy 940 TCATCAAGCGAAGTATGATGCTGCGAGTGGCGGACGCTACGACGGCGGACGCGACG 999
 Db 311 TCCACTATCGAGATCATGCTGTAGAGACAGCCAGGCGCTACAACACGACAGACAGTGT 370
 Qy 1000 GTGCTGTTCCGGAACAACAGGCGGTACACGCGGACAACTACCGCAAGGCGGCGAT--G 1056
 Db 371 ATCACTTCTTGAAGGACTTCACTACGCAAGAGACACTTCCACCGTGAGGCGCTGCG 430
 Qy 1057 TCCTACGTCTACGAGGACCTGCTGCATCTTCTGCGTGTATGTACTCCATGAGCATGGAC 1116
 Db 431 GTGGAGTTTATCAACCCATCTTCGAGTTCTCGGGGCCATCGGCGGCTGGAC 490
 Qy 1117 AATGTGCACTACGCGCTGCTCAACCGCCATCGTTTATATCT--CAGACCGGCGAGGCTC 1173
 Db 491 GAGCGTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCGCAACGTG 550
 Qy 1174 GAGCAACCCCTTTTGTGGAGGAATCCAGAGATCTACTTGAAGACGCTGCGGGTTTAC 1233
 Db 551 CAGGAGCGGCGCGCGTGGAGGCGTTGACAGAGCCCTACGTGGAGGCGCTGCTCTCTAC 610
 Qy 1234 ATTTTAAATCAGCACAGCGGCTGCGCTCGCTGCGCGCTGCTGTTTCGGCAAGATCCTCGGC 1293
 Db 611 AC-----GCGCATCAAGAGGCGCGAGACGAGCTGCGCTTCCCGCGCATGCTCATG 661
 Qy 1294 GTGCTGAGGAACTGCGGACGCTCGGCAAGTCCCAACATGTCATCTCGCTGAG 1353

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

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662 AAGTGGTGAAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGAGGTCTTCGCTTGGCG 721
1354 CTGAGAAACAGAAACTTCGCGCATCTCCGAGGAGATCTGGAGTGGCCCAA 1407
722 CTCCAGGACAAGAAGCTGCGGCTCTGCTGGTGGAGATCTGGAGCTGCCCAA 775

RESULT 11
BQ214241 918 bp mRNA linear EST 02-MAY-2002
AGENCOURT 7589981 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070455
5', mRNA sequence.
ACCESSION BQ214241
VERSION BQ214241.1 GI:20395641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13354 row: m column: 16
High quality sequence stop: 626.
Location/Qualifiers
1. 918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6070455"
/tissue types="large cell carcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
source
Query Match 8.1%; Score 134.6; DB 5; Length 918;
Best Local Similarity 54.3%; Pred. No. 3.4e-25;
Matches 344; Conservative 0; Mismatches 274; Indels 15; Gaps 3;

QY 820 CCCTTCGTCAGATCAGAGATGACATCTTAACAGTCGAGCTTATTGTAGAAATCGCA 879
DB 32 CGCTTTGCCACCTTCACGAGCTGGCCATCATCTCAGTCGAGAGATCGTGGACTTCGCT 91
QY 880 AAGGGACTACGGGATCTCCAAGATATCTCAGTCGATCAAAATTAATATTAAAGGCG 939
DB 92 AAGCAAGTGTCTGTTCTTCGAGCTGGCGGGAGAGACCAGATCGCCCTCTGAGGCA 151
QY 940 TCATCAAGCGAAGTATGATCTGTCGAGTGGCGGAGCGGTCAGACGGCGGCGAGCAGC 999
DB 152 TCCACTATCAGATCATGCTGCTAGACAGCAGCGGCGCTACACACACAGACAGAGTGT 211
QY 1000 GTGCTGTTCCGAACACACAGCGGTACACGGGAGCAACTACCGAGCGGGCAT---G 1056
DB 212 ATCACTTCTTGAAGGACTTCACATACGAAAGGACGACTTCCACCGTCGAGCGTCGAG 271
QY 1057 TCCTACCTCATCAGGACCTGCTGCACTCTGTGCGGTGTATGTACTCCATGAGCATGGAC 1116
DB 272 GTGAGGTTTCATCAACCCCATCTTCGAGTTCTTCGGCGGCGCATGCGGCGGCTGGGCTGGAC 331
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QY 1117 AATGTGACTACGGCTGCTCACGCCATCGTTATATTCT---CAGACGGCCAGGCCTC 1173
DB 332 GAGCGTAGTAGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACGGCCCAACGTG 391
QY 1174 GAGCAACCCCTTTAGTGGAGAAATCCAGAGATACTTGAAGACCTCGGGTTTAC 1233
DB 392 CAGGAGCGGGCGCGTGGAGCGTTGCAGCAGCGCCCTACGTGGAGGCGCTGCTGTCTTAC 451
QY 1234 ATTTTAAATACGACAGCGCGTGCCTCGCTGCGCGCTGCTTTCGCAAGATCTCTCGGC 1293
DB 452 A-----CGGCATCAAGAGCGCGAGACAGCTGCGCTTCCCGCATGCTCATG 502
QY 1294 GTGCTGACGGAATCTCGCACGCTCGGCACGAGAACTCAACATGTGATCTTCGCTGAAG 1353
DB 503 AAGCTGGTGGAGCTGCGCACGCTGAGCTCTGTGCACCTCGGAGAGGTCTTCGCTTGGCG 562
QY 1354 CTGAAGAACAGAACTTCGCCCATCTCCGAGGAGATCTGGAGCTGGCCGAGGTGTCG 1413
DB 563 CTCCAGGACAAGAAGCTGCGGCTCTGCTGCGGAGATCTGGGACGTCCACGAGTGAGGG 622
QY 1414 AGCAGGAAGCTTGCCCCCGCCGACCGATGTGACG 1446
DB 623 GCTGCCACCCAGCCCAAGCCTTGCCTGAGC 655

RESULT 12
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LOCUS AGENCOURT 7503312 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018964
DEFINITION 5', mRNA sequence.
ACCESSION BQ222200
VERSION BQ222200.1 GI:20403609
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13220 row: 1 column: 05
High quality sequence stop: 674.
Location/Qualifiers
1. 867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6018964"
/tissue type="epithelioid carcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_70"
/notes="Organ: Páncrëas; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 Kb. Library constructed by Life
Technologies."
ORIGIN
source
Query Match 8.1%; Score 134.4; DB 5; Length 867;
Best Local Similarity 55.3%; Pred. No. 3.8e-25;
Matches 330; Conservative 0; Mismatches 252; Indels 15; Gaps 3;

QY 820 CCCTTCGTCAGATCAGAGATGACGATCTTAACAGTCGAGCTTATTGTAGAAATCGCA 879
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Db 96 CGCTTGGCCACTTCAGGAGCTGCCATCATCTCAGTCAGGAGATCGTGACTTCGCT 155
Qy 880 AAGGACATACCGGATTCCTCAAGATATCTCAGTCGATCAAAATTAATTAAAGGCG 939
Db 156 AAGCAAGTGCCTGGTTCTCAGCTGGGCGGAGGACCATAGTCGCCCTCCTGAAGGCA 215
Qy 940 TCATCAACGGAAGTATGATCTGCTGGAGTGGCGGACGCTACGAGCGGCGACCGACAGC 999
Db 216 TCCACTATCGAGATCATCTGCTAGAGACAGCCAGGCGCTACACCCAGACAGAGTGT 275
Qy 1000 GTGCTGTTTCGGACCAACAGCGGTACACGCGCGACAACTACCCCAAGCGGGCAT--G 1056
Db 276 ATCACTTCTTGAAGGACTTCACTACAGCAAGACGACTTCCACCGTCAGGCGCTGCAG 335
Qy 1057 TCCTACGTCATCGAGGACCTCTGCACTTCTGTGCGTGTATGTACTCCATGAGATGGAC 1116
Db 336 GTGGAGTTTCAACCCCATCTTGGAGTTCTCGCGGGCCATCGCGGCTGGGCTGGAC 395
Qy 1117 AATGTGACTAGCGCTCTCACGCCCATCGTTATATCT--CAGACCGGCGAGGCTC 1173
Db 396 GACGCTGAGTACGCGCTCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCCAACGTG 455
Qy 1174 GAGCAACCCCTTTAGTGGAGGAAATCCAGAGATACTACTTGAAGAGCTCGCGGTTTAC 1233
Db 456 CAGGAGCGCGCGCTGGAGCGTTGAGCAGCGCTACGTGGAGGCGCTGCTGCTCTAC 515
Qy 1234 ATTTTAAATAGCACAGCGCTCGCTCGCTGCGCGGCTGTGTCGGCAAGATCCTCGGC 1293
Db 516 AC-----GCGCATCAAGAGGCGCGAGGACAGCTGCGCTTCCGCGCATGCTCATG 566
Qy 1294 GTGCTGACGGAACCTTCGCGACGCTCGGACGCGAGACTCCACATGTGCATCTCGCTGAAG 1353
Db 567 AAGCTGTGAGCTGCGCAGCGTGAAGTCTGTGCACTCGGAGAGGTTTTCGCTTGGCG 626
Qy 1354 CTGAAGAACAGGAACTTTCGCGCATCTCCTCGAGAGATCTGGGAGCTGGCGCAAGTG 1410
Db 627 CTCAGGACAGAGAGCTCGCGCTCTGCTGTCGGAGATCTGGAGCTCCACAGNTG 683
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RESULT 13
LOCUS CD673041 667 bp mRNA linear EST 24-JUN-2003
DEFINITION fg19g05.v1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
            fg19g05.5, mRNA sequence.
ACCESSION CD673041
VERSION CD673041.1 GI:32174772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 667)
AUTHORS Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
        Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
        Expressed sequence tag analysis of adult human iris for the NEIBank
        Project: steroid-response factors and similarities with retinal
        pigment epithelium
JOURNAL Mol. Vis. 8 (4), 185-195 (2002)
MEDLINE 22103462
PUBMED 12107412
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```
COMMENT Contact: Wistow G
        Section on Molecular Structure and Function
        National Eye Institute
        6/331, NIH, Bethesda, MD 20892-2740, USA
        Tel: 301 402 3452
        Fax: 301 496 0078
        Email: graeme@helix.nih.gov
        Plate: 19 row: G column: 05
        Seq primer: M13RP1 reverse primer (ABI).
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            1..667
                /organism="Homo sapiens"
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FEATURES
        source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fg19g05"
/tissue_type="iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Eye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."
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ORIGIN

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Query Match 8.1%; Score 134.2; DB 6; Length 667;
Best Local Similarity 54.6%; Pred. No. 4e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;

Qy 820 CCCTTCGTCAGATCAAGAGATGACGATCTTAACAGTCAGCTTATTGTAGATTTCGCA 879
Db 10 CGCTTTGCCCACTTTCAGGAGCTGGCCATCATCTCAGTCAGGAGATCGTGGAGCTTCGCT 69

Qy 880 AAGGACTACCGGATTTCTCAAGATATCTCAGTCCGATCAAAATTAATTAAAGCG 939
Db 70 AAGCAAGTGCCTGTTTCTGAGCTGGGCGGAGGACCATGTCGCTCTCTGAAGGCA 129

Qy 940 TCATCAAGCGAAGTATGATGCTTCGAGTCGGCGAGCGGTACGACGGCGGACGAGCAGC 999
Db 130 TCCACTATCGAGATCATGCTGTAGAGACAGCCAGCGCTACAACCAAGACAGACAGATGT 189

Qy 1000 GTGCTGTTTCGGACAAACAGGCGGTACACGCGGACAACTACCGCAAGGCGGCAT--G 1056
Db 190 ATCACTTCTTGAAGGACTTTCACCTACGCAAGACGACTTCCACCGTCGAGGCTGCAG 249

Qy 1057 TCCTACGTCATCGAGGACCTGCTGCATCTTCTGCGGTGTATGTACTCCTATGAGCATGGAC 1116
Db 250 GTGGAGTTTCAATCAACCCCATCTTCGAGTTCTCGCGGCCATGCGGCGCTGGGCTGGAC 309

Qy 1117 AATGTGCACTACGCGCTGCTCACGCCCATCGTTATATCT--CAGACCGGCGCAGGCTC 1173
Db 310 GACGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCCAACGTG 369

Qy 1174 GAGCAACCCCTTTAGTGGAGGAAATCCAGAGATACTACTTGAAGACGCTCGCGGTTTAC 1233
Db 370 CAGGAGCGGCGCGCTGGAGGCGGTTTCAGAGCCCTACGTGAGGCGCTGCTGCTCTAC 429

Qy 1234 ATTTTAAATCAGCACAGCGGTGCGCTTCGCTGCGCGCTGCTGTTTCGGCAAGATCCTCGGC 1293
Db 430 AC-----GCGCATCAAGAGCGCGCAGGACCATGCTGCTTCCGCGCATGCTCATG 480

Qy 1294 GTGCTGACGGAATCTGCGCAGCTCGGCAAGAGACTCCAACTGTCATCTCCTGTAAG 1353
Db 481 AAGCTGTGAGCGCTGCGCAGCTGAGCTCTGTGCATCTCGGAGCAGGTTCTTCGCTTCGG 540

Qy 1354 CTGAAGAACAGGAACTTTCGCCCATCTCCTCAGAGAGATCTGGGACGTGGCGCAAGTGTGCG 1413
Db 541 CTCAGGACAGAGAGCTGCGCGCTCTCTGCTGTGGAGATCTGGGACGTCACAGAGTGGGG 600

Qy 1414 ACAGCAAGCTTGCCCCCCCCGAC 1436
Db 601 GCTGCCACCCAGCCCCCAGGCC 623
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RESULT 14

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CR614375      1585 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS      full-length cDNA clone CS0DM011YB14 of Fetal liver of Homo sapiens
DEFINITION      (human).
ACCESSION      CR614375
VERSION      CR614375.1 GI:50495182
KEYWORDS      HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1685)
AUTHORS      Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
Paradise Avenue
2 (bases 1 to 1685)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1685
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM011YB14"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match      8.1%; Score 134.2; DB 3; Length 1685;
Best Local Similarity 54.6%; Pred. No. 5.2e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;

QY      820 CCCTCCGTCAGATCACAGATGACGATCTTAAACAGTCGAGTATTGTAGAAATCGCA 879
DB      731 CGCTTTGCCCACTTACGAGAGTGGCCATCATCTCAGTCCAGAGATCGTGACTTCGT 790
QY      880 AAGGGAATACCGGATTCTCCAAGATATCTCAGTCCGATCAAAATTAATTAAGGCG 939
DB      791 AAGCAAGTGCCTGTTCTCTGAGTGGCGGGAGGACAGATCGCCCTCTCTGAAGGCA 850
QY      940 TCATCAAGCGAAGTGATGATGCTGCGAGTGGCGCGACGATGACGACGCGGCGACGAC 999
DB      851 TCCACTATCGAGATCATGCTGCTAGAGACAGCGCGGCTACAAACACGACAGAGTGT 910
QY      1000 GTGCTTTCCGAAACACAGGGGTACACGCGCGACAACTACCGAAGGGGGCAT---G 1056
DB      911 ATCACCTTCTGAAGGACTTCACTACAGCAAGGACGACTTCCACCGTCGAGCCCTGCGAG 970
QY      1057 TCCTAGCTCATCAGGACCTGCTGCACTTCTGCGTGATGTACTCCATGACATGGAC 1116
DB      971 GTGGAGTTTCATCAACCCCATCTTCGAGATTCTCGGGCCATGCGGGCTGGGCTGGAC 1030
QY      1117 AATGTGCATACGCGCTGCTCACCGCCATCGTTATATCTC---CAGACCGGCGAGGCTC 1173
DB      1031 GACGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCGCCACGCTG 1090
QY      1174 GAGCAACCCCTTTTGTGAGGAGAAATCCAGAGATACACTTGAAGACGCTCGCGGTTTAC 1233
DB      1091 CAGGAGCGGCGCGCTGGAGGGGCTTTCAGCAGCGCCCTACGTCGAGGGCGCTGCTCTCTAC 1150
QY      1234 ATTTTAATCAGCACACGCGCTCGCTCGCGCTGCTGTTTCGSCAAGATCTCTCGGC 1293

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1151 AC-----GGCATCAAGAGCGCCGACGACGAGCTGGCTTCCCGCGCATCTCATG 1201
1294 GTGCTGACGAACTGCGCAGCGCTCGGACGCGAGAACTCCAAATGTGATCTCTGCTGAAG 1353
1202 AAGCTGTGAGCCTGCGCAGCGCTGAGCTCTGTGACTCGGAGCAGGTCTTCGCTTGGCG 1261
1354 CTGAAGAACAGGAACTTCGCGCCATTCCTCGAGAGAGATCTCGGACGTCGGCGAAGTGTG 1413
1262 CTCAGGACAAGAGCTGCGCGCTCTGCTGTGCGAGATCTGGGACGCTCCACGAGTGAGGG 1321
1414 ACGACGAGCTTGGCCCGCCGAC 1436
1322 GCTGCCACCGACCGCCACAGCC 1344

RESULT 15
LOCUS      CR610600      1763 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION      full-length cDNA clone CS0DJ010YB16 of T cells (Jurkat cell line)
                Cot 10-normalized of Homo sapiens (human).
ACCESSION      CR610600
VERSION      CR610600.1 GI:50491407
KEYWORDS      HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1763)
AUTHORS      Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
Paradise Avenue
2 (bases 1 to 1763)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1763
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ010YB16"
/tissue_type="T cells (Jurkat cell line)"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match      8.1%; Score 134.2; DB 3; Length 1763;
Best Local Similarity 54.6%; Pred. No. 5.3e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;

QY      820 CCCTTCCGTCAGATCACAGATGACGATCTTAAACAGTCGAGTATTGTAGAAATCGCA 879
DB      817 CGCTTTGCCCACTTACGAGAGTGGCCATCATCTCAGTCCAGAGATCGTGACTTCGT 876
QY      880 AAGGGAATACCGGATTCTCCAAGATATCTCAGTCCGATCAAAATTAATTAAGGCG 939
DB      877 AAGCAAGTGCCTGTTCTCTGAGTGGCGGGAGGACAGATCGCCCTCTCTGALGGCA 936
QY      940 TCATCAAGCGAAGTGATGATGCTGCGAGTGGCGCGACGCTACGACGCGGCGACGACG 999
DB      937 TCCACTATCGAGATCATGCTGCTAGAGACAGCGCGGCTACAAACACGACAGAGTGT 996
QY      1000 GTGCTTTCCGAAACACAGGCGGTACACGCGCGACAACTACCGCAAGGGGGCAT---G 1056

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Db	997	ATCACCTTCCTGTAAGGACTTCACCTCAGCAAGGACGACTTCCACCGTGAGCGCTGCAG	1056
Qy	1057	TCCTACGTCATCGAGGACCTGCTGCATCTTGTGCGGTATGTACTCATGAGCATGGAC	1116
Db	1057	GTGGAGTTCATCAACCCCATCTTCGAGTCTCGCGGCCATCGCGGGCTGGCGCTGGAC	1116
Qy	1117	AATGTGCATCAGCGCTGCTCACCGCCATCGTTATATTCT--CAGACCGCGCAGGCGCTC	1173
Db	1117	GACGCTGAGTAGCCCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGCGCCAACGCTG	1176
Qy	1174	GAGCAACCCCTTTTAGTGGAGGAAATCCAGAGATACTACTTGAAGACGCTGCCGGTTTAC	1233
Db	1177	CAGGAGCCGGCCGCTGGAGGCGTTTCGACGAGCCCTACGTGGAGGCGCTGCTGTCTCTAC	1236
Qy	1234	ATTTTAAATCAGCACAGCGGTCCGCTCGCTGCTGTTTCGGCAAGATCCCTCGGC	1293
Db	1237	AC-----GCGCATCAAGAGGCCGAGGACGAGCTGCGCTCCCGCGCATGCTCATG	1287
Qy	1294	GTGCTGACGGAACTGCGCACGCTCGGCACGAGAACTCCAACTGTCATCTCGCTGAAG	1353
Db	1288	AAGCTGTGAGCCTTGGCAACGCTGAGCTCTGTGCACTCGGAGCAGGTCTTCGCGCTGCGG	1347
Qy	1354	CTGAAGAACAGGAAACTTCGSCCATTCCTCGAGAGATCTTGGGACGTGGGCCGAAGTGTCTG	1413
Db	1348	CTCCAGGACAAGAAGTCGCGCCTCTGTGTGCGAGATCTGGGACGTCCGACGATGAGGG	1407
Qy	1414	ACGAGGAAGCTTGCCCCCGAC	1436
Db	1408	GCTGGCCACCCAGGCCACACGCC	1430

Search completed: April 14, 2005, 18:41:11
Job time : 5679.37 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	681	41.0	2126	4	US-09-393-839-1	Sequence 1, Appli
2	660.4	39.7	1934	3	US-08-653-648A-2	Sequence 2, Appli
3	660.4	39.7	1934	4	US-09-564-418-2	Sequence 2, Appli
C	660.4	39.7	1934	4	US-09-564-418-61	Sequence 61, Appli
5	660.4	39.7	2464	3	US-08-653-648A-3	Sequence 3, Appli
6	660.4	39.7	2464	4	US-09-564-418-3	Sequence 3, Appli
C	660.4	39.7	2464	4	US-09-564-418-62	Sequence 62, Appli
8	660.4	39.7	2745	4	US-08-653-648A-4	Sequence 4, Appli
9	660.4	39.7	2745	4	US-09-564-418-4	Sequence 4, Appli
C	657.6	39.6	2463	3	US-08-653-648A-10	Sequence 10, Appli
11	652.2	39.2	2711	3	US-08-891-298-2	Sequence 2, Appli
C	650.8	39.2	1934	3	US-08-653-648A-9	Sequence 9, Appli
13	623.2	37.5	948	3	US-08-653-648A-6	Sequence 6, Appli
14	623.2	37.5	948	4	US-09-564-418-6	Sequence 6, Appli
C	623.2	37.3	948	4	US-09-564-418-63	Sequence 63, Appli
16	620	37.3	948	3	US-08-653-648A-64	Sequence 64, Appli
17	443.4	26.7	10060	3	US-09-479-122-25	Sequence 25, Appli
18	443.4	26.7	10060	4	US-09-484-997-25	Sequence 25, Appli
19	443.4	26.7	10060	4	US-09-481-355-25	Sequence 25, Appli
20	443.4	26.7	10060	4	US-09-481-382-25	Sequence 25, Appli
21	443.4	26.7	10060	4	US-09-455-559A-25	Sequence 25, Appli
22	443.4	26.7	10060	4	US-09-484-996-25	Sequence 25, Appli
23	443.4	26.7	10060	4	US-09-479-123-25	Sequence 25, Appli
24	443.4	26.7	10060	4	US-09-484-317A-25	Sequence 25, Appli
25	442.4	26.6	546	2	US-08-477-493-2	Sequence 2, Appli
26	442.4	26.6	546	3	US-09-798-070-3	Sequence 3, Appli
27	442.4	26.6	546	4	US-10-142-373-3	Sequence 3, Appli

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QY 690 GAAACAGAGTCCCTGATCGAGGCTCGTGTGTGTACAGAGGGGTACGAGGAGCGTC 749
Db 1240 CAACAGCAGTTCCTGATCGGAGGCTGTGTGTGTACAGAGGATACGAGGAGCTTC 1299
QY 750 GGAGGAGATCTCAAGAGAGTTACACAGACATGCGAGTTAGAAAGAGAGGAGGA 809
Db 1300 GGAAGAGATCTCAAAAGGGTGACGACATTTGGCAATCAGACATGAAGAAGACGAGA 1359
QY 810 AACTGACATGCCCTTCCCTCAGATCACAGAGATGACGATCTTAAACAGTGCAGCTTATTGT 869
Db 1360 CTCAGACATGCCATTCGCCAGATCACAGAAATGACCATCTCTCAGGTACAGCTAAATGT 1419
QY 870 AGAATTCGAAGGGAATACCGGATTTCTCAAGATATCTCAGTCCGATCAATTAATTT 929
Db 1420 CGAGTTTCCAAAGGCTTACCTGTGTTTCTCAAGATCTTCAAACTGTACACAGATCAAT 1479
QY 930 ATTAAGGCGTCAACAGGAGTATGATGCTCGAGTGGCGGAGGTACGACGCGGC 989
Db 1480 ATTAAGGCGATGCTCAAGCGAAGTATGATGCTCCGAGTACGAGGCGGTACGACGCGT 1539
QY 990 GACGACAGCGTGTCTTTCGGGAAACAACAGGCGGTACACGCGGCAACTACCCGAAGGC 1049
Db 1540 GTCGATAGCGTCTGTTCGCCCAACAACAGGCGGTACACTCGGACAACTACCCGAAGGC 1599
QY 1050 GGGCATGTCTACGTCATGAGGAGCTCTGCACTTCTGTGCGGTATGTATCTCATGAG 1109
Db 1600 GGGCATGTGCTACGTCATGAGGAGCTCTGCACTTCTGTGCGGTATGTATCTCATGATC 1659
QY 1110 CATGACAAATGTGCACTACGCGTCTCAACGCGCATCGTTATATTTCTCAGACCGGCCAGG 1169
Db 1660 GATGACAAATGTGCACTACGCGTCTCACTGCGCATCGTTATTTCTCGGATCGGCCGG 1719
QY 1170 CCTCAGCAACCCCTTTTAGTGGAGAAATCCAGAGATATCTATGAAAGACGCTGCGGGT 1229
Db 1720 CCTCAGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAAACAGCTGCGGGT 1779
QY 1230 TTACATTTTAATCAGCAGCGGCTGCGTCTGCGCGGTGCTGTTTGGCAGAGATCCT 1289
Db 1780 GTACATCATGAACACGACAGCGCGTGCACGCTGCGCGGTATCTACGCGAAGATTC 1839
QY 1290 CGGCGTGTGACGGAACCTGCGCAGCTCGGACGAGAACTCCAAACATGTGCATCTCGCT 1349
Db 1840 GTCGCTGTATTACGAGTTTGGGACGCTGGGCAATTCGAACATGTGCATCTCGCT 1899
QY 1350 GAAGCTGAAGAACAGGAACTTCCGCCATTTCTCGAGGAGATCTGGGACGTGGCGGAAGT 1409
Db 1900 GAACTCAAGAACAGGAAAGTCCGCCGTTCTCGAGGAGATTTGGGACGTGGCGCAAGT 1959
QY 1410 GTCGAGGAGAGCTTGCCCCCGACCGATGTACGCTGGGAGACGAGCTCCACTTAGA 1469
Db 1960 GTCGAGGCGGACGCGCGCTGTGTGGCGAGCGGCGCTACGGCGCTCTAGCGCGGCGCAG 2019
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Db 2020 CGATCGCGCGCTCGCCCGCGCCCGCGGCTTGCTCTAGCGTAGTGAT 2068
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RESULT 2

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US-08-653-648A-2
; Sequence 2, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
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; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-08-653-648A-2
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Query Match 39.7%; Score 660.4; DB 3; Length 1934;
Best Local Similarity 80.7%; Pred. No. 2.3e-181; Indels 27; Gaps 2;
Matches 807; Conservative 0; Mismatches 166;

QY 435 TGTATCGACCGGTATGAGGCCGAGTGCCTGCCAGAGTCCACGTCGACGAGCAAAAG 494
Db 733 TCTTGGGTGGGCATGAGGCCCGAGTGGTGGCGGAGAACGAGTGTGCAATGAAACG 792
QY 495 AAGAGAAAGGAAAGCAGAGAGAAAGAAAGAACTCCAGTCCAGTACGACGAGTGA 554
Db 793 GAAAGAGAAAGGCGCAGAGGGGAAAGAAATTTGCCCGTCAGTACGACGACAGTAGA 852
QY 555 CGATCATATGCTGCCATAATGCAATGTGACCTCCGCCGCCAGAGGCGGCAAGGATT-- 612
Db 853 CGATCATATGCTGCCATCATGCAATGTGACCTCCGCCGCCAGAGGCGGCTAGATTCT 912
QY 613 -----CACGAACTGTGCCAGGTTCCTAAACGAGAGAGTCTAATGAGAGCAAA 659
Db 913 GGAATGTGTGACGACGAGGTGGTGCACGATTCCTGAATGAGAAAGCTAATGGAACAGAA 972
QY 660 CAGACTGAAGAAATGTGACGCGCTGTGCGGCAACGAGAACTCCTGTATCGCGAGCTCGT 719
Db 973 CAGATTGAAGAACTGTGCGGCCCTCTACTGCGCAATCAGAAAGTGTGTATCGCAAGGCTCGT 1032
QY 720 GTGTATCCAGAGGGGTACGAGCAGCGTCCGAGGAGAGATCTCAAGAGAGTTACACAGAC 779
Db 1033 GTGTATCCAGAGGGCTATGAAACCTCTCGAGGAGAGACTGAGAGGGTTACACAGTC 1092
QY 780 ATGCGAGTTAGAAAGAAAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCAACAGA 839
Db 1093 -----GSAACGAGCAGCAGAAAGCTCGATATGCCGTTCCGTCAGATTACCGA 1140
QY 840 GATGACGATCTTAACAGTGCAGCTTATGTAGATTCGCAAGAGGAGTACCGGAGTCTC 899
Db 1141 GATGACGATTTCTCAGTGCAGCTCATCGTAGAAATTCGTAAGGGGCTTCCCGGCTTCGC 1200
QY 900 CAAGATATCTCAGTCCGATCAAAATTACATTTAAAGGCGGTATCAAGCGAAGTGTATGAT 959
Db 1201 CAAGATCTCGAGTCCGACCCAGATCACGTTTAAAGCGGTGCTCAAGTAGAGTGTATGAT 1260
QY 960 GCTGCGAGTGGCGCAGCGGTACGACGCGGCGAGCGGACAGCGGTGCTGTTCGCGAACAACCA 1019
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Db 1321 GGCGTACACTCGCGACAACTACCGCAAGGGGCGATGGCGTACGTCATTCGAGGACCTGCT 1380
QY 1080 GCATTTCTGCGGTGTATGTACTCCATGAGCATGGCAAAATGTGCACTACGCGCTGCTCAC 1139
Db 1381 GCATTTCTGCGGTGCATGTACTCCATGATGATGATAACGTCATTTATGCGTGTCTTAC 1440
QY 1140 CGCATCGTTATATTTCTCAGACCGGCGGCTCGAGCAACCCCTTTTAGTGGAGGAAT 1199
Db 1441 AGCATTTGTCTATCTTCTCAGACCGGCGGCGCTTGAGCAACCCCTGTGTGGTGGAGGACAT 1500
QY 1200 CCAGATATCTACTTTGAAGCGCTGCGGTTTACATTTTAAATCAGACACGCGGTGCGC 1259
Db 1501 CCAGATATTTACTCTGAACACGCTTACGCGGTGTATCTCTGNAACCAAGACGCGGTGCGC 1560
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QY 1260 TCGCTGGCGCTGTCTTGGCAAGATCCTCGCGTGTCTGACGAAGTGCACGCTCGG 1319
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QY 1320 CACGAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGAAATTCGSCCAAT 1379
Db 1621 CATGAGAACTCCAAACATGTGCATCTCCTCAAGCTGAAGAACAGAAAGTTCGCGCCGT 1680
QY 1380 CCTCAGAGAGATCTGGGACGTGGCGCAAGTGTGACGACG 1419
Db 1681 CCTCAGAGAGATCTGGGACGTGGCGCAAGTGTGACGACG 1720

RESULT 3
US-09-564-418-2
; Sequence 2, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-09-564-418-2

Query Match 39.7%; Score 660.4; DB 4; Length 1934;
Best Local Similarity 80.7%; Pred. No. 2.3e-181;
Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

QY 435 TGTATCGACGCGTATGAGCGCCGAGTGGCTGCTCCAGAGTCCAGTGAAGAACAAAG 494
Db 733 TCTTGGCGTGGCATGAGCGCCGAGTGGCTGCTCCGAGAACCACTGTGCAATGAACG 792
QY 495 AAGAGAAAAGGAGACACAGAGAGAAAAGACAAACTGCCAGTCACTACGACACAGTGA 554
Db 793 GAAAGAGAAAAGGCGCAGAGGAGAAAAGACAAATTTGCCGTCAGTACGACGACAGTGA 852
QY 555 CGATCATATGCTGCTCCATATGCAATGTGACCCCTCCGCGCCCGCAGAGCGCGCAAGGATT-- 612
Db 853 CGATCATATGCTGCTCCATATGCAATGTGACCCCTCCGCGCCCGCAGAGCGCGTGAATTTCT 912
QY 613 -----CAGCAAGTGTGCTCCGAGGTTCTTAACGGAGAACTAATGAGACAGAA 659
Db 913 GGNATGTGACACGACGAGTGTGCGCACGATTCCTGAATGAGAACTAATGAGAACAGAA 972
QY 660 CAGACTGAAGAAATGTGACGCGCTGTGCGGGAACACAGAGTCCCTGATCGGAGGCTCGT 719
Db 973 CAGATTGAAGAACTGTGCGCCCTCCCTCACTGCGCAATCAGAACTGCTTGAATGCGCAAGGCTCGT 1032
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Db 1033 GTGGTACCAGAGGGGTATGAAACACCTTCGAGGAGAGACCTGAAGAGGGTTACAGATC 1092
QY 780 ATGCGAGTTAGAGAGAAAGAGAGGAGGAAACTGACATCCCTTCGCTCAGATCAGAA 839
Db 1093 -----GGACGAGACGACGAGACTCGGATATCCGTTCCGTCAGATTACCGA 1140
QY 840 GATGACGATCTTAACAGTGCAGCTTATGTAGAAATTCGAAAGGAGTACCGGATCTC 899
Db 1141 GATGACGATCTTCAAGTGCAGCTTATGTAGAAATTCGTAAGGGCTCCCGGGCTTCG 1200
QY 900 CAAGATATCTCAGTCCGATCAATTTACATTTATTAAGGCGTCAACGCAAGTGTATGAT 959
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Db 1201 CAAGATCTCGCAGTCCGACAGATCAGCTTATTAAGCGCGTCTCAAGTGAAGTGTATGAT 1260
QY 960 GCTCGAGTGGCGGACGCTACGACGCGGCGACGACGAGCTGTGTTTCGGGAAACAAACA 1019
Db 1261 GCTCCGAGTGGCTCGGCGGTATGACGCGGCACCGACAGCTACTGTTTCGGGAAACAAACA 1320
QY 1020 GGCGTACACGCGGCACAACTACCGCAAGCGCGGCGATGTCTTACGTCACTCGAGGACCTGCT 1079
Db 1321 GGCGTACACTCGCGCAACTACCGCAAGCGGACGCAATGGCGTACGTCACTCGAGGACCTGCT 1380
QY 1080 GCATTTCTGCTCGTGTATGTACTCTCATGAGCATGGAACHATGTGCACTACGCGCTGCTCAC 1139
Db 1381 GCATTTCTGCTCGTGTATGTACTCTCATGAGCATGGAACHATGTGCACTATGCGCTGCTTAC 1440
QY 1140 CGCCATCGTTATATTTCTCAGACCGCGCAGGCTCGAGCAACCCCTTTTAGTGGAGGAAAT 1199
Db 1441 AGCCATTTGTCATCTTCTCAGACCGCGCGGCTTGAGCAACCCCTTTTAGTGGAGGACAT 1500
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Db 1501 CCAGAGATTTACTCTGAACACGCTACGGTGTACATCTCTGAACCAAGAACAGCGCTGCGC 1560
QY 1260 TCGTGGCGCGTGTGTTTCGCAAGATCCTCGCGCTGTGACGGAATCTCGCACGCTCGG 1319
Db 1561 CCGGGCGCGCTCATCTTTCGCGAGATCCTCGGCACTACTGACGGAGATCCGCGACGCTGG 1620
QY 1320 CACGAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGAAATTTCCGCAAT 1379
Db 1621 CATGCAAACTCCAAACATGTGCATCTCCTCAAGCTGAAGAACAGAAAGTTCGCGCGTT 1680
QY 1380 CCTCAGGAGATCTGGGACGTGGCGCAAGTGTGACGACG 1419
Db 1681 CCTCAGGAGATCTGGGACGTGGCGCAAGTGTGACGACG 1720

RESULT 4
US-09-564-418-61/c
; Sequence 61, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-09-564-418-61

Query Match 39.7%; Score 660.4; DB 4; Length 1934;
Best Local Similarity 80.7%; Pred. No. 2.3e-181;
Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

QY 435 TGTATCGACGCGTATGAGCGCCGAGTGGCTGCTCCAGAGTCCAGTGAAGAACAAAG 494
Db 1202 TCTTGGCGTGGCATGAGCGCCGAGTGGCTGCTCCGAGAACCACTGTGCAATGAACG 1143
QY 495 AAGAGAAAAGGAGACACAGAGAGAAAAGACAAACTGCCAGTCACTACGACGAGTGA 554
Db 1142 GAAAGAGAAAAGGCGCAGAGGAGAAAAGACAAATTTGCCGTCAGTACGACGACAGTGA 1083
QY 555 CGATCATATGCTGCTCCATATGCAATGTGACCCCTCCGCGCCCGCAGAGCGCGCAAGGATT-- 612
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Db	1082	CGATCAGATGCTCCCATCATGCAATGTGACCTCCGCCCCAGGAGCGGCTAGAAATCT	1023
Qy	613	-----CACGAAGTGGTCCGAGGTTCTTAACGGAGAGCTAATGAGAGAGAA	659
Db	1022	GGAAATGTGTGAGCAGCAGAGTGGTCCACGATTCCTGAATGAGAAGCTAATGGAACAGAA	963
Qy	660	CAGACTGAAGAAATGTAGCGCGCTGTGGCGAAACAGAAAGTCCCTGATCGGAGGCTCGT	719
Db	962	CAGATTGAAGAACTGCGCCCTCCCTACCTGCAATCAGAAAGTCTGTGATCGCAAGGCTCGT	903
Qy	720	GTGGTACAGAGGGGTACGAGCAGCGCTCGGAGGAGAGATCTCAAGAGAGTTACACAGAC	779
Db	902	GTGGTACAGAGGCTATGACAACTTCCGAGGAGAGCTGAAGAGGGTTACACAGTC	843
Qy	780	ATGGCAGTTAGAAAGAAAGAGGAGGAGAACTGACATGCCCTTCGTCAGATCAGACA	839
Db	842	-----GGACGAGGAGCGACGAAGACTCGGATATGCCGTTCCGTCAGATTAACCGA	795
Qy	840	GATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGGAGCTACCGGATTTCTC	899
Db	794	GATGACGATTTCTCAGTGCAGCTCATCTGTAATTCGTAAGGCGCTCCCGGCTTCGC	735
Qy	900	CAAGATATCTCAGTCCGATCAAAATTAATTAAAGCGCTCATCAAGCAGAGTGAATGAT	959
Db	734	CAAGATCTCGCAGTCGGACCATCACTGTTTAAAGGCGTCTCAAGTGAGGTGATGAT	675
Qy	960	GCTGCGAGTGGCGACCGGTACGAGCGCGGACCGAGCGGTGCTGTTGCGGAAACCA	1019
Db	674	GCTCGAGTGGTCCGCGGTATGACGCGGCCACCGACAGCGTACTGTTTCGCGAAACCA	615
Qy	1020	GGCGTACACGCGCGCAACTACCGCAAGCGGCGATGCTCTACGTATCGAGGACCTGCT	1079
Db	614	GGCGTACACTCCGCAACTACCGCAAGCGGCGATGCGGTACGTATCGAGGACCTGCT	555
Qy	1080	GCATCTTGTGCGGTATGTATCTCATCAGCATGGAATGTGCACTACGCGCTGCTCAC	1139
Db	554	GCATCTTGTGCGGTGATGATCTCCATGATGATGATTAACGTGCTATGCGCTGCTTAC	495
Qy	1140	CGCCATCGTTATTTCTCAGACCGCGGCGGCTCGAGCAACCCCTTTTGTGAGGAGAA	1199
Db	494	AGCCATTTGTCATCTTCTCAGACCGCGCGGCTTGAACACCCCTGTTGGTGGAGGACAT	435
Qy	1200	CCAGAGATACTACTTGAAGACGCTCGGCTTTTACATTTTAAATCAGCACAGCGGCTCGCC	1259
Db	434	CCAGAGATATTACTGACACGCTAGCGGTGTACATCTGTAACAGACAGCGGCTCGCC	375
Qy	1260	TCGCTGCGCGCTGTGTCGCAAGATCTCGGCGTGTGACGGAATCGCGCAAGCTCGG	1319
Db	374	CGCGCGCGCGTCACTTTCGCGAGATCTCGGCGCATCTGCGGAGATCCGCAAGCTCGG	315
Qy	1320	CACGAGACTCCACATGTGCATCTCGCTGAAGCTGAAGAACAGGAACTTCGCGCAAT	1379
Db	314	CATGAGAACTCCACATGTGCATCTCCCTCAAGCTGAAGAACAGGAAAGCTCGCGCGTT	255
Qy	1380	CCTCGAGGAGATCTGGAGCTGGCGAAGTGTGACGAGC	1419
Db	254	CCTCGAGGAGATCTGGAGCTGGCGAGCTGGCGAGCG	215
RESULT 5			
US-08-653-648A-3			
; Sequence 3, Application US/08653648A			
; Patent No. 6379945			
; GENERAL INFORMATION:			
; APPLICANT: Jepson, Ian			
; APPLICANT: Greenland, Andrew			
; APPLICANT: Martine, Alberto			
; TITLE OF INVENTION: A Gene Switch			
; FILE REFERENCE: PPD50047/US			
; CURRENT APPLICATION NUMBER: US/08/653,648A			
; CURRENT FILING DATE: 1996-05-24			
; PRIOR APPLICATION NUMBER: GB 9510759.5			
; PRIOR FILING DATE: 1995-05-26			

; PRIOR APPLICATION NUMBER: GB 9605656.9			
; PRIOR FILING DATE: 1996-03-18			
; PRIOR APPLICATION NUMBER: GB 9513882.2			
; PRIOR FILING DATE: 1995-07-07			
; PRIOR APPLICATION NUMBER: GB 9517316.7			
; PRIOR FILING DATE: 1995-08-24			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 3			
; LENGTH: 2464			
; TYPE: DNA			
; ORGANISM: Heliothis virescens			
; FEATURE:			
; NAME/KEY: Unsure			
; LOCATION: (2241)..(2241)			
; OTHER INFORMATION: Unsure			
; US-08-653-648A-3			
Query Match 39.7%; Score 660.4; DB 3; Length 2464;			
Best Local Similarity 80.7%; Pred. No. 2.7e-181;			
Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;			
Qy	435	TGATGACCGCTATGAGCCCGAGTGGCTCCAGAGTCCACGTGCAAGACAAAAG	494
Db	612	TCTTGGCGTGGCATGAGCCCGAGTGGTGGCGGAGAACGAGTGTCAATGAACG	671
Qy	495	AAGAGAAAAGGAGACAGAGAGAAAAGAACTGCCAGTCCAGTACGACGAGTGA	554
Db	672	GAAAGAGAAAAGCGCAGAGGAGAAAAGCAANTTCCCGTCACTACGACGAGTAGA	731
Qy	555	CGATCATATGCTCCCATTAATGCAATGTGACCTCCGCCCCAGAGGCGCAAGGATT	612
Db	732	CGATCATGCTCCCATCATGCAATGTGACCTCCGCCCCAGAGGCGCTAGAAATCT	791
Qy	613	-----CAGCAAGTGTCCCGAGGTTCTTAACGAGAGCTAATGAGAGCAAA	659
Db	792	GGAATGTGTGACGACGAGGTGGTCCACGATTCCTGAATGAGAGCTAATGAGACAA	851
Qy	660	CAGATGAAAGAAATGTGACGCGCTGTGCGGCAACAGAACTCCCTGATCGCGAGGCTCGT	719
Db	852	CAGATTGAGAAACGTGCCCCCTCTACTGCCAATCAGAACTGTTGATCGCAAGGCTCGT	911
Qy	720	GTGTTACAGAGGGGTACAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGAC	779
Db	912	GTGTTACAGAGGGCTATGAACAACTTCCGAGGAGAGCTGAAAGAGGTTACACAGTC	971
Qy	780	ATGCGACTTAGAAGAAAGAGAGGAGAACTGACATGCCCTTCCGTTCAGATCAGACA	839
Db	972	-----GGACGAGGACGACGAGACTCGGATATGCCGTTCCGTTCAGATTACCGA	1019
Qy	840	GATGACGATCTTAACTGTCAGCTTATTGTAGAAATTCGCAAGAGGACTACCGGATTTCTC	899
Db	1020	GATGACGATTTCTACAGTGCAGCTCATCGTAGAAATTCGTTAAAGGGCTCCCGGCTTCG	1079
Qy	900	CAAGATATCTCAGTCCGATCAATTAATTAATTAAGGCGCTCACTCAAGCGAAGTGTGAT	959
Db	1080	CAAGATCTCGAGTCGGACCATGATCAGTTATTAAAGGCGTCTCAAGTGAAGTGTGAT	1139
Qy	960	GCTCGAGTGGCGGACGCTACGACGCGGACGAGCAGGCTGCTGTTTCGCGAACAACCA	1019
Db	1140	GCTCCGAGTGGCTCGGCGGTATGACGCGGCCACCGACAGCGTACTGTTTCGCGAACAACCA	1199
Qy	1020	GGCGTACACGCGCAAACTACCGCAAGGGGGGATGCTCTACGTCTACGAGGACCTGCT	1079
Db	1200	GGCGTACACTCGCGCAAACTACCGCAAGGGGAGGATGCGGTACGTCTACGAGGACCTGCT	1259
Qy	1080	GCATTTCTGTCGGTGTATGTACTCCATGAGCATCGACAAATGTGCACTACGCGTGTCTCAC	1139
Db	1260	GCATTTCTGTCGGTGTATGTACTCCATGATGATGAATGATTAATGCGCTGCTTAC	1319
Qy	1140	CGCCATCGTTTATTTCTCAGACCGCGGCGCTCGAGCAACCCCTTTTGTGAGGAGAAAT	1199
Db	1320	AGCCATTTGTCATCTTCTCAGACCGCGGCGCTTGAACAACTTGTGTTGGAGGACAT	1379

QY 1200 CCAGAGATACTTGAAGACGCTCGCGTTTACATTTTAAATCAGACAGCGCTCGCC 1259
 Db 1380 CCAGAGATATTACCTGAAACACGCTACGGGTGTACATCTCTGAACACAGACGCGTCCGC 1439
 QY 1260 TCGTTCGCCCGTGTCTTTCGCGCAAGATCTCGCGGTGTCTGACGGAATCTGCGACGCTCGG 1319
 Db 1440 CCGCGCGCGTGTCTTTCGCGGAGATCTTGGGATCTGACGAGATCTCGACGCTCGG 1499
 QY 1320 CACGAGAACTCCAAATCTGTCATCTCGTGAAGCTGAAGAACAGGAACTTTCGCCCATTT 1379
 Db 1500 CATGCAGAACTCCAAATCTGTCATCTCTCTCAAGCTGAAGAACAGGAACTTTCGCCCATTT 1559
 QY 1380 CCTCAGAGATCTCGGACGCTGCGCAAGTGTGCGACGAG 1419
 Db 1560 CCTCAGAGATCTCGGACGCTGCGGACGCTGCGGACGAG 1599

RESULT 6

US-09-564-418-3

; Sequence 3, Application US/09564418

; Patent No. 6610828

; GENERAL INFORMATION:

; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2464

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: misc

; LOCATION: (2241)..(2241)

; OTHER INFORMATION: n is a, c, g, or t

US-09-564-418-3

Query Match 39.7%; Score 660.4; DB 4; Length 2464;

Best Local Similarity 80.7%; Pred. No. 2.7e-181;

Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

QY 435 TGTATCGACGCGTATGAGCCCGAGTGCCTGCCAGAGTCCACGTGCAAGAACAAAG 494
 Db 612 TCTTGGGTGGGATGAGCCCGAGTGCCTGCCAGAGTCCACGTGCAAGAACAAAG 671
 QY 495 AAGAGAAAGGAGACAG 554
 Db 672 GAAAGAGAAAGGAG 731
 QY 555 CGATCATATGCTTCCCATATGCAATGTGACCTCCGCCCGCCAGAGCGCGCAAGGATT-- 612
 Db 732 CGATCATATGCTTCCCATATGCAATGTGACCTCCGCCCGCCAGAGCGCGCTAGAAATCT 791
 QY 613 -----CAGCAAGTGTCCGAGGTTCTTAAACGAGAGAACTAATGAGAGAGAA 659
 Db 792 GGAATGTGTGACGACGAGGTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
 QY 660 CAGACTGAAGATGTGACGCGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
 Db 852 CAGATTGAAGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
 QY 720 GTGGTACAG 779
 Db 912 GTGGTACAG 971

QY 780 ATGCGAGTTAGAAGAAGAAG 839
 Db 972 -----GGAAG 1019
 QY 840 GATGACGATCTTAACAGTGCAGCTTATGTAGAAATTCGCAAGAGAGAGAGAGAGAGAGAG 899
 Db 1020 GATGACGATCTTAACAGTGCAGCTTATGTAGAAATTCGCAAGAGAGAGAGAGAGAGAGAG 1079
 QY 900 CAAGATATCTCAGTCCGATCAAAATTAATTAAGGCGCTCATCAAGCGAAGTGAATGATGAT 959
 Db 1080 CAAGATCTCGAGTCCGAG 1139
 QY 960 GCTCGAGTGCAG 1019
 Db 1140 GCTCGAGTGCAG 1199
 QY 1020 GCGGTACAGCGGAG 1079
 Db 1200 GCGGTACAGCGGAG 1259
 QY 1080 GCATCTCTGCTGCTGATGTATCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139
 Db 1260 GCATCTCTGCTGCTGATGTATCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319
 QY 1140 CGCATCGTTATATTTCTCAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
 Db 1320 AGCATTTGTCATCTTCTCAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
 QY 1200 CCAGAGATCTTGAAG 1259
 Db 1380 CCAGAGATCTTGAAG 1439
 QY 1260 TCGTTCGCCCGTGTCTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319
 Db 1440 CCGCGCGCGGAG 1499
 QY 1320 CACGAG 1379
 Db 1500 CATGCAG 1559
 QY 1380 CCTCAG 1419
 Db 1560 CCTCAG 1599

RESULT 7

US-09-564-418-62/c

; Sequence 62, Application US/09564418

; Patent No. 6610828

; GENERAL INFORMATION:

; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 62

; LENGTH: 2464

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2241)..(2241)

; OTHER INFORMATION: n = a, c, g, or t, or i

US-09-564-418-62

Query Match 39.7%; Score 660.4; DB 4; Length 2464;

[illegible]

RESULT 8

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US-08-653-648A-4
; Sequence 4, Application US/08653648A
; Patent NO. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (2522)..(2522)
; OTHER INFORMATION: Unsure
US-08-653-648A-4

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Query Match	39.7%	Score 660.4	DB 3	Length 2745
Best Local Similarity	80.7%	Pred. No. 2.9e-181		
Matches 807	Conservative 0	Mismatches 166	Indels 27	Gaps 2
QY	435	TGTTATCGACGCGTATGAGGCCGAGTGCCTGCGTCCCGAGAGTCCACGTCGAAGAACAAAAAG	494	
DB	893	TCITGCGGTGGGCATGAGGCCGCGAGTGCCTGCGTGCCTGGAGAACCGTGTGCAATGAAACG	952	
QY	495	AAGAGAAAAGGAAGCAGAGAGAGAAAAGACAAACTGCCAGTCAAGTACGACGACAGTGA	554	
DB	953	GAAGAAGAAAAGCGCAGAGGGAAGAACAAATTTGCCGCTCAGTACGACGACAGTAGA	1012	
QY	555	CGATCATATGCTGCCCATATGCAATGTGACCTCCGCCCCCAGAGCGCGCAAGSATT--	612	
DB	1013	CGATCATATGCTGCCCATATGCAATGTGACCTCCGCCCCCAGAGCGCGTAAATTC	1072	
QY	613	-----CACGAATGGTCCCGAGGTTCTTAACGGAGAACGTAATGGAGCAGAA	659	
DB	1073	GGAATGTGTGCAGCAGCAGGTGGTGCACGATTTCTTGAAATGGAAGCTAATGAAACAGAA	1132	
QY	660	CAGACTGAAGAAATGTGACGCGCTGTCCGGCGAACACGAAGTCCCTGATCCGAGGCTCGT	719	
DB	1133	CAGATTGAAGAACTGCCCCCTCATCTGCCATCAGAAGTCGTTGATCGCAAGGCTCGT	1192	
QY	720	GTGGTACCGAGAGGGTACGAGCAGCCGTCGGAGGAAGATCTCAAAGAGATTACACAGAC	779	
DB	1193	GTGGTACCGAAGGCTATGAACAACTTCGAGGAGAGACTGAAGAGGGTTACACAGTC	1252	
QY	780	ATGCGAGTTAGAAAGAGAGAGGAGGAGAACTGCATCCCTTCGTCAGATCACAGA	839	
DB	1253	-----GGACGAGGACGACGAGACTCGGATATGCCGTTCCGTCAGATTACCGA	1300	
QY	840	GATGACGATCTTAAACAGTCGAGCTTATTGTAGAAATTCGAAAGGACTACCGGGATTCTC	899	
DB	1301	GATGACGATCTTCAACAGTCGAGCTCATCTGAGAAATTCGCTTAAGGGCCCTCCCGGCTTCG	1360	
QY	900	CAAGATATCTCAGTCCGATCAAAATTTACATATTTAAAGCGCTCATCAAGCGAAAGTGATGAT	959	
DB	1361	CAAGATATCTCGCAGTCGGACCAAGATCACTTTATTAAAGCGTGTCTCAAGTCAGGTGATGAT	1420	
QY	960	GCTCGAGTGGCGGACGGTACGACGCGGGCAGCGACAGCGTGTCTTCCGGAACAAACCA	1019	

Db 1421 GCTCGAGTGGCTCGCGGTATGACGCGGCACACGACGAGTACTGTTTCGGGAACAACA 1480
Qy 1020 GCGGTACACGCGGCAAACTACCGCAAGCGGGCATGTCCTACGTCATCGAGGACCTGCT 1079
Db 1481 GCGGTACACTCGCGCAAACTACCGCAAGCGAGCATGGCGTACGTCATCGAGGACCTGCT 1540
Qy 1080 GCATCTCTGTCGCTGTATGTCATCTCCATGAGCATGACATGTCACATGTCACATGTCAC 1139
Db 1541 GCATCTCTGTCGCTGTATGTCATCTCCATGATGATGATGATGATGATGATGATGATGAT 1600
Qy 1140 CCGCATCTGTTATATCTCAGACCGCGCGCGCTCGAGCAACCCCTTTTATGTCGAGAAAT 1199
Db 1601 AGCCATCTGTCATCTCTCAGACCGCGCGCGCTCGAGCAACCCCTTTTATGTCGAGAAAT 1660
Qy 1200 CCAGAGATACCTCTGAGACCGCTCGCGGTATGTCATCTTAAATGACGACGCGCTCGCC 1259
Db 1661 CCAGAGATATTAACCTGAAACACGCTACGCGGTGATCATCTCTGAAACCGAGACGCGCTCGCC 1720
Qy 1260 TCGCTCGCGCGCTGTTTCGGCAAGATCTCGCGGTGTCGAGCAACTGCGCACGCTCGG 1319
Db 1721 CCGCGCGCGCTGATCTTCGGCGAGATCTCGCGCATATGCGGAGATCTGCGGAGATCTCGG 1780
Qy 1320 CACGAGAACTCCAACTGTCATCTCGCTGAGCTGAAAGACAGGAAATCTTCCGCCATT 1379
Db 1781 CATGAGAACTCCAACTGTCATCTCTCAAGCTGAGAGATCTGCGGAGATCTCGGAGATCT 1840
Qy 1380 CCTCGAGGAGATCTGGAGCTGGCGCAAGTGTGCGAGCG 1419
Db 1841 CCTCGAGGAGATCTGGAGCTGGCGCAAGTGTGCGAGCG 1880

RESULT 9
US-09-564-418-4
; Sequence 4, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURES:
; NAME/KEY: misc
; LOCATION: (2522)..(2522)
; OTHER INFORMATION: n=a, c, g, or t
US-09-564-418-4
Query Match 39.7%; Score 660.4; DB 4; Length 2745;
Best Local Similarity 80.7%; Pred. No. 2.9e-181;
Matches 807; Conservative 0; Mismatches 156; Indels 27; Gaps 2;
Qy 435 TGTATCGACCGGTATGAGCCGAGTGGCTGCTCCAGAGTCCACGTGCAAGAACAAAG 494
Db 893 TCTTGGCGTGGGATGAGCCGAGTGGCTGGTGGTGGGAGAACAGTGTGCAATGAAACG 952
Qy 495 AAGAGAAAGGAGACACAGAGAAAGAAAGAAAGTCCAGTCTAGTACGACGAGTGA 554
Db 953 GAAAGAGAAAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1012
Qy 555 CGATCATGCTCCCATATGCAATGTGACCTTCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 612
Db 1013 CGATCATGCTCCCATATGCAATGTGACCTTCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 1072

Qy 613 -----CA CGAAGTGGTCCGAGGTTCTTAACGAGAGAGCTTAATGGACAGAA 659
Db 1073 GGAATGTGTGAGCAGCAGAGTGGTCCACGATTTCTGAATGAGAAGCTTAATGGACAGAA 1132
Qy 660 CAGACTGAAGAAATGTGACGCGCTGTTCGGGAAACGAGAGTCCCTGATCGCGAGGCTGCT 719
Db 1133 CAGATTGAAGAAACGTCGCCCTCACTGCCCAATCAGAAAGTGGTGAATCGCAAGGCTGCT 1192
Qy 720 GTGGTACAGAGGAGTACGAGCAGCGCTCGAGGAGATCTCAAGAGAGTTCACAGAC 779
Db 1193 GTGGTACAGAGGAGTATGAAACACCTTCGAGGAGACCTGAGAGAGGTTACAGATC 1252
Qy 780 ATGCGAGTTAGAAAGAGAGAGAGGAGGAAACCTGACATGCCCTTTCCGTGAGATCAGAG 839
Db 1253 -----GGACGAGGAGCAGAGAGACTCGGATATGCCGTTCCGTGAGATACCGA 1300
Qy 840 GATGACGATCTTAAACAGTGCAGCTTATTTAGAAATTCGCAAGGAGCTACCCGGATTC 899
Db 1301 GATGACGATCTTCAAGTGCAGCTCATGCTAGAAATTCGTAAGGGCTCTCCCGGCTTC 1360
Qy 900 CAGAGATATCTCAGTCCGATCAAAATTAATTTAAAGGCTCATCAAGCGAAGTGTATGAT 959
Db 1361 CAGATCTCGCAGTCCGACCATGATCACGTTATTTAAAGGCGTCTCAAGTGAAGTGTATG 1420
Qy 960 GCTCGAGTGGCGCGACGCTACGACGCGCGCAGCAGCAGCGTGTCTGTTCCGAAACAACA 1019
Db 1421 GCTCGAGTGGCTCGCGGTATGACGCGGCGCACCAGCAGCGTACTGTTCCGAAACAACA 1480
Qy 1020 GCGGTACACGCGGCAAACTACCGCAAGCGGGCATGTCCTACGTCATCGAGACCTGCT 1079
Db 1481 GCGGTACACTCGCGCAAACTACCGCAAGCGAGCATGGCGTACGTCATCGAGGACCTGCT 1540
Qy 1080 GCATCTCTGTCGCTGTATGTCATCTCCATGAGCATGCAATGTCATCGCTGCTCAC 1139
Db 1541 GCATCTCTGTCGCTGTATGTCATCTCCATGATGATGATGATGATGATGATGATGATGAT 1600
Qy 1140 CGCCATCGTTATATTTCTCAGACCGCGCGCGCTCGAGCAACCCCTTTTATGTCGAGAAAT 1199
Db 1601 AGCCATGTGCTCTCTCAGACCGCGCGCGCTGAGCAACCCCTGTTGTCGAGGAGAT 1660
Qy 1200 CCAGAGATACCTTAAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCAGCGCTCGCC 1259
Db 1661 CCAGAGATATTAACCTGAAACACGCTACGCGGTGATCATCTCTGAAACAGACGCGCTCGCC 1720
Qy 1260 TCGCTCGCGCTGCTGTTTCGGCAAGATCTCGCGGTGTCGAGGAGTCCGCGACGCTCGG 1319
Db 1721 CCGCGCGCGCTGATCTTCGGCGAGATCTTCGGGATGATGATGATGATGATGATGATGATG 1780
Qy 1320 CAGCAGAACTCCAACTGTCATCTCGCTGAGCTGAAAGACAGGAAATCTTCCGCCATT 1379
Db 1781 CATGAGAACTCCAACTGTCATCTCTCAAGCTGAGAGATCTGCGGAGATCTCGGAGATCT 1840
Qy 1380 CCTCGAGGAGATCTGGAGCTGGCGCAAGTGTGCGAGCG 1419
Db 1841 CCTCGAGGAGATCTGGAGCTGGCGCAAGTGTGCGAGCG 1880

RESULT 10
US-08-653-648A-10/c
; Sequence 10, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9

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; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent version 3.0
; SEQ ID NO 10
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (224)..(224)
; OTHER INFORMATION: 1
US-08-653-648A-10

Query Match 39.6%; Score 657.6; DB 3; Length 2463;
Best Local Similarity 80.4%; Pred. No. 1.8e-180;
Matches 806; Conservative 0; Mismatches 169; Indels 27; Gaps 2;

QY 435 TGTATCGACGGTATGAGCCCGAGTGGTGTGCTCCAGAGTCCAGTGCACAGAAACAAAG 494
Db 1852 TCTTCGGTGGCATGAGCCCGAGTGGTGTGCGGAGAACCAAGTGTGCAATGAACG 1793
QY 495 AAGAGAAAGGAAGCACAGAGAGAGAAACAACTGCCAGTACAGACAGACAGTGA 554
Db 1792 GAAAGAGAAAGGCGCAGAGAGAGAGAAATTTGCCCGTACAGACAGACAGTAGA 1733
QY 555 GCATCATATGCTGCTCAATATGCAATGACCTCCGCCCCCAGAGGGGGCAAGATT-- 612
Db 1732 CGATCACATGCTCCCATCATGCAATGACCTCCGCCCCCAGAGGGCGGTAGAAATCT 1673
QY 613 -----CACGAAGTGGTCCCGAGGTTCTTAACGGAGAGCTTAATGGAGCAGAA 659
Db 1672 GGAATGTGTGACAGCAGAGTGTGTCACGATTCTCTGAATGAGAAGCTAATGGAACAA 1613
QY 660 CAGACTGAAGATGTGACGCCCTGTGCGGAGAACAGAGTCCCTGATCGCGAGCTGCT 719
Db 1612 CAGATTGAAGAACGTGCCCTCTCACTGCCAATCAGAAAGTGGTTGATCGCAAGGCTCGT 1553
QY 720 GTGGTACAGAGAGGGGTACGACGCGTCCGAGAGAGATCTCAAGAGAGTTACACAGAC 779
Db 1552 GTGGTACAGAGAGGGGTATGAACACCTTCCGAGAGAGCTGAAGAGGGTTACACATC 1493
QY 780 ATGGCAGTTAGAGAGAGAGAGAGAGAACTGACATGCCCTTCCGTCAGATCACAGA 839
Db 1492 -----GGACGAGGACGACGAGACTCGGATATGCCGTTCCGTCAGATTACCGA 1445
QY 840 GATGACGATCTTAAACAGTCCAGCTTATTTAGAAATTCGCAAGGAGCTACCGGATTCTC 899
Db 1444 GATGACGATCTTCAACAGTCCAGCTTATTTAGAAATTCGCAAGGAGCTTCCCGGGCTTCG 1385
QY 900 CAAGATATCTCAGTCCGATCAATTAATTAATTAAGGGCTCATCAAGCGAAGTGTATGAT 959
Db 1384 CAGATCTCGAGTCCGACAGATCACTGTTATTAAGGGCTCTCAAGTGAAGTGTATGAT 1325
QY 960 GTTCCGAGTGGCGCAGCGTACGACGCGGAGAGAGAGTGTGCTGTTGCGGAAACACCA 1019
Db 1324 GCTCCGAGTGGCTCGCGGTATGACGCGGCCACCGACAGCTACTGTTTCGCGAACAACCA 1265
QY 1020 GGGGTACACGCGGACAACTACCGAAGGGGGCATGCTTACGTCATCGAGGACTGCT 1079
Db 1264 GCGGTACACTCGGACAACTACCGAAGGGGAGGAGGAGTGGGTAGCTCATCGAGGACTGCT 1205
QY 1080 GCATTTCTGCGGTGATGTACTTCCATGAGCATGGAACAATGTGCACTACGCGCTGCTCAC 1139
Db 1204 GCATTTCTGCGGTGATGTACTTCCATGATGATGATGATGATGATGATGATGATGATGAT 1145
QY 1140 CGCCATGTTATTTCTCAGACCGCGGAGCGCTTCGAGCAACCCCTTTTAGTGGAGGAAT 1199
Db 1144 AGCCATTGTCATTTCTCAGACCGCGGCTTTGAGCAACCCCTTTGTTGGTGGAGACAT 1085

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QY 1200 CCAGAGATACTACTTGAAGACGCTGCGGTTTACATTTTAAATCAGACAGCGCGTCGCC 1259
Db 1084 CCAGAGATATTACTTGAACACGCTACGCTGCTGATCATCTCTGAACCAAGACAGCGCGTCGCC 1025
QY 1260 TCGCTGCGCGCTGCTGTTCCGGCAAGATCTCGCGCTGCTGAGCGAACTGCGCACGCTCGG 1319
Db 1024 CCGCGCGCGCTCATCTTCCGGCAGATCTTGGGCATCTGACGAGATCCGCAACGCTGGG 965
QY 1320 CACGAGAACTCCAAACATGTGATCTGCTGAGCTGAAGACAGGAACTTCCGCCATT 1379
Db 964 CATGCAAGAACTCCAAACATGTGATCTTCCCTCAAGCTGAAGAACAGGAAGCTGCCGCCGT 905
QY 1380 CTTCCAGGAGATCTGGAGCTGGCGCGAAGTGTGACGAGCAA 1421
Db 904 CTTCCAGGAGATCTGGAGCTGGCGCGAGCTGGCGGCAACGGA 863

RESULT 11
US-08-891-298-2
; Sequence 2, Application US/08891298
; Patent No. 630488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; APPLICANT: Suhr, Steven T.
; TITLE OF INVENTION: Modified Lepidopteran Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 185..2002
; OTHER INFORMATION:
; US-08-891-298-2

Query Match 39.2%; Score 652.2; DB 3; Length 2711;
Best Local Similarity 77.7%; Pred. No. 7e-179;
Matches 815; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

QY 405 GAGTAGTAAAGGTCAGACAGATTTGACTGTATCGACGCGTATGAGCGCGAGTGGGT 464

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Db      955 GAAATGTCAGAGTGTGATTAAGAAATGCTAGCGGTAGGAATGAGGCTGTAATGTGT 1014
Qy      465 COTCCAGAGTCCAGTCAAGAAACAAAGAGAGAAAGGAGACACAGAGAGAAAGA 524
Db      1015 CATACAGAGCCAGTAAATAAAGACAGGCAAGAAAGAAAGAAAGAAAGAAATA-- 1072
Qy      525 CAAATCGCCAGTCAGTACGACACAGTGGACCATCATATGCTGCTGCATATCAATGTGA 584
Db      1073 -TTATTACCTGTGTAGTACACACAGTCAAGACCATATGCCCGATCATCATGTGA 1131
Qy      585 CCTCCGCCCCAGAGGCGGCAAGATTCAAGAGTGTGCTCCGAGGTCTTCAACGAGAA 644
Db      1132 TCCACTTCGCCGAGCGCCAGGATTCACGAGTGTGCTCCGAGGTATCTTTCCGAGAA 1191
Qy      645 GCTAATGAGAGACAGACTGAAGATGTGACGCGCTGTGCGGGAACAGAGTCCCT 704
Db      1192 GCTGATGAGACAGACAGGACAGAAACATACCACTTGTGCGGCAATCGAAGTCTCT 1251
Qy      705 GATCGGAGCTCGTGTGTACAGGAGGCTACGAGCAGCGCTCGAGGAAAGATCTCAA 764
Db      1252 GATCGGAGCTCGTGTGTACAGGAGGATATGAGCAGCGCTCGAGGAGATCTCAA 1311
Qy      765 GAGAGTTACACAGATGCGAGTTAGAAAGAGAGAGAGAGAACTGACATGCCCTT 824
Db      1312 AAGAGTTAAGCAGACTTGGCAGT---CGGATGAAGAGGACGAGGATCGATCTACCTT 1368
Qy      825 CCGTCAGATCACAGAGATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAGG 884
Db      1369 CCGCCAGATCACGAGATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAGG 1428
Qy      885 ACTACCGGATCTCAAGATCTCAGTCCGATCAAAATTAATTAAGGCGTCATC 944
Db      1429 TCTACCGGCTTTTCAAGATATCAAGTCTGATCAAAATTAATTAAGGCGTCATC 1488
Qy      945 AAGCGAAGTGTATGATGCTGCGAGTGGCGGACGCTGACGAGCGCGGACGAGCGTGT 1004
Db      1489 CAGCGAGTGTATGATGCTGCGGTTGGGAGGCGATACGAGCGCGCTCCGACAGCGTGT 1548
Qy      1005 GTTCGCGAAACACAGCGGTACAGCGCGGACAACTACCGAAGCGCGGATGTCACGT 1064
Db      1549 GTTCGCGAAACACAGCGGTACAGCGCGGACAACTACCGAAGCGCGGATGTCACGT 1608
Qy      1065 CATCGAGGACCTGCTGCACTTCTGCTGCTGTATGCTTCTCATGAGTGGACAAATGCA 1124
Db      1609 CATCGAAGACCTCTTACACTTCTGCGGTCATGTTTCTCATGAGTGGACAAATGCA 1568
Qy      1125 CTACGCGTCTCACCGCCATCGTTATTTCTCAGACCGGCGGCGCTCGAGCAACCCCT 1184
Db      1669 CTTTGCAGTCTCACGCGCATCGTTATTTCTCAGATCGGCGCGGCTCGAGCAGCGTC 1728
Qy      1185 TTTAGTGGAGAAATCCAGAGATACCTACTTGAAGACGCTCGGCTTTTACATTTTAATCA 1244
Db      1729 GCTGTTAGAGAGATCCAGAGATACCTACTTGAACACGCTTTCGGAATTTACATCAACCA 1788
Qy      1245 GCACAGCGCTCGCTGCTGCGCGCTGCTGTTGCGCAAGATCTCGGCGTCTGACGGA 1304
Db      1789 GAACAGCGCTGCTGCGCGCTGCTGTTGCGCAAGATCTCGGCGGATCTGAGCGTGTGACCGA 1848
Qy      1305 ACTCGCAGCTCGGCGACGAGAACTCAACATGTGATCTCGCTGAAGCTGAAGAACAG 1364
Db      1849 GCTACGCAAGCTCGGCGACGAGAACTCAACATGTGATCTCGCTGAAGCTGAAGAACAG 1908
Qy      1365 GAAATTCGCGCATTCCTCGAGGAGATCTGCGGAGTGGCGGAGTTCGACGAGAGCT 1424
Db      1909 GAAGCTGCGCGCTTCTCGAGGAGATCTGCGGAGTGGCGGAGTGGCGGACGAGCTCC 1968
Qy      1425 TCGCCCCCGGACCATGTGACCTTGGGG 1453
Db      1969 CACGGTGTGCGCGCCACCAACCCGGTGG 1997

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; Sequence 9, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
; US-08-653-648A-9

Query Match      39.2%; Score 650.8; DB 3; Length 1934;
Best Local Similarity 80.1%; Pred. No. 1.5e-178;
Matches 801; Conservative 0; Mismatches 172; Indels 27; Gaps 2;

Qy      435 TGTATCGACGCGTATGAGCCCGAGTGTGCTGCTCCAGAGTCCAGTGCAGTCAAGAAAG 494
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Qy      495 AAGAGAAAGGAGGACGACAGAGAGAAAGAAACAAATTCGCCCGTCAAGACGAGTAGA 554
Db      1142 GAAAGAGAAAGGCGCAGAGGAGAAAGAAACAAATTCGCCCGTCAAGACGAGTAGA 1083
Qy      555 CGATCATATGCTGCCATATGCAATGTCACCTCCGCCCGCCAGAGCGGCAAGGATT-- 612
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Qy      720 GTGGTACGAGGAGGCTGACGAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGAC 779
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Db      842 -----GGACGAGGACGACCAAGACTCGGATATGCCGTTCCTGATGATACCGA 795
Qy      840 GATGACGATCTTAAAGTGTGAGCTTATGTAAGTTCGCAAGGAGTCCCGGATTCCTC 899
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Db      734 CAAGATCTCGAGTCCGACCGATCACTGTTTAAAGGCGTCTCAAGTGAAGTATGAT 675
Qy      960 GCTCGGAGTGGCGGACGAGTACGACGCGGACGAGCAGCGTCTGTTTCGCAACAAACCA 1019
Db      674 GCTCCGAGTGGCTGGCGGATGACGCGGCGCAACGACAGCGTACTGTTTCGCAACAAACCA 615
Qy      1020 GCGGTACACGCGGACAACTACCGAAGGCGGAGTGTCTCATCGTCAATCAGGACCTGCT 1079
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Db 242 CTTGAGCTAACCCCTGTTGGTGGAGGAGATCCAGAGATATTACCTGAACACGCTGGGGTG 183
Qy 1231 TACATTTTAAATCAGCACAGCGGTGCGCTCGCTGCGCCGTGCTGTTGCGCAAGATCCTC 1290
Db 182 TACATCCTGAACCAAGAACAGTCGGTGGCGGTGCTGCCCTGTCACTAGCGCTAAGATCCTC 123
Qy 1291 GCGGTGCTGACGGAACCTGCGCACGCTGGGCACGAGAACTCCAACATGTGCATCTCGCTG 1350
Db 122 GGCATCCTGACGGAGCTCGGACCCCTGGGCATGCAGAACTCCAAATGTGCATCTCACTC 63
Qy 1351 AAGCTGAAGAACAGGAAACTTCCGCCATTCTCGAGGAGATCTGGGACGTGGCCGA 1406
Db 62 AAGCTGAAGAACAGGAACTGCGGCCGTTCTTCGAGGATATCTGGGACGTCTCTCGA 7

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Job time : 292.825 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:19:52 ; Search time 999.495 Seconds
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Title: US-10-087-167-104_COPY_2007_3668
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1662	100.0	3972	16	Sequence 104, App
2	1612.8	97.0	1767	16	Sequence 122, App
3	1552.2	93.4	1800	16	Sequence 126, App
4	1441.6	86.7	1776	16	Sequence 118, App
5	1431.8	86.1	1863	16	Sequence 136, App
6	1426.6	85.8	1848	16	Sequence 134, App
7	1425	85.7	1428	16	Sequence 128, App
8	1424	85.7	1767	16	Sequence 120, App
9	1422	85.6	1809	16	Sequence 142, App
10	1314.2	79.1	1782	16	Sequence 124, App
11	1216.6	73.2	1518	16	Sequence 93, App

12	1167.4	70.2	1500	16	US-10-087-167-69	Sequence 69, Appl
13	1166	70.2	1800	16	US-10-087-167-147	Sequence 147, Appl
14	1109.8	66.8	1533	16	US-10-087-167-79	Sequence 79, Appl
15	996.2	59.9	1509	16	US-10-087-167-65	Sequence 65, Appl
16	978.6	58.9	1500	16	US-10-087-167-67	Sequence 67, Appl
17	976.6	58.8	1500	16	US-10-087-167-67	Sequence 67, Appl
18	976.6	58.8	2840	15	US-10-083-842A-6	Sequence 6, Appl
19	954.6	57.4	1551	16	US-10-087-167-1	Sequence 1, Appl
20	954.6	57.4	1551	16	US-10-087-167-71	Sequence 71, Appl
21	951.8	57.3	1464	16	US-10-087-167-89	Sequence 89, Appl
22	899.4	53.5	1524	16	US-10-087-167-83	Sequence 83, Appl
23	871.8	52.5	1515	16	US-10-087-167-77	Sequence 77, Appl
24	831.6	50.0	838	16	US-10-087-167-75	Sequence 75, Appl
25	799.8	48.1	1506	16	US-10-087-167-7	Sequence 7, Appl
26	760.2	45.7	1503	16	US-10-087-167-63	Sequence 63, Appl
27	734.2	44.2	1542	16	US-10-087-167-91	Sequence 91, Appl
28	715	43.0	1491	16	US-10-087-167-73	Sequence 73, Appl
29	681	41.0	2126	14	US-10-087-167-85	Sequence 85, Appl
30	681	41.0	2126	15	US-10-292-356-1	Sequence 1, Appl
31	681	41.0	2126	15	US-10-292-324-1	Sequence 1, Appl
32	660.4	39.7	1934	17	US-10-606-060A-2	Sequence 2, Appl
33	660.4	39.7	2464	17	US-10-606-060A-3	Sequence 3, Appl
34	660.4	39.7	2464	17	US-10-606-060A-4	Sequence 4, Appl
35	652.2	39.2	2711	9	US-09-952-559-2	Sequence 2, Appl
36	623.4	37.5	1110	9	US-09-965-703-2	Sequence 2, Appl
37	623.4	37.5	1110	17	US-10-239-134-2	Sequence 2, Appl
38	623.4	37.5	1288	9	US-09-965-703-1	Sequence 1, Appl
39	623.4	37.5	1288	17	US-10-239-134-1	Sequence 1, Appl
40	623.4	37.5	1288	17	US-10-468-199-59	Sequence 59, Appl
41	623.4	37.5	1542	9	US-09-965-703-58	Sequence 58, Appl
42	623.2	37.5	1542	17	US-10-239-134-49	Sequence 49, Appl
43	623.2	37.5	948	17	US-10-606-060A-6	Sequence 6, Appl
44	617	37.1	1054	9	US-09-965-703-3	Sequence 3, Appl
45	617	37.1	1054	17	US-10-239-134-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-087-167-104
Sequence 104, Application US/10087167
Publication No. US20030154509A1
GENERAL INFORMATION:
APPLICANT: Pascal, Erica
APPLICANT: Valentine, Scott
APPLICANT: Brown, Jeffrey
APPLICANT: Cockrell, Adam
APPLICANT: Johnson, Brian
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
FILE REFERENCE: 50018A
CURRENT APPLICATION NUMBER: US/10/087,167
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/242,969
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 3972
TYPE: DNA
ORGANISM: synthetic construct
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(3972)
OTHER INFORMATION: GAL4-Manduca ECR-VP16 fragment in pCGS202
NAME/KEY: CDS
LOCATION: (2007)..(3668)
OTHER INFORMATION: GAL4-Manduca ECR-VP16 chimera
US-10-087-167-104

Query Match 100.0%; Score 1662; DB 16; Length 3972;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGCTACTGCTTCTATCGAAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG	60
Db	2007	ATGAAGCTACTGCTTCTATCGAAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG	2066
Qy	61	TGCTCCAAAGAAAAACCGAAGTGCGCCAAAGTGTCGAAAGAAACAACCTGGGAGTGTCCTAC	120
Db	2067	TGCTCCAAAGAAAAACCGAAGTGCGCCAAAGTGTCGAAAGAAACAACCTGGGAGTGTCCTAC	2126
Qy	121	TCCTCCAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCAAGG	180
Db	2127	TCTCCCAAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCAAGG	2186
Qy	181	CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAAGACCTTGACATGATTT	240
Db	2187	CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAAGACCTTGACATGATTT	2246
Qy	241	TTGAAATTGGATTTCTTACAGGATATTAAGACATTTGTTAACAGGATATTTGTACAAAGAT	300
Db	2247	TTGAAATTGGATTTCTTACAGGATATTAAGACATTTGTTAACAGGATATTTGTACAAAGAT	2306
Qy	301	AATGTGAATAAGATGCGCTCACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTCTTA	360
Db	2307	AATGTGAATAAGATGCGCTCACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTCTTA	2366
Qy	361	ACATTGAGACAGCATAGAATAAGTGCACATCATCTCGAAGAGAGTAGTAAACAAGGT	420
Db	2367	ACATTGAGACAGCATAGAATAAGTGCACATCATCTCGAAGAGAGTAGTAAACAAGGT	2426
Qy	421	CAAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCGTCCGACAGAGTCCACG	480
Db	2427	CAAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCGTCCGACAGAGTCCACG	2486
Qy	481	TGCAAGAACAAAAGAGAAAAAGAAAGACACAGAGAGAAAAAGACAAACTGCCAGTCAGT	540
Db	2487	TGCAAGAACAAAAGAGAAAAAGAAAGACACAGAGAGAAAAAGACAAACTGCCAGTCAGT	2546
Qy	541	ACGACGACAGTGGACGATCATATGCTTGCCATAATGCAATGTGACCTCCGCCCCCAGAG	600
Db	2547	ACGACGACAGTGGACGATCATATGCTTGCCATAATGCAATGTGACCTCCGCCCCCAGAG	2606
Qy	601	CGCGCAGGATTCACGAGTGGTCCCGAGGTTCCCTAACGGAGAAGCTAATGGAGCAGAAC	660
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Qy	661	AGACTGAAGAATGTGACGCCCTGTGCGCGAACACAGAAGTCCCTGATCGCGAGGCTCGTG	720
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Qy	721	TGGTACAGGAGGGGTACGAGCACCGTCGAGGAGAAGATCTCAAGAGAGTTACACAGACA	780
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Qy	781	TGGCAGTTTAGAAGAAGAAAGAGAGAGGAACTCACATGCCCTTCCCTCGAGATCACAGAG	840
Db	2787	TGGCAGTTTAGAAGAAGAAAGAGAGAGGAACTCACATGCCCTTCCCTCGAGATCACAGAG	2846
Qy	841	ATGACGATCTTAAACAGTGCAGCTATTATTGTAGAATTCGCAAAAGGACTACCGGATTTCTCC	900
Db	2847	ATGACGATCTTAAACAGTGCAGCTATTATTGTAGAATTCGCAAAAGGACTACCGGATTTCTCC	2906
Qy	901	AAGATATCTCAGTCCGATCAAAATTACATTTAAGCGGTCATCAAGCGAAGTGTATGATG	960
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Qy	961	CTGCGAGTGGCGACGCTACGACGCGCGACGACACGCTGCTGTTTCGGGAAACAAACGAG	1020
Db	2967	CTGCGAGTGGCGACGCTACGACGCGCGACGACACGCTGCTGTTTCGGGAAACAAACGAG	3026
Qy	1021	CGGTACACGCGGCAACACTACCGCAAGCGGGGCAATGCTTACGTCTATCGAGGACCTGCTG	1080
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Qy	1081	CAC	TTCTGTCGGTGATGTACTCCATGAGCATGGACAATGTGCACTACGGCTGCTCACC	1144
Db	3087	CAC	TTCTGTCGGTGATGTACTCCATGAGCATGGACAATGTGCACTACGGCTGCTCACC	3146
Qy	1141	GCC	ATCGTTATATTTCTCAGACCGGCAGGCGCTCGAGCAACCCCTTTTAGTGGAGGAAATC	1200
Db	3147	GCC	ATCGTTATATTTCTCAGACCGGCAGGCGCTCGAGCAACCCCTTTTAGTGGAGGAAATC	3206
Qy	1201	CAG	AGATACTACTTTGAAGACGCTCGCGGTTTACATTTTAAATCAGCAACGGCGTTCGCCT	1260
Db	3207	CAG	AGATACTACTTTGAAGACGCTCGCGGTTTACATTTTAAATCAGCAACGGCGTTCGCCT	3266
Qy	1261	CGT	GCGCCGCTGCTGTTGGCGAAGATCTCTCGGCGTGCTGACGGAATCTGCACGCTCGGC	1320
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Db	3327	ACC	CAGAACTCCAACTGTCATCTCGCTCAAGCTGAAGAAACAGGAAATCTTCGCGCAATTC	3386
Qy	1381	CTC	GAGGAGATCTGGGACGTGGCGCGAAGTGTGCAACGACGAAGCTTGCCCCCGCACCGAT	1440
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Qy	1501	GC	GTACACGATTTTCGATCTGGACATGTTCTGGGGACGGGGATTTCCCGGGTTCGGGATTT	1560
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Qy	1561	AC	CCCCCAGCACTCCGCCCCCTACGGCGCTCTGGATATGGCCGCACTTCGAGTTTGACGAG	1620
Db	3567	AC	CCCCCAGCACTCCGCCCCCTACGGCGCTCTGGATATGGCCGCACTTCGAGTTTGACGAG	3626
Qy	1621	AT	GTTTACCAGATGCCCTTGGAAATTGACGAGTACGGTGGGTAG	1662
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RESULT 2
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; Sequence 122, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatencIn version 3.1
; SEQ ID NO 122
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)FV
US-10-087-167-122

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Query Match	97.0%;	Score 1612.8;	DB 16;	Length 1767;
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			Indels	18;
			Gaps	1;

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DB |||||
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QY 244 TGCTCCAAAGAAAAACCGAAGTGCAGAGTCTGAAAGAAACAACTGGAGTGTGCTTAC 303
DB |||||
QY 181 CTGAAAGAGCTGGAACAGCTATTTCTTACTGATTTTCTCGAAGAGACCTTCGACATGATT 240
DB |||||
QY 304 CTGAAAGAGCTGGAACAGCTATTTCTATGATTTTCTCGAAGAGACCTTCGACATGATT 363
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QY 241 TTGAAATATGGAATCTTTTACAGGATATAAAGCAATTTTAAACAGGATTTTGTACAAGAT 300
DB |||||
QY 364 TTGAAATATGGAATCTTTTACAGGATATAAAGCAATTTTAAACAGGATTTTGTACAAGAT 423
DB |||||
QY 301 AATGTGAATAAAGATGCGGCTCAGATAGATTGGCTTCAGTGGAGACGATATGCTCTTA 360
DB |||||
QY 424 AATGTGAATAAAGATGCGGCTCAGATAGATTGGCTTCAGTGGAGACGATATGCTCTTA 483
DB |||||
QY 361 ACATTGAGACAGATAGATAGTGCAGATCATCATCGAAGAGAGTAGTAACAAAGGT 420
DB |||||
QY 484 ACATTGAGACAGATAGATAGTGCAGATCATCATCGAAGAGAGTAGTAACAAAGGT 543
DB |||||
QY 421 CAAAGACAGTTGACTGTATCGAGCGGTATGAGCGCGGTGCTGCTCGTCCAGAGTCCAG 480
DB |||||
QY 544 CAAAGACAGTTGACTGTATCGAGCGGTATGAGCGCGGTGCTGCTCGTCCAGAGTCCAG 603
DB |||||
QY 481 TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAGAAACAACTGCCAGTCAGT 540
DB |||||
QY 604 TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAGAAACAACTGCCAGTCAGT 663
DB |||||
QY 541 ACAGACAGAGTGCAGCATATGCTGCTGCATATGCAATGTGACCTCGCGCCCGCAGAG 600
DB |||||
QY 664 ACAGACAGAGTGCAGCATATGCTGCTGCATATGCAATGTGACCTCGCGCCCGCAGAG 723
DB |||||
QY 601 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGGAGAGCTTAATGAGAGAGAAC 660
DB |||||
QY 724 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGGAGAGCTTAATGAGAGAGAAC 783
DB |||||
QY 661 AGACTGAAGATGTGACGGCTGTGCGGAAACAGAGTCCCTGATCGGAGGCTCGTG 720
DB |||||
QY 784 AGACTGAAGATGTGACGGCTGTGCGGAAACAGAGTCCCTGATCGGAGGCTCGTG 843
DB |||||
QY 721 TGGTACAGAGGGGTACGAGCAGCGCTCGGAGAGAGTCTCAAGAGAGTTACACAGACA 780
DB |||||
QY 844 TGGTACAGAGGGGTACGAGCAGCGCTCGGAGAGAGTCTCAAGAGAGTTACACAGACA 903
DB |||||
QY 781 TGTCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCTCCCTTCGCTCAGATCAAGAG 840
DB |||||
QY 904 TGTCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCTCCCTTCGCTCAGATCAAGAG 963
DB |||||
QY 841 ATGACGATCTTAAACAGTGCAGTTATTTGTAAGATTTGCAAGAGGACCTACCGGATTTCTCC 900
DB |||||
QY 964 ATGACGATCTTAAACAGTGCAGTTATTTGTAAGATTTGCAAGAGGACCTACCGGATTTCTCC 1023
DB |||||
QY 901 AAGATATCTCAGTCCGATCAAAATTAATTAAGGCGTCATCAAGCGAAGTGTGATG 960
DB |||||
QY 1024 AAGATATCTCAGTCCGATCAAAATTAATTAAGGCGTCATCAAGCGAAGTGTGATG 1083
DB |||||
QY 961 CTGCGAGTGGCGGACCGGTACGACGCGCGGACGAGCGGTGCTGTTTCGCGAAACAAACCGAG 1020
DB |||||
QY 1084 CTGCGAGTGGCGGACCGGTACGACGCGCGGACGAGCGGTGCTGTTTCGCGAAACAAACCGAG 1143
DB |||||
QY 1021 GCGTACACGCGGACAACTACCGCAAGCGGGGATGCTTCTACGTCATCGAGGACCTGCTG 1080
DB |||||
QY 1144 GCGTACACGCGGACAACTACCGCAAGCGGGGATGCTTCTACGTCATCGGGGACCTGCTG 1203
DB |||||
QY 1081 CACTTCTGTCGCTGATGTACTCCATGAGCATGAGCAATGTGACATGCGGCTGCTCACC 1140
DB |||||

DB 1204 CACTTCTGTCGCTGATGTACTCCATGAGCATGACAAATGTGCATACGCGTGTCTACC 1263
QY |||||
QY 1141 GCGATCGTTATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTGTAGTGGAGAAATC 1200
DB |||||
QY 1264 GCGATCGTTATTTCTCAGACCGCGGCTCGAGCAACCCCTTTTGTAGTGGAGAAATC 1323
DB |||||
QY 1201 CAGAGATACTACTTGAAGACGCTCGGCTTTTACATTTTAAATCAGACAGCGGCTGCGCT 1260
DB |||||
QY 1324 CAGAGATACTACTTGAAGACGCTCGGCTTTTACATTTTAAATCAGTACAGCGCTGCGCT 1383
DB |||||
QY 1261 GCGTGGCGGCTGCTGTTTCGGCAAGATCTCGCGCTGCTGACGGAACTGCGCACTGCGG 1320
DB |||||
QY 1384 GCGTGGCGGCTGCTGTTTCGGCAAGATCTCGCGCTGCTGACGGAACTGCGCACTGCGG 1443
DB |||||
QY 1321 ACGCAGAACTCCAACTGTCATCTCGTGAAGCTGAAGAAACAGGAAACTTCGCGCATTC 1380
DB |||||
QY 1444 ACGCAGAACTCCAACTGTCATCTCGTGAAGCTGAAGAAACAGGAAACTTCGCGCATTC 1503
DB |||||
QY 1381 CTCGAGGAGATCTGCGACGCTGCGGCGAAAGTGTGCGACGACGAAAGCTTGCCTCCCGACCGAT 1440
DB |||||
QY 1504 CTCGAGGAGATCTGCGGAGCT-----GAGCTTTGCGCCCGACCGAT 1545
DB |||||
QY 1441 GTCAGCTGGGGGACGAGCTCCATTAAGACGCGGAGGAGCTGCGCATGCGCGCATGCGGAC 1500
DB |||||
QY 1546 GTCAGCTGGGGGACGAGCTCCATTAAGACGCGGAGGAGCTGCGCATGCGCGCATGCGGAC 1605
DB |||||
QY 1501 GCGCTAGACGATTTGATCTGACATGTTGGGGGAGCGGGATTTCCCGGCTCGGGATTT 1560
DB |||||
QY 1606 GCGCTAGACGATTTGATCTGACATGTTGGGGGAGCGGGATTTCCCGGCTCGGGATTT 1665
DB |||||
QY 1561 ACCCGCCACGACTCCGCGCCCTTACGCGCTCTGATATGCGGACTTCGAGTTTGAGCAG 1620
DB |||||
QY 1666 ACCCGCCACGACTCCGCGCCCTTACGCGCTCTGATATGCGGACTTCGAGTTTGAGCAG 1725
DB |||||
QY 1621 ATGTTTACGATGCTTGGAAATTAAGTACGATGCGTGGGTAG 1662
DB |||||
QY 1726 ATGTTTACGATGCTTGGAAATTAAGTACGATGCGTGGGTAG 1767
DB |||||

RESULT 3

US-10-087-167-126
; Sequence 126, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087, 167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1800)
; OTHER INFORMATION: Ecdysone receptor chimera G(B)MV
US-10-087-167-126

Query Match 93.4%; Score 1552.2; DB 16; Length 1800;

Best Local Similarity 95.9%; Pred. No. 0;

Matches 1609; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAAGTACTGCTCTTCTATCGAAACAGCATGCGATATTTGCGGACTTTAAAGCTCAAG 60

Db 124 ATGAAGTACTGTCTTCTTATCGAACAGCATGCGATATTGTCGAGCTTAAAGAGCTCAAG 183
 Qy 61 TGCTCAAGAAAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCTTAC 120
 Db 184 TGCTCAAGAAAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCTTAC 243
 Qy 121 TCTCCAAAAACCAAGAGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGAATCAAGG 180
 Db 244 TCTCCAAAAACCAAGAGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGAATCAAGG 303
 Qy 181 CTAGAAAGACTGGAACAGACTATTTCTACTGATTTTTCTCGAGAAAGACTTGACATGATT 240
 Db 304 CTAGAAAGACTGGAACAGACTATTTCTACTGATTTTTCTCGAGAAAGACTTGACATGATT 363
 Qy 241 TTGAAAAATGGATTTCTTTACAGATATTAAGCAATTTGTTAAACAGGATTTATTTGTAAGANT 300
 Db 364 TTGAAAAATGGATTTCTTTACAGATATTAAGCAATTTGTTAAACAGGATTTATTTGTAAGANT 423
 Qy 301 AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
 Db 424 AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 483
 Qy 361 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAGGT 420
 Db 484 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAGGT 543
 Qy 421 CAAAGACAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTGTGCCAGAGTCCAGG 480
 Db 544 CAAAGACAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTGTGCCAGAGTCCAGG 603
 Qy 481 TCGAAGAACAAAGAGAGAAAGGAGGACACAGAGAGAAAGACAACTGCCAGTCACT 540
 Db 604 TCGAAGAACAAAGAGAGAAAGGAGGACACAGAGAGAAAGACAACTGCCAGTCACT 563
 Qy 541 ACAGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCAGAG 600
 Db 664 ACAGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCAGAG 723
 Qy 601 GCGGCAAGGATTCAGAAAGTGTGTCGAGGTTCTTAACGGAGAGAGCTAATGAGAGCAGAAC 660
 Db 724 GCGGCAAGGATTCAGAAAGTGTGTCGAGGTTCTTAACGGAGAGAGCTAATGAGAGCAGAAC 783
 Qy 661 AGACTGAAGAAATGTGACGGCTGTGCGGACCAAGTCCCTGATCGCGAGGTCGTG 720
 Db 784 AGACTGAAGAAATGTGACGGCTGTGCGGACCAAGTCCCTGATCGCGAGGTCGTG 843
 Qy 721 TGTGTACAGAGGGGTACAGAGAGCGGTGCGAGGAAAGATCTCAAGAGAGTTACACAGACA 780
 Db 844 TGTGTACAGAGGGGTATGAAACCTTCAGAGGAGAGCTCAAGAGGGGTGACGAGACC 903
 Qy 781 TGCAGGTTAGAAAGAGAGAGAGGAGAACTGACATGCCCTTCGTCAGATCAGAGAG 840
 Db 904 TGCAGGTTAGAAAGAGAGAGAGGAGAACTGACATGCCCTTCGTCAGATCAGAGAG 960
 Qy 841 ATGACAGTCTTAACAGTGGAGCTTATGTAAGATTCGAAAGGAGCTACCGGATTTCTCC 900
 Db 961 ATGACAGTCTTAACAGTGGAGCTTATGTAAGATTCGAAAGGAGCTACCGGATTTCTCC 1020
 Qy 901 AAGATATCTCAGTCCGATCAAAATACATTTAAAGGCGTTCATCAAGCGAAGTGTATG 960
 Db 1021 AAGATCTCGAGTCCGATCAAAATACATTTAAAGGCGTTCATCAAGCGAAGTGTATG 1080
 Qy 961 CTGCGAGTGGCGGAGCGGTACGACGGCGGACCGGACAGCGTGTGTTGCGGAAACACCCAG 1020
 Db 1081 CTGCGAGTGGCGGAGCGGTACGACGGCGGACCGGACAGCGTGTGTTGCGGAAACACCCAG 1140
 Qy 1021 GCGTACAGCGGACCAACTACCGAAGCGGCGATGCTTCACTGATCGAGGACCTGCTG 1080
 Db 1141 GCGTACTCCGCGCAACACTACCGAAGCGGCGATGCTTCACTGATCGAGGATCTCTTG 1200
 Qy 1081 CACTTCTGTCGGTGTATGTAATCTCCATGAGCATGACAAATGTGCACTACGCGCTGCTCACC 1140
 Db 1201 CACTTCTGTCGGTGTATGTAATCTCCATGATGATGATGATGATGATGATGATGATGATG 1260

Qy 1141 GCCATCGTTATATTTCTCAGACCGCGCAGGCTTCAGACAAACCCCTTTTATGTGAGGAAATC 1200
 Db 1261 GCCATGTCTATTTCTCAGACCGCGCCTGGCTCGAGCAACCCCTTATTGTTGGAAGAAATC 1320
 Qy 1201 CAGAGATATTAATTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1260
 Db 1321 CAGCGGTTATTAACCTGAAACACGCTCGGGGTACATCTTTGAACCAAAACAGTGCCTCGCG 1380
 Qy 1261 CGCTGCGCGCTGCTTCGGCAAGATCCTCGCGTGTGAGGAACTTCGCAACGCTCGGC 1320
 Db 1381 CGCTGCGCGCTGCTTCGGCAAGATCCTCGCGTGTGAGGAACTTCGCAACGCTCGGC 1440
 Qy 1321 ACGAGAACTCAACATGTGATCTGCTGAAGTGAAGAAACAGGAAATCTTCGCGCATTC 1380
 Db 1441 ATGAGAACTCAACATGTGATCTGCTGAAGTGAAGAAATCTTCGCGCATTC 1500
 Qy 1381 CTCGAGAGATCTCGGACGCTGCCGAGTGTGACGAGCAAGCTTGCCTCCCGACCGAT 1440
 Db 1501 CTCGAGAGATCTCGGACGCTGCCGAGTGTGACGAGCAAGCTTGCCTCCCGACCGAT 1554
 Qy 1441 GTCAGCTTGGGGAGAGCTCCACTTAGACGCGAGGAGCTGGCGATGGCGATGCCGAC 1500
 Db 1555 GTCAGCTTGGGGAGAGCTCCACTTAGACGCGAGGAGCTGGCGATGGCGATGCCGAC 1614
 Qy 1501 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGACGCGGATTTCCCGGATTT 1560
 Db 1615 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGACGCGGATTTCCCGGATTT 1674
 Qy 1561 ACCCCCCACGACTCCGCCCCCTACCGCGCTCTGGATATGCGGACTTCGAGTTGAGCAG 1620
 Db 1675 ACCCCCCACGACTCCGCCCCCTACCGCGCTCTGGATATGCGGACTTCGAGTTGAGCAG 1734
 Qy 1621 ATGTTTACGATGCTTCGATTTGCAATTCAGCAGTACGTTGGGTAG 1662
 Db 1735 ATGTTTACGATGCTTCGATTTGCAATTCAGCAGTACGTTGGGTAG 1776

RESULT 5

US-10-087-167-136
 ; Sequence 136, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 136
 ; LENGTH: 1863
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (1863)
 ; OTHER INFORMATION: Ecdysone receptor chimera G(M)MD
 US-10-087-167-136

Query Match 86.1%; Score 1431.8; DB 16; Length 1863;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 ATGAAGTACTGTCTTCTTATCGAACAGAGCTGATATTTGCGGACTTAAAGAGCTCAAG 60
 Db 124 ATGAAGTACTGTCTTCTTATCGAACAGAGCTGATATTTGCGGACTTAAAGAGCTCAAG 183

Qy 61 TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGAGTGCCTAC 120
Db 184 TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGGAGTGCCTAC 243
Qy 121 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCAAGG 180
Db 244 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCAAGG 303
Qy 181 CTAGAAAGACTGGAAACAGCTATTCTCTGATATTTTCTCGAAGACCTTGAATGATT 240
Db 304 CTAGAAAGACTGGAAACAGCTATTCTCTGATATTTTCTCGAAGACCTTGAATGATT 363
Qy 241 TTGAATAATGGATCTTTACAGGATATAAAGCATTTTAAACAGGATTTTGTACAAGAT 300
Db 364 TTGAATAATGGATCTTTACAGGATATAAAGCATTTTAAACAGGATTTTGTACAAGAT 423
Qy 301 AATGTGAATAAAGATGCGCGTCAAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA 360
Db 424 AATGTGAATAAAGATGCGCGTCAAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA 483
Qy 361 ACATTGAGACAGCATAGAAATAGTCGACATCATCATCGGAAGAGTAGTAAACAAAGGT 420
Db 484 ACATTGAGACAGCATAGAAATAGTCGACATCATCATCGGAAGAGTAGTAAACAAAGGT 543
Qy 421 CAAAGACAGTTGACTGTATCGACCGGTATAGGCGCGAGTGGCTCCACAGATCCACG 480
Db 544 CAAAGACAGTTGACTGTATCGACCGGTATAGGCGCGAGTGGCTCCACAGATCCACG 603
Qy 481 TGCAAGAAACAAAGAAAGAAAGAAAGCAAGACAGAGAGAGAAAGCAAACTGCCAGTCAGT 540
Db 604 TGCAAGAAACAAAGAAAGAAAGAAAGCAAGACAGAGAGAGAAAGCAAACTGCCAGTCAGT 663
Qy 541 ACGACGACAGTGGACATCATATGCTGCTGCATATATGCAATGTGACCTCCGCCGCCACAG 600
Db 664 ACGACGACAGTGGACATCATATGCTGCTGCATATATGCAATGTGACCTCCGCCGCCACAG 723
Qy 601 GCGCAAGATTCACGAAGTGTCCGAGGTTCCTTAACGAGAGAGCTAATGGAGCAGAAC 660
Db 724 GCGCAAGATTCACGAAGTGTCCGAGGTTCCTTAACGAGAGAGCTAATGGAGCAGAAC 783
Qy 661 AGACTGAAGAATGTGACGCGCTGTCCGCGAACACAGAAAGTCCCTGATCGCAGGCTCGTG 720
Db 784 AGACTGAAGAATGTGACGCGCTGTCCGCGAACACAGAAAGTCCCTGATCGCAGGCTCGTG 843
Qy 721 TGGTACCAGAGGGGTACAGACAGCGTCCGAGGAAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAGAGGGGTACAGACAGCGTCCGAGGAAGATCTCAAGAGAGTTACACAGACA 903
Qy 781 TGGCAGTTTGAAGAAGAAAGAGAGAGGAACTGACATGCCCTTCCGTCAAGTACACAGAG 840
Db 904 TGGCAGTTTGAAGAAGAAAGAGAGGAACTGACATGCCCTTCCGTCAAGTACACAGAG 963
Qy 841 ATGACGATCTTAACAGTCAGCTTATTTAGAAATTCGAAAGGGACTACCGGATTTCC 900
Db 964 ATGACGATCTTAACAGTCAGCTTATTTAGAAATTCGAAAGGGACTACCGGATTTCC 1023
Qy 901 AGATATCTCAGTCGATCAAAATTTACATTTAAAGGGCTCATCAAGCGAGTGTATGATG 960
Db 1024 AGATATCTCAGTCGATCAAAATTTACATTTAAAGGGCTCATCAAGCGAGTGTATGATG 1083
Qy 961 CTGCGAGTGGCGGACGGTACACGCGGACGGACAGCGTCTGTTCCGGAACACCCAG 1020
Db 1084 CTGCGAGTGGCGGACGGTACACGCGGACGGACAGCGTCTGTTCCGGAACACCCAG 1143
Qy 1021 GCGTACACGCGGACAACTACCGCAAGCGGCGCATGTCTCACTCATCGAGGACCTGTG 1080
Db 1144 GCGTACACGCGGACAACTACCGCAAGCGGCGCATGTCTCACTCATCGAGGACCTGTG 1203
Qy 1081 CACTTCTGTCGTTGATGTACTCCATGACATGGCAATGTGCACTACGCGTGTCTACC 1140
Db 1204 CACTTCTGTCGTTGATGTACTCCATGACATGGCAATGTGCACTACGCGTGTCTACC 1263

Qy 1141 GCCATGTTATATTTCTCAGACCGGCAGGCTCTGACAAACCCCTTTTAGTGGAGAAATC 1200
Db 1264 GCCATGTTATATTTCTCAGACCGGCAGGCTCTGACAAACCCCTTTTAGTGGAGAAATC 1323
Qy 1201 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCACAGCGCTGCGCT 1260
Db 1324 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCACAGCGCTGCGCT 1383
Qy 1261 CGCTGCGCGTGTCTGTTTCGCAAGATCTCTCGGGGTCTGACGGAACTGCGCACGCTCGGC 1320
Db 1384 CGCTGCGCGTGTCTGTTTCGCAAGATCTCTCGGGGTCTGACGGAACTGCGCACGCTCGGC 1443
Qy 1321 ACGCAGAACTCCAACATGTSCATCTCGCTGAAGCTGAAGAAAGGAAACTTTCGCCCATTC 1380
Db 1444 ACGCAGAACTCCAACATGTSCATCTCGCTGAAGCTGAAGAAAGGAAACTTTCGCCCATTC 1503
Qy 1381 CTGAGAGATCTGGGACGCTGGCGGAGTGTCTGACGAGGCTTGCCTCCCGCCGACCGAT 1440
Db 1504 CTGAGAGATCTGGGACGCTGGCGGAGTGTCTGACGAGGCTTGCCTCCCGCCGACCGG 1563
Qy 1441 GTGAGCTGGG 1451
Db 1564 GCGACCCAGG 1574

RESULT 6

US-10-087-167-134
; Sequence 134, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1848)
; OTHER INFORMATION: Bcdysone receptor chimera G(M)MC
US-10-087-167-134

Query Match 85.8%; Score 1426.6; DB 16; Length 1848;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 34; Indels 6; Gaps 1;

Qy 1 ATGAAGCTACTGTCTTCTATCGAAACAGCATGCGATATTTCCGACTTAAAGCTCAAG 60
Db 124 ATGAAGCTACTGTCTTCTATCGAACAGCATGCGATATTTCCGACTTAAAGCTCAAG 183
Qy 61 TGCTCCAAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACTGGAGTGTGCTAC 120
Db 184 TGCTCCAAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACTGGAGTGTGCTAC 243
Qy 121 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCAAGG 180
Db 244 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCAAGG 303
Qy 181 CTAGAAAGACTGGAAACAGCTATTCTCTGATATTTTCTCGAAGACCTTGAATGATT 240
Db 304 CTAGAAAGACTGGAAACAGCTATTCTCTGATATTTTCTCGAAGACCTTGAATGATT 363


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QY 361 ACATTGACAGCAGTAAATAGTGCAGCATCATCGGAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 361 ACATTGACAGCAGTAAATAGTGCAGCATCATCGGAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 421 CAAGACAGTTGACTGTATCGACGGTATAGGCCGAGTGCCTGCCAGAGTCCACG 480
Db |||||||
QY 421 CAAGACAGTTGACTGTATCGACGGTATAGGCCGAGTGCCTGCCAGAGTCCACG 480
Db |||||||
QY 481 TGCAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db |||||||
QY 481 TGCAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db |||||||
QY 541 ACGACAGAGTGGAGCATATATGCTCGCCATATGCAATGATGACCTCCGCCCCAGAG 600
Db |||||||
QY 541 ACGACAGAGTGGAGCATATATGCTCGCCATATGCAATGATGACCTCCGCCCCAGAG 600
Db |||||||
QY 601 GCGGCAAGGATTACGAAAGTGTCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAGAAC 660
Db |||||||
QY 601 GCGGCAAGGATTACGAAAGTGTCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAGAAC 660
Db |||||||
QY 661 AGACTGAAGATGTGACGCGGTGTCGGGCAACAGAAAGTCCCTGATCGCGAGGTCGTG 720
Db |||||||
QY 661 AGACTGAAGATGTGACGCGGTGTCGGGCAACAGAAAGTCCCTGATCGCGAGGTCGTG 720
Db |||||||
QY 721 TGGTACCAAGGGGTACGAGCAGCGTCCGAGGAGATCTCAAGAGAGTTACACAGACA 780
Db |||||||
QY 721 TGGTACCAAGGGGTACGAGCAGCGTCCGAGGAGATCTCAAGAGAGTTACACAGACA 780
Db |||||||
QY 781 TGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db |||||||
QY 781 TGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db |||||||
QY 841 ATGACGATCTTAAAGTGCAGCTTATGTAGAAATTCGCAAGGAGTACCGGGATTCCTCC 900
Db |||||||
QY 841 ATGACGATCTTAAAGTGCAGCTTATGTAGAAATTCGCAAGGAGTACCGGGATTCCTCC 900
Db |||||||
QY 901 AGATATCTCAGTCCGATCAATTAATATTTAAAGGCGTCAATCAAGGAGAGTATGATG 960
Db |||||||
QY 901 AGATATCTCAGTCCGATCAATTAATATTTAAAGGCGTCAATCAAGGAGAGTATGATG 960
Db |||||||
QY 961 CTGCGAGTGGCGGACGCTACGACGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db |||||||
QY 961 CTGCGAGTGGCGGACGCTACGACGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db |||||||
QY 1021 GCGTACACGCGGACAACTACCGAGGCGGAGTCTTACGTCATCGAGGAGCTGCTG 1080
Db |||||||
QY 1021 GCGTACACGCGGACAACTACCGAGGCGGAGTCTTACGTCATCGAGGAGCTGCTG 1080
Db |||||||
QY 1081 CACTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
Db |||||||
QY 1081 CACTTCTGCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
Db |||||||
QY 1141 GCCATCGTTATATCTCAGACCGGCGCTCGAGCAACCCCTTTTATGTGAGGAGAAATC 1200
Db |||||||
QY 1141 GCCATCGTTATATCTCAGACCGGCGCTCGAGCAACCCCTTTTATGTGAGGAGAAATC 1200
Db |||||||
QY 1201 CAGAGATACCTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGGCGCTCGCT 1260
Db |||||||
QY 1201 CAGAGATACCTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGGCGCTCGCT 1260
Db |||||||
QY 1261 CGCTGCGCGGTGTGTTTGGGCAAGATCTCTCGCGGTGCTGACGGAACTCGCGACGCTCGGC 1320
Db |||||||
QY 1261 CGCTGCGCGGTGTGTTTGGGCAAGATCTCTCGCGGTGCTGACGGAACTCGCGACGCTCGGC 1320
Db |||||||
QY 1321 ACGCAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db |||||||
QY 1321 ACGCAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db |||||||
QY 1381 CTCGAGGAGATCTGGGAGGCTGCGGAGGTCGAGACGAGAGCTT 1425
Db |||||||
QY 1381 CTCGAGGAGATCTGGGAGGCTGCGGAGGTCGAGACGAGAGCTT 1425
Db |||||||
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```
RESULT 8
US-10-087-167-120
; Sequence 120, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)EV
US-10-087-167-120
```

```
Query Match      85.7%; Score 1424; DB 16; Length 1767;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 120; Indels 18; Gaps 1;

QY 1 ATGAAGTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
Db |||||||
QY 124 ATGAAGTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
Db |||||||
QY 61 TGTCTCCAAAAGAAAACCGAAGTGCGCCAGTGTCTGAAGAAACAACTGGGAGTGTGCTAC 120
Db |||||||
QY 184 TGTCTCCAAAAGAAAACCGAAGTGCGCCAGTGTCTGAAGAAACAACTGGGAGTGTGCTAC 243
Db |||||||
QY 121 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACTCTGACAGAAAGTGGAAATCAAG 180
Db |||||||
QY 244 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACTCTGACAGAAAGTGGAAATCAAG 303
Db |||||||
QY 181 CTAGAAAGACTGGAAACAGACTATTTCTACTGATTTTCTCTCGAGAAAGACCTTGACATGAT 240
Db |||||||
QY 304 CTAGAAAGACTGGAAACAGACTATTTCTACTGATTTTCTCTCGAGAAAGACCTTGACATGAT 363
Db |||||||
QY 241 TTGAAAATGGATTTCTTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
Db |||||||
QY 364 TTGAAAATGGATTTCTTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 423
Db |||||||
QY 301 AATGTGAATAAAGATCCGTCACAGATAGATTTGCTTTCAGTGGAGACTGATATGCTCTTA 360
Db |||||||
QY 424 AATGTGAATAAAGATCCGTCACAGATAGATTTGCTTTCAGTGGAGACTGATATGCTCTTA 483
Db |||||||
QY 361 ACATTGAGACAGCATAGAATAAGTGCACATCATCATCGGAAAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 484 ACATTGAGACAGCATAGAATAAGTGCACATCATCATCGGAAAGAGAGTAGTAACAAAGGT 543
Db |||||||
QY 421 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCGAGTGCCTGCCAGAGTCCACG 480
Db |||||||
QY 544 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCGAGTGCCTGCCAGAGTCCACG 603
Db |||||||
QY 481 TGCAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db |||||||
QY 604 TGCAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
Db |||||||
QY 541 ACGACAGAGTGGACGATCATATGCTCGCCATATGCAATGTGACCTCCGCCCCAGAG 600
Db |||||||
QY 664 ACGACAGAGTGGACGATCATATGCTCGCCATATGCAATGTGACCTCCGCCCCAGAG 723
Db |||||||
QY 601 GCGCAAGGATTACGAGAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAGAAC 660
Db |||||||
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Db 724 GCGGCAAGGATTCACGAAGTGTGTCGAGTTCTTAACGGAAGCTAATGAGCAGAAC 783
QY 661 AGACTGAAGAAATGTAGCGCGCTGTGCGGAAACCAAGAGTCCCTCATCGCAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTAGCGCGCTGTGCGGAAACCAAGAGTCCCTCATCGCAGGCTCGTG 843
QY 721 TGGTACCAAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACT 903
QY 781 TGGCAGTTAGAAAGAAAGAGAGGAGGAACTGCATGCTCCCTTCGTCAGATCAAGAG 840
Db 904 TGGCAATCAGCAGATGAAGACGCAAGACTCAGACATGCCATTTCGCCAGATCAAGAA 963
QY 841 ATGACGATCTTAACAGTGAGCTTATTGTAGAAATTCGCAAGGGAGTACCGGATTCCTCC 900
Db 964 ATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCCTCAAGGCTTACCTGTTTCA 1023
QY 901 AGATATCTCAGTCCGATCAAAATTAATTAAGGCGTTCATCAAGCGAGTGATGATG 960
Db 1024 AAGATCTCAACCTGACAGATCAATTAATAAGGCGATGCTCAAGCGAGTGATGATG 1083
QY 961 CTGCGAGTGGCGGACGCTACGACGCGGCGAGCAGCGTGTCTGTTCGCGAACCAACAG 1020
Db 1084 CTGCGAGTGGCGGCGTACGACGCGGTGTGCGATAGGTTCTGTTCGCGAACCAACAG 1143
QY 1021 GCGTACACGCGGACAACTACCGCAAGCGGCGATGCTCTAGTCATACGAGACCTGCTG 1080
Db 1144 GCGTACCTCGGACAACTACCGCAAGCGGCGATGCGCTAGCTCATCAAGACCTGCTG 1203
QY 1081 CACTTCTGCGGTGTATGTACTCCATGAGCATGGCAATGTGCATACCGCGTGTCTACC 1140
Db 1204 CACTTCTGCGGTGTATGTACTCCATGAGCATGGCAATGTGCATACCGCGTGTCTACC 1263
QY 1141 GCGATCGTTATATCTCAGACGCGGCGGCTCGAGCAACCCCTTTTGTGGAGGAAATC 1200
Db 1264 GCGATCGTTATATCTCAGATCGGCGGCGCTAGACGCGCACAGCTAGTAGAGATC 1323
QY 1201 CAGAGATCTACTTGAAGACGCTGCGGTTTACATTTTAAATCAGACAGCGGCTGCT 1260
Db 1324 CAGCGGTATTACCTGAACGCTGCGGTTGTATCATCATGAACGAGCAGCGCTGCGCG 1383
QY 1261 CGTGGCGGCTGTGTTGCGCAAGATCTCGGCGTGTCTACGGAATCTGCGCAGCTCGCG 1320
Db 1384 CGTGGCGGCTCATCTACGGAAGATTTCTGCGGTGCTTACCGAGTTGCGGACGCTGGG 1443
QY 1321 ACGCAGAACTCCAAATGTGATCTCGCTGAAGCTGAAGAACAGGAACTTCGCGCATTC 1380
Db 1444 ATCAGAAATTCGAACATGTGATCTCTGCTGAAGCTCAAGAACAGGAGCTGCGCGCT 1503
QY 1381 CTGAGGAGATCTGGGACGCTGGCGAAGTGTGACGACGAAGCTTCCCGCCCGACCGAT 1440
Db 1504 CTGAGGAGATCTGGGACGT-----GAAGCTTCCCGCCCGACCGAT 1545
QY 1441 GTAGCCTGGGAGACGAGTCTCACTTAGACGCGGAGACGCTGCGGATGCGGATGCGGAC 1500
Db 1546 GTAGCCTGGGAGACGAGTCTCACTTAGACGCGGAGACGCTGCGGATGCGGATGCGGAC 1605
QY 1501 GCGCTAGACATTTGATCTGGACATGTTGGGGGAGGGGATTCGCGGCTCGGATTT 1560
Db 1606 GCGCTAGACATTTGATCTGGACATGTTGGGGGAGGGGATTCGCGGCTCGGATTT 1665
QY 1561 ACCCCCCAGACTCCGCCCCCTACGGGCTCTCGATATGCGGACTTCGAGTTTGAAGCAG 1620
Db 1666 ACCCCCCAGACTCCGCCCCCTACGGGCTCTCGATATGCGGACTTCGAGTTTGAAGCAG 1725
QY 1621 ATGTTTACGATGCTTGAATTTGACGATACGCTGGGTAG 1662
Db 1726 ATGTTTACGATGCTTGAATTTGACGATACGCTGGGTAG 1767

US-10-087-167-142
; Sequence 142, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1809)
; OTHER INFORMATION: Bcdysone receptor chimera VG(M)M
US-10-087-167-142

Query Match 85.6%; Score 1422; DB 16; Length 1809;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGTACTGTCTTCTATCGAACAGCATGCGATTTTCGCGACTTAAAGAGCTCAAGTGC 63
Db 385 AAGTACTGTCTTCTATCGAACAGCATGCGATTTTCGCGACTTAAAGAGCTCAAGTGC 444
QY 64 TCCAAAGAAAAACCGAAGTGGCCAAAGTGTCTGAAAGAACAACTGGGAGTGTGCTACTCT 123
Db 445 TCCAAAGAAAAACCGAAGTGGCCAAAGTGTCTGAAAGAACAACTGGGAGTGTGCTACTCT 504
QY 124 CCCAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGAGTGAATCAAGGCTA 183
Db 505 CCCAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGAGTGAATCAAGGCTA 564
QY 184 GAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAGAGCTTGACATGATTTG 243
Db 565 GAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAGAGCTTGACATGATTTG 624
QY 244 AAAATGGATTCTTTACAGGATATAAAAGCATTTTAAACAGGATTTTGTACAGATAT 303
Db 625 AAAATGGATTCTTTACAGGATATAAAAGCATTTTAAACAGGATTTTGTACAGATAT 684
QY 304 GTGAATAAGATGCCGTACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTCTAAC 363
Db 685 GTGAATAAGATGCCGTACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTCTAAC 744
QY 364 TTGACAGACATAGAAATAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAAGCTCAA 423
Db 745 TTGACAGACATAGAAATAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAAGCTCAA 804
QY 424 AGACAGTTGACTGTATCGACGCTATAGGCCGAGTGGCTCGTCCAGAGTCCAGCTGC 483
Db 805 AGACAGTTGACTGTATCGACGCTATAGGCCGAGTGGCTCGTCCAGAGTCCAGCTGC 864
QY 484 AAGAACAAAGAGAGAAAGAAAGAACGACAGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 543
Db 865 AAGAACAAAGAGAGAAAGAAAGAACGACAGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 924
QY 544 ACGCAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCGCCCGCAGAGGCG 603
Db 925 ACGCAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCGCCCGCAGAGGCG 984
QY 604 GCAAGGATTACGAAAGTGGTCCCGAGGTTCTTAACGGAAGAGCTTAATGAGGAGAAACAG 663

QY 1340 GCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCAATTCCTCGAGAGATCTGGGACG 1399
DB 1196 GCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCAATTCCTCGAGAGATCTGGGACG 1255
QY 1400 TGGCCGAAGTGTTCACACGACGAAGCTTGGCCCCCGGACCGATGTGAGCTGTGGGGACGAGC 1459
DB 1256 TGGCCGAAGTGTTCACACGACGAAGCTTGGCCCCCGGACCGATGTGAGCTGTGGGGACGAGC 1315
QY 1460 TCCACTTAGACGGGACGAGACGTGGCGATGGCGCATGGCGACGCGCTAGACGATTCGATC 1519
DB 1316 TCCACTTAGACGGGACGAGACGTGGCGATGGCGCATGGCGACGCGCTAGACGATTCGATC 1375
QY 1520 TGGACATGTTCGGGACGCGGATTCGCCGGGTTCGGGATTTACCCGCCACGACTCCGCC 1579
DB 1376 TGGACATGTTCGGGACGCGGATTCGCCGGGTTCGGGATTTACCCGCCACGACTCCGCC 1435
QY 1580 CCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTG 1639
DB 1436 CCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTG 1495
QY 1640 GAATTGACGAGTACGGTGGGTAG 1662
DB 1496 GAATTGACGAGTACGGTGGGTAG 1518

RESULT 12

US-10-087-167-69
; Sequence 69, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1500)
; OTHER INFORMATION: Ecdysone Receptor chimera MFV
US-10-087-167-69

Query Match 70.2%; Score 1167.4; DB 16; Length 1500;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 6; Indels 18; Gaps 1;

QY 440 CGACGGGTATGAGGCCGCGAGTCCGTCCTCCAGAGTCCACGTGCGAAGAACAAAGAG 499
DB 296 CGGTGGGATATGAGGCCGCGAGTCCGTCCTCCAGAGTCCACGTGCGAAGAACAAAGAG 355
QY 500 AAAAGGAACACAGAGAGAAAGACAACTGCCAGTCACTAGTACGACGACGAGTGGACGATC 559
DB 356 AAAGGAGACACAGAGAGAAAGACAACTGCCAGTCACTAGTACGACGACGAGTGGACGATC 415
QY 560 ATATGCTCCCAATATGCAATGTGACCTTCGCGCCCGAGAGCGGCGAAGGATTCAGGAG 619
DB 416 ATATGCTCCCAATATGCAATGTGACCTTCGCGCCCGAGAGCGGCGGAGGATTCAGGAG 475
QY 620 TGGTCCCGAGGTTCTTAACGGAGAGACTAATGGACGAGAACAGACTGAAGATGTGACGC 679
DB 476 TGGTCCCGAGGTTCTTAACGGAGAGACTAATGGACGAGAACAGACTGAAGATGTGACGC 535

RESULT 13

US-10-087-167-147
; Sequence 147, Application US/10087167
; Publication No. US20030154509A1

QY 680 CGCTGTCCGCGAACCAAGTCCCTGATCGCGAGGTCGTGTGGTACCAAGAGGGGTACG 739
DB 536 CGCTGTCCGCGAACCAAGTCCCTGATCGCGAGGTCGTGTGGTACCAAGAGGGGTACG 595
QY 740 AGCAGCCGTCCGAGGAGAGATCTCAAGAGTGTACACAGATCGCAGTTTAAAGAGAG 799
DB 596 AGCAGCCGTCCGAGGAGAGATCTCAAGAGTGTACACAGATCGCAGTTTAAAGAGAG 655
QY 800 AACAGAGGAGAACTGACATGCCCTTCGCTCAGATCACAGAGATGACGATCTTAAACAGTGC 859
DB 656 AAGAGAGGAGAACTGACATGCCCTTCGCTCAGATCACAGAGATGACGATCTTAAACAGTGC 715
QY 860 AGCTTATTTAGAAATTCGAAAGGAGTACCGGATTTCTCAAGATATCTCAGTCCGATC 919
DB 716 AGCTTATTTAGAAATTCGAAAGGAGTACCGGATTTCTCAAGATATCTCAGTCCGATC 775
QY 920 AAATTACATTTTAAAGGCGTCAATCAAGCGAAGTGTATGCTGCGAGTGGCGGACGCT 979
DB 776 AAATTACATTTTAAAGGCGTCAATCAAGCGAAGTGTATGCTGCGAGTGGCGGACGCT 835
QY 980 ACAGCCGCGGACGAGCAGCGTGTCTTTCGCGAAACCAAGGCGTACACGCGGACAACT 1039
DB 836 ACAGCCGCGGACGAGCAGCGTGTCTTTCGCGAAACCAAGGCGTACACGCGGACAACT 895
QY 1040 ACCGCAAGCGGCGATGTCTCATCTCATTCAGGACCTGTGCACTTCTGTCGGTGTATGT 1099
DB 896 ACCGCAAGCGGCGATGTCTCATCTCATTCAGGACCTGTGCACTTCTGTCGGTGTATGT 955
QY 1100 ACTCCATGACATGGACATGTGCACTTACGCGGTGTCTACCGCCATCTGTTATATTCACG 1159
DB 956 ACTCCATGACATGGACATGTGCACTTACGCGGTGTCTACCGCCATCTGTTATATTCACG 1015
QY 1160 ACCGCGGCGGCTCGAGCAACCCCTTTTGTAGTGGAGGAAATCCAGAGATCTACTTTGAAGA 1219
DB 1016 ACCGCGGCGGCTCGAGCAACCCCTTTTGTAGTGGAGGAAATCCAGAGATCTACTTTGAAGA 1075
QY 1220 CGCTGCGGGTTTAAATTTAAATCAGACACGCGGTGCGCTCGTGGCGCGTGTGTTCG 1279
DB 1076 CGCTGCGGGTTTAAATTTAAATCAGACACGCGGTGCGCTCGTGGCGCGTGTGTTCG 1135
QY 1280 GCAAGATCCTCGGCGTCTGACGAACTGCGCGCTCGGCGAGAACTCCAGAACTCTTCAACATGT 1339
DB 1136 GCAAGATCCTCGGCGTCTGACGAACTGCGCGCTCGGCGAGAACTCCAGAACTCTTCAACATGT 1195
QY 1340 GCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCAATTCCTCGAGAGATCTGGGACG 1399
DB 1196 GCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCAATTCCTCGAGAGATCTGGGACG 1255
QY 1400 TGGCCGAAGTGTGACACGAGAGTTCGCCCGGCGGATGTGAGCTGTGGGACGAGC 1459
DB 1256 T-----GAAAGCTTGGCGCGGCGGATGTGAGCTGTGGGACGAGC 1297
QY 1460 TCCACTTAGACGGGAGAGCTGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATC 1519
DB 1298 TCCACTTAGACGGGAGAGAGCTGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATC 1357
QY 1520 TGGACATGTTGGGGGACGCGGATTTCCCGGGTCCGGGATTTACCCCGACGACTCCGCGCC 1579
DB 1358 TGGACATGTTGGGGGACGCGGATTTCCCGGGTCCGGGATTTACCCCGACGACTCCGCGCC 1417
QY 1580 CTTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTG 1639
DB 1418 CTTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTG 1477
QY 1640 GAATTGACGAGTACGGTGGGTAG 1662
DB 1478 GAATTGACGAGTACGGTGGGTAG 1500


```

; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1800)
; OTHER INFORMATION: Ecdysone receptor chimera GV(M)M
; US-10-087-167-147

Query Match          70.2%; Score 1166; DB 16; Length 1800;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 1425; Conservative 0; Mismatches 0; Indels 249; Gaps 1;

QY      1  ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTCGCGACTTAAAAAGCTCAAG 60
DB      124 ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTCGCGACTTAAAAAGCTCAAG 183

QY      61  TGTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGGAAGAAACAACTGGGAGTGTGCTTAC 120
DB      184 TGTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGGAAGAAACAACTGGGAGTGTGCTTAC 243

QY      121 TCTCCAAACCAAAAGGTTCTCGCTGACTAGGGACATCTGACAGAAGTGGAAATCAAGG 180
DB      244 TCTCCAAACCAAAAGGTTCTCGCTGACTAGGGACATCTGACAGAAGTGGAAATCAAGG 303

QY      181 CTAGAAAGACTGGAAACAGCTATTCTTACTGATTTTCTCGAAGAACCTTGACATGATT 240
DB      304 CTAGAAAGACTGGAAACAGCTATTCTTACTGATTTTCTCGAAGAACCTTGACATGATT 363

QY      241 TTGAAATGGATTCTTTACGGATATAAAGCATTTGTTAAACAGGATTTTGTACAGAT 300
DB      364 TTGAAATGGATTCTTTACGGATATAAAGCATTTGTTAAACAGGATTTTGTACAGAT 423

QY      301 AATGTGAATAAGATCCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCTTA 360
DB      424 AATGTGAATAAGATCCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCTTA 483

QY      361 ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAAGGT 420
DB      484 ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAAGGT 543

QY      421 CAAAGACAGTTGATGTATGACGCGTATAGAGCCCGAGTGGCTGCTCCAGAGTC----- 476
DB      544 CAAAGACAGTTGATGTATGACGCGTATAGAGCCCGAGTGGCTGCTCCAGAGTCCACG 603

QY      477 ----- 476
DB      604 TGAAGCTTCCCCCCCCGACCGATGTGACGCTGGGGGACGAGCTCCACTTAGACGGCGAG 663

QY      477 ----- 476
DB      664 GACGTGGCGATGGCGATGGCGCGCTAGACGATTTTCGATCTGGACATGTTGGGGGAC 723

QY      477 ----- 476
DB      724 GGGGATTCGGGGTCCGGGATTTACCCCCACGACTCCGCCCCCTACGGCGCTCTGGAT 783

QY      477 ----- 476

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DB      784 ATGCCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGT 843
QY      477 -----CAGCTGCAAGNACAAAAGAGAGAAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
DB      844 GGGAAACAGCTGCAAGAACAAAAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
QY      532 CCAGTCAGTACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGCAATGCAATGCAATGCAATG 591
DB      904 CCAGTCAGTACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGCAATGCAATGCAATG 963
QY      592 CCCCAGAGGCGGCAAGATTACGAAGTGTGTCGAGGTTCTTAACGAGAGAGAGAGAGAGAGAGAGAG 651
DB      964 CCCCAGAGGCGGCAAGATTACGAAGTGTGTCGAGGTTCTTAACGAGAGAGAGAGAGAGAGAGAG 1023
QY      652 GAGCAGACAGACTGAAGATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCG 711
DB      1024 GAGCAGAAACAGACTGAAGATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCG 1083
QY      712 AGGCTCGTGTGTACCCAGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTT 771
DB      1084 AGGCTCGTGTGTACCCAGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTT 1143
QY      772 ACACAGACATGCGCAGTTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
DB      1144 ACACAGACATGCGCAGTTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1203
QY      832 ATCAGAGATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGAGTACCG 891
DB      1204 ATCAGAGATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGAGTACCG 1263
QY      892 GATTTCTCCAGATATCTCAGTCCGATCAAAATTAATTAATAAGGCGTCATCAAGCGAA 951
DB      1264 GATTTCTCCAGATATCTCAGTCCGATCAAAATTAATTAATAAGGCGTCATCAAGCGAA 1323
QY      952 GTGATGATGCTGCGAGTGGCGGACGGTACGACGCGGCGACGAGCAGCGTGTGTTCCGG 1011
DB      1324 GTGATGATGCTGCGAGTGGCGGACGGTACGACGCGGCGACGAGCAGCGTGTGTTCCGG 1383
QY      1012 AACACACAGGCGTACACGCGGACAACTACGCAAGGCGGCGATCTCTACGTCATCGAG 1071
DB      1384 AACACACAGGCGTACACGCGGACAACTACGCAAGGCGGCGATCTCTACGTCATCGAG 1443
QY      1072 GACCTGCTGCACTTCTGTCGGTGTATGATCTCATGAGCATGGACAAATGTGCACTACGCG 1131
DB      1444 GACCTGCTGCACTTCTGTCGGTGTATGATCTCATGAGCATGGACAAATGTGCACTACGCG 1503
QY      1132 CTGCTCACCGCCATCGTTATATTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTG 1191
DB      1504 CTGCTCACCGCCATCGTTATATTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTG 1563
QY      1192 GAGGAAATCCAGAGATATCTTTGAAGAGCGTGGGGTTTACATTTTAATTCAGCACAGC 1251
DB      1564 GAGGAAATCCAGAGATATCTTTGAAGAGCGTGGGGTTTACATTTTAATTCAGCACAGC 1623
QY      1252 GCGTCGCTCGCTGCGCGCTGCTGTTTCGGAAGATCTCTCGGCGTGTGACGGAATCGCGC 1311
DB      1624 GCGTCGCTCGCTGCGCGCTGCTGTTTCGGAAGATCTCTCGGCGTGTGACGGAATCGCGC 1683
QY      1312 AGCGCTCGGCACGACAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAAGAACAGGAAACTTT 1371
DB      1684 AGCGCTCGGCACGACAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAAGAACAGGAAACTTT 1743
QY      1372 CGCGCATTTCTCGAGAGATCTGGGACGTCGGCGGAGTGTGACACGACGAGCTT 1425
DB      1744 CGCGCATTTCTCGAGAGATCTGGGACGTCGGCGGAGTGTGACACGAGCTT 1797

```

RESULT 14
 US-10-087-167-79
 ; Sequence 79, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:

```
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION: Ecdysone Receptor chimera EMV
US-10-087-167-79

Query Match      66.8%; Score 1109.8; DB 16; Length 1533;
Best Local Similarity 92.8%; Pred. No. 1.2e-313; Indels 15; Gaps 1;
Matches 1181; Conservative 0; Mismatches 77;

Qy 405 GAGTAGTAACAAAGGTCAAAGACAGTGTGATCGACCGGTATGAGGCCGCCGAGTGGT 464
Db 261 GAAATGTCAAGATGCGCGTTGAGAAAGTGTAGCGGTGGCATGAGGCCGCGAGTGGT 320
Qy 465 CGTCCAGAGTCCAGTCAGAACAAAGAAAGAGAAAGAAAGAACAGACAGAGAAAGA 524
Db 321 GGTGCCAGAAACGCGAGTGTGCGCAAAAGAAAGAAAGAAAGAACAGACAGAGAAAGA 380
Qy 525 CAAACTGCCAGTCAGTAGCAGACAGTGCAGATCATATGCTGCGCAATATGCAATGTGA 584
Db 381 CAAACTACAGTAGCAGCAACAGACAGTAGACATATATGCCCCCAATCATGCAAGTGA 440
Qy 585 CCCCCTCCGCCCCAGAGCGCGCAAGATT-----CACGAAGTGGTCCCGAG 629
Db 441 TCCACACCCCGGAGCGAGGAGATTCTGGAATGTTTGACGAGCATGAAGTGGTCCCGCG 500
Qy 630 GTTCTTAACGGAGAGCTAATGGACAGAACAGATGGAATGTGACGCCGTGTGGC 689
Db 501 GTTCTCTCGGAGAGAGCTGATGGAGCAAGATCGGCTGAAGAAACATACCCCCCTCACCGC 560
Qy 690 GAACAGAGAGTCCCTGATCGCGAGGCTCGTGTGGTACCAGAGGGGTACGAGCAGCCGTC 749
Db 561 CAAACAGCAGTTCCTGATCGCGAGGCTGTGTGGTACCAGAGGGGTACGAGCAGCCGTC 620
Qy 750 GGAGGAAGATCTCAAGAGAGGTACACAGACATGGCAGTTAGAAAGAAAGAGAGGAGGA 809
Db 621 GGAGGAAGATCTCAAGAGAGGTACACAGACATGGCAGTTAGAAAGAAAGAGAGGAGGA 680
Qy 810 AACTCAGATGCCCTTCCTGATCAGATCAGACAGATGACGATCTTAACAGTGCAGCTTATGT 869
Db 681 AACTCAGATGCCCTTCCTGATCAGATCAGACAGATGACGATCTTAACAGTGCAGCTTATGT 740
Qy 870 AGAATTTCGAAAGGAGCTACCGGGATTTCCAAAGATATCTCAGTCCGATCAAAATTACATT 929
Db 741 AGAATTTCGAAAGGAGCTACCGGGATTTCCAAAGATATCTCAGTCCGATCAAAATTACATT 800
Qy 930 ATTAAGGCGTCATCAAGCGAAGATGATGATGTCGAGTGGCGCGACCGGTACGACCGGC 989
Db 801 ATTAAGGCGTCATCAAGCGAAGTATGATGTCGAGTGGCGCGACCGGTACGACCGGC 860
Qy 990 GACGACAGCGTGTCTTCGCAACACACAGCGGTACAGCGCGCAACTACCGCAAGGC 1049
Db 861 GACGACAGCGTGTCTTCGCAACACACAGCGGTACAGCGCGCAACTACCGCAAGGC 920
Qy 1050 GGGCATGTCTACGTATCGAGGACCTGTGCACTTCTGTGGTGTATGTACTCCATGAG 1109
```

```
Db 921 GGGCATGTCTACGTATCGAGGACCTGTGCACTTCTGTGGTGTATGTACTCCATGAG 980
Qy 1110 CATGGACAATGTGCACTAGCGCTGTCAACGCCATCGTTATATTCTCAGACCGCGCAGG 1169
Db 981 CATGGACAATGTGCACTAGCGCTGTCAACGCCATCGTTATATTCTCAGACCGCGCAGG 1040
Qy 1170 CCTCAGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTCTTGAAGACGCTGGCGGT 1229
Db 1041 CTTGAGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTCTTGAAGACGCTGGCGGT 1100
Qy 1230 TTACATTTTAAATCAGACAGCGCTGCGCTCGCTCGCGCTGCTGTGGGCAAGATCCT 1289
Db 1101 TTACATTTTAAATCAGACAGCGCTGCGCTCGCTCGCGCTGCTGTGGGCAAGATCCT 1160
Qy 1290 CGGCGTGTGACGGAACTGGCAAGCTCGGACGCGTCCGACGAGAACTCCAACATGTGCATCTCGCT 1349
Db 1161 CGGCGTGTGACGGAACTGGCAAGCTCGGACGCGTCCGACGAGAACTCCAACATGTGCATCTCGCT 1220
Qy 1350 GAAGCTGAAGAACAGGAACTTCCGGCATTTCTTCGAGGAGATCTGGGACGCTGGCCGGAAGT 1409
Db 1221 GAAGCTGAAGAACAGGAACTTCCGGCATTTCTTCGAGGAGATCTGGGACGCTGGCCGGAAGT 1280
Qy 1410 GTCGACGACGAAGCTTTCGCCCCCGGACCGATGTACGCTGGGGGACGAGCTCCACTTAGA 1469
Db 1281 GTCGACGACGAAGCTTTCGCCCCCGGACCGATGTACGCTGGGGGACGAGCTCCACTTAGA 1340
Qy 1470 CGGCGAGGACGTGGCGATGCGCATGCCGACGCGTAGACGATTTTCGATCTGGACATGTT 1529
Db 1341 CGGCGAGGACGTGGCGATGCGCATGCCGACGCGTAGACGATTTTCGATCTGGACATGTT 1400
Qy 1530 GGGGACGCGGGAATTCGCCCGGTCGGGATTTTACCCCCCAGACTCCGCCCCCTACGCGCG 1589
Db 1401 GGGGACGCGGGAATTCGCCCGGTCGGGATTTTACCCCCCAGACTCCGCCCCCTACGCGCG 1460
Qy 1590 TCTGGATATGCGCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAAATTGACGA 1649
Db 1461 TCTGGATATGCGCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAAATTGACGA 1520
Qy 1650 GTACGGTGGGTAG 1662
Db 1521 GTACGGTGGGTAG 1533
```

RESULT 15

```
US-10-087-167-65
; Sequence 65, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1509)
; OTHER INFORMATION: Ecdysone Receptor chimera MBV
US-10-087-167-65
```

```
Query Match      59.9%; Score 996.2; DB 16; Length 1509;
Best Local Similarity 89.6%; Pred. No. 2.3e-280;
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Matches	1096;	Conservative	0;	Mismatches	118;	Indels	9;	Gaps	2;
Qy	440	CGACGCGTATGAGGCCGAGTGCCTCGTCCAGAGTCCA	CGTGCAGAAACAAAGAGAG	499					
Db	296	CGGTGGSCATGAGGCCGAGTGCCTCGTCCAGAGTCCA	CGTGCAGAAACAAAGAGAG	355					
Qy	500	AAAAGGAGCACAGAGAAAAGACAAACTGCCAGTCA	GCAGACAGTGGACGATC	559					
Db	356	AAAAGGAAGCACAGAGAAAAGACAAACTGCCAGTCA	GCAGACAGTGGACGATC	415					
Qy	560	ATATGCCCTGCATAATGSCAATGTGACCTTCGCGCC	CCAGAGCGGCAAGGATTCACGAAG	619					
Db	416	ATATGCCCTGCATAATGSCAATGTGACCTTCGCGCC	CCAGAGCGGCAAGGATTCACGAAG	475					
Qy	620	TGCTCCCGAGGTTCTTAACCGAGAAGCTAATGAGC	AGAACAGACTGAAGATGTGACGC	679					
Db	476	TGCTCCCGAGGTTCTTAACCGAGAAGCTAATGAGC	AGAACAGACTGAAGATGTGACGC	535					
Qy	680	CGCTGTCGGCGAACACAGAACTCCCTGATCCGAGG	CTCGTGGTACCAAGGAGGTACG	739					
Db	536	CGCTGTCGGCGAACACAGAACTCCCTGATCCGAGG	CTCGTGGTACCAAGGAGGTACG	595					
Qy	740	AGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACA	CAGACATCGCAGTTAGGAAGAAG	799					
Db	596	AACAACCTTCAGAGGAAGACCTCAAGAGGAGTGA	CGCAGACTGCGACGAGATG	655					
Qy	800	AAGAGGAGGAACCTGACATGCCCTTCGTCAGATCA	CAGAGATGACGATCTTAAACAGTGC	859					
Db	656	AAGAGGAGTCA--GATATGCCGTTCCGCGAGATCA	CCGAGATGACGATCTCGACAGTTTC	712					
Qy	860	AGCTTATGTAGAAATTCGCAAAAGGGACTACGGG	ATCTCAGAGATATCTCAGTCCGATC	919					
Db	713	AACTCATCGTAGAAATTCGCAAAAGGCTTCGCGAG	CTTCGCAAGATCTCGCAGTCCGATC	772					
Qy	920	AAATTCATTTATTAAGCGCTCATCAGCGAAGTGAT	GCCTCGAGTGGCGCGACGCT	979					
Db	773	AAATTCACGTTACTTAAAGCGGTTCATAGTGAGTG	ATGATGCTCCGAGTGGCCCGCGGT	832					
Qy	980	ACGACGGGCGACGACGAGCGTCTGTTTCGCAACAA	CCAGGGGTACAACGCGCAAACT	1039					
Db	833	ACGACGGGCGACGACGAGCTACTGTTTCGCAACAA	CCAGGGGTACTCCGCGCAAACT	892					
Qy	1040	ACCSCAAGGCGGCGATGTCTCATCGTAGACCTGCT	GCATCTTCTGTCGCTGTATGT	1099					
Db	893	ACCSCAAGGCGGCGATGTCTCATCGTAGAGTCTCT	TTCGCACTTCTGTCGCTGTATGT	952					
Qy	1100	ACTCGATGAGCATGGACAATGTGCACATACGGCTG	CTCACGGCCATCGTTATTTCTCAG	1159					
Db	953	ACTCGATGATGGATAACGTGCATACGCGCTGCTTA	CGGCGATTTCAITTTCTCAG	1012					
Qy	1160	ACCGCCAGGCTCGAGCAACCCCTTTTATGGAGGAAT	TCCAGAGATACTATTGAAGA	1219					
Db	1013	ACCGCCCTGGGCTCGAGCAACCCCTTATGGTGGAA	GAANTCCAGCGTATTACTGNACA	1072					
Qy	1220	CGCTCGCGGTTTACATTTTAATCAGCACAGCGCGT	TCGCTCGCTGCGCGCTGTGCT	1279					
Db	1073	CGCTCGCGGTGTACATCTTGAACCAAAACAGTGC	GTGCGCTGCCCGTAGTCTTCG	1132					
Qy	1280	GGAAGATCCTCGGCGTGTGACGGAATGCGCGCA	CGCTCGGACCGCAACTCCAAATGT	1339					
Db	1133	CCAAATCCTCGGGATATTTGACGAGCTCGGAGCCCT	CGGCGATTCAGAACTCCAAATGT	1192					
Qy	1340	GCATCTCGCTGAAGCTGAAGAACAGGAAATCTTCG	CCATTCTCGAGAGATCTGGGACG	1399					
Db	1193	GCATCTCGTGTGAAGCTGAAGAAATAGGAAGCTG	CGCCCGTTCTCGAGAGATCTGGGACG	1252					
Qy	1400	TGGCCGGAATGTTCGACGACGAGCTTGGCCCCCG	CGACCGATGTTCAGCTTGGGGACGAGC	1459					
Db	1253	TG-----GAATCCCGCGGAAGCTTGGCCCCCG	ACCGATGTTCAGCTTGGGGACGAGC	1306					
Qy	1460	TCCACTTAGACGGCGAGGACGTGGCGATGGCGCAT	TGCGCATGCGCAGCTGTAGATTTTCATC	1519					
Db	1307	TSCACTTAGACGGCGAGGACGTGGCGATGGCGCAT	TGCGCATGCGCAGCTGTAGATTTTCATC	1366					

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 173 Seconds
(without alignments)
1236.292 Million cell updates/sec

Title: US-10-087-167-105

Perfect score: 2856

Sequence: 1 MKLSSIEQACDICKLKLK.....ADFFEQMTDALGIDYGG 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2856	100.0	553	5	ABJ05371 Ecdysone
2	2856	100.0	553	7	ADP49177 Ecdysone
3	2803	98.1	588	5	ABJ05374 Chimeric
4	2803	98.1	588	7	ADP49195 Ecdysone
5	2786.5	97.6	599	5	ABJ05376 Chimeric
6	2786.5	97.6	599	7	ADP49199 Ecdysone
7	2738.5	95.9	591	5	ABJ05372 Chimeric
8	2738.5	95.9	591	7	ADP49191 Ecdysone
9	2731	95.6	588	5	ABJ05373 Chimeric
10	2731	95.6	588	7	ADP49193 Ecdysone
11	2661.5	93.2	593	5	ABJ05375 Chimeric
12	2661.5	93.2	593	7	ADP49197 Ecdysone
13	2442.5	85.5	615	5	ABJ05378 Chimeric
14	2442.5	85.5	615	7	ADP49207 Ecdysone
15	2440	85.4	620	5	ABJ05379 Chimeric
16	2440	85.4	620	7	ADP49209 Ecdysone
17	2433	85.2	475	5	ABJ05377 Chimeric
18	2433	85.2	475	7	ADP49201 Ecdysone
19	2428	85.0	602	5	ABJ05380 Chimeric
20	2428	85.0	602	7	ADP49215 Ecdysone
21	2381.5	83.4	599	5	ABJ05381 Chimeric
22	2381.5	83.4	599	7	ADP49220 Ecdysone
23	2100	73.5	505	5	ABJ05369 Chimeric
24	2100	73.5	505	7	ADP49166 Ecdysone
25	2047	71.7	499	5	ABJ05357 Chimeric

26	2047	71.7	499	7	ADP49142	Adf49142 Ecdysone
27	2030.5	71.1	510	5	ABJ05362	Abj05362 Chimeric
28	2030.5	71.1	510	7	ADP49152	Adf49152 Ecdysone
29	1982.5	69.4	502	5	ABJ05355	Abj05355 Chimeric
30	1982.5	69.4	502	7	ADP49138	Adf49138 Ecdysone
31	1975	69.2	499	5	ABJ05356	Abj05356 Chimeric
32	1975	69.2	499	7	ADP49140	Adf49140 Ecdysone
33	1913	67.0	507	5	ABJ05361	Abj05361 Chimeric
34	1913	67.0	507	7	ADP49150	Adf49150 Ecdysone
35	1905.5	66.7	504	5	ABJ05360	Abj05360 Chimeric
36	1905.5	66.7	504	7	ADP49148	Adf49148 Ecdysone
37	1816	63.6	521	5	ABJ05367	Abj05367 Chimeric
38	1816	63.6	521	7	ADP49162	Adf49162 Ecdysone
39	1791.5	62.7	516	5	ABJ05358	Abj05358 Chimeric
40	1791.5	62.7	516	7	ADP49144	Adf49144 Ecdysone
41	1763	61.7	487	5	ABJ05364	Abj05364 Chimeric
42	1763	61.7	487	7	ADP49156	Adf49156 Ecdysone
43	1725.5	60.4	500	5	ABJ05368	Abj05368 Chimeric
44	1725.5	60.4	500	7	ADP49164	Adf49164 Ecdysone
45	1712	59.9	501	5	ABJ05354	Abj05354 Chimeric

ALIGNMENTS

RESULT 1

ABJ05371
ID ABJ05371 standard; protein; 553 AA.

AC ABJ05371;

DT 07-NOV-2002 (first entry)

DE Ecdysone receptor encoded by vector pCGS202 SEQ ID NO: 105.

XX Plant; gene expression control; insect; hormone receptor; fertility;
ecdysonic receptor.

OS Synthetic.

FN WO200261102-A2.

PD 08-AUG-2002.

PF 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

FR (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2002-619259/66.

XX N-PSDB; ABT07353.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

XX Claim 27; Page 258-261; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (Ecr) of an insect, a ligand binding domain of an insect Ecr, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a protein described in the exemplification of the invention

```

SQ      Sequence 553 AA;
Query Match      100.0%; Score 2856; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 8.6e-229;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Qy      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Db      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Qy      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Db      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Qy      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Db      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Qy      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Db      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Qy      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Db      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Qy      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Db      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Qy      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Db      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Qy      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540
Db      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540

SQ      Sequence 553 AA;
Query Match      100.0%; Score 2856; DB 7; Length 553;
Best Local Similarity 100.0%; Pred. No. 8.6e-229;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Qy      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Db      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Qy      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Db      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Qy      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Db      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Qy      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Db      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Qy      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Db      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Qy      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Db      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Qy      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Db      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Qy      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540
Db      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540

RESULTS 2
ADFA9177
ID ADFA9177 standard; protein; 553 AA.
XX
AC ADFA9177;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/Vp16 transactivation domain seq id 105.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; Vp16 transactivation domain.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
XX
XX 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.

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XX      24-OCT-2001; 2001US-00087167.
XX      (PASC/) PASCAL E J.
XX      (VALE/) VALENTINE S A.
XX      (BROW/) BROWN J A.
XX      (COCK/) COCKRELL A S.
XX      (JOHN/) JOHNSON B D.
XX      Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX      WPI; 2003-897756/82.
XX      New receptor cassette encoding a chimeric receptor polypeptide, useful
XX      for regulating the expression of target polypeptides in plants in the
XX      presence of appropriate chemical ligands.
XX      Example 11; SEQ ID NO 105; 186pp; English.
XX      The invention describes a receptor cassette encoding a chimeric receptor
XX      polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX      (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX      (E) domain that is heterologous with respect to the D domain, and an
XX      activation domain. The receptor cassette and method are useful in
XX      regulating the expression of target polypeptides in plants in the
XX      presence of appropriate chemical ligands. The transgenic seeds and plants
XX      can be used for the breeding of improved plant lines that, for e.g.,
XX      increase the effectiveness of conventional methods such as herbicide or
XX      pesticide treatment. This is the amino acid sequence of an ecdysone
XX      receptor-Vp16 transactivation domain fusion protein.
XX      Sequence 553 AA;
Query Match      100.0%; Score 2856; DB 7; Length 553;
Best Local Similarity 100.0%; Pred. No. 8.6e-229;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db      1 MKLLSSIEQACDLCRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Qy      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Db      61 LERLEQLFLILFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Qy      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Db      121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRREKEAQREKDKLPVS 180
Qy      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Db      181 TTTVDHMPAIMQCDPPPEAARIHEVVPRLTEKLMQNLKNVTPLSANQKSLIARLV 240
Qy      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Db      241 WYQEGYEQPSSEDLKRVTTQWLEEEEEETDMPFRQITMTILTQVLIIVEFAKGLPGFS 300
Qy      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Db      301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
Qy      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Db      361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYLINQHSASP 420
Qy      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Db      421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKLNKRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Qy      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540
Db      481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFFFEQ 540

```


New receptor cassette encoding a chimeric receptor polypeptide, useful for regulating the expression of target polypeptides in plants in the

PT presence of appropriate chemical ligands.

PS Example 23; SEQ ID NO 123; 186pp; English.

XX The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding (E) domain that is heterologous with respect to the D domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants can be used for the breeding of improved plant lines that, for e.g., increase the effectiveness of conventional methods such as herbicide or pesticide treatment. This is the amino acid sequence of an ecdysone receptor-Vp16 transactivation domain fusion protein.

XX Sequence 588 AA;

Query Match 98.1%; Score 2803; DB 7; Length 588;
Best Local Similarity 98.6%; Pred. No. 2.4e-224;
Matches 545; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

Qy 1 MKLLSSIEQACDLCRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPPLTRAHLTEVESR 60
Db |||||
Qy 42 MKLLSSIEQACDLCRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPPLTRAHLTEVESR 101
Db |||||
Qy 61 LERLEQLFLIFPREDLDMLKWSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
Db |||||
Qy 102 LERLEQLFLIFPREDLDMLKWSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
Db |||||
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNRKEAQRKDLPLVS 180
Db |||||
Qy 162 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNRKEAQRKDLPLVS 221
Db |||||
Qy 181 TTTVDHMPAIMQCDPPPPPEAARIHEVVPRFLTEKLMQNLKNVTPLSANQKSLIARLV 240
Db |||||
Qy 222 TTTVDHMPAIMQCDPPPPPEAARIHEVVPRFLTEKLMQNLKNVTPLSANQKSLIARLV 281
Db |||||
Qy 241 WYQEGYEQPSSEDLKRVTTQWLESEEEETDMPFRQITENTILTVQLIVEFAKGLGFS 300
Db |||||
Qy 282 WYQEGYEQPSSEDLKRVTTQWLESEEEETDMPFRQITENTILTVQLIVEFAKGLGFS 341
Db |||||
Qy 301 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
Db |||||
Qy 342 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIGDLL 401
Db |||||
Qy 361 HFCRCWMSMDNVHYALLTAIVIPSDRPGLEQPLLVVEEIQRYLKTIRVYILNQHSASP 420
Db |||||
Qy 402 HFCRCWMSMDNVHYALLTAIVIPSDRPGLEQPLLVVEEIQRYLKTIRVYILNQHSASP 461
Db |||||
Qy 421 RCVLFGKILGVLTRELRTLTQNSNMCI SLKLNKRLPPFLLEEIMDVAVSTTKLAPPTD 480
Db |||||
Qy 462 RCVLFGKILGVLTRELRTLTQNSNMCI SLKLNKRLPPFLLEEIMDVAVSTTKLAPPTD 515
Db |||||
Qy 481 VSLGDELHLDGEDVAMAHADLDDFDLMDLGDGSPGPGFTPHDSAPYGALDMDADFFEQ 540
Db |||||
Qy 516 VSLGDELHLDGEDVAMAHADLDDFDLMDLGDGSPGPGFTPHDSAPYGALDMDADFFEQ 575
Db |||||
Qy 541 MFTDALGIDEXYGG 553
Db |||||
Qy 576 MFTDALGIDEXYGG 588
Db |||||

RESULT 5
ABJ05376
ID ABJ05376 standard; protein; 599 AA.

XX AC ABJ05376;

XX 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 127.

XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.

XX Ostrinia nubilalis.

OS Manduca sexta.

OS Chimeric.

PN W0200261102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EU, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

DR N-PSDB; ABT07370.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

PS Example 23; Page 288-291; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect EcR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a protein described in the exemplification of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 599 AA;

Query Match 97.6%; Score 2786.5; DB 5; Length 599;
Best Local Similarity 96.8%; Pred. No. 5.9e-223;
Matches 540; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

Qy 1 MKLLSSIEQACDLCRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPPLTRAHLTEVESR 60
Db |||||
Qy 42 MKLLSSIEQACDLCRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPPLTRAHLTEVESR 101
Db |||||
Qy 61 LERLEQLFLIFPREDLDMLKWSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
Db |||||
Qy 102 LERLEQLFLIFPREDLDMLKWSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
Db |||||
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNRKEAQRKDLPLVS 180
Db |||||
Qy 162 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNRKEAQRKDLPLVS 221
Db |||||
Qy 181 TTTVDHMPAIMQCDPPPPPEAARI-----HEVVPRFLTEKLMQNLKNVTPLSANQKSL 235
Db |||||
Qy 222 TTTVDHMPAIMQCDPPPPPEAARI-----HEVVPRFLTEKLMQNLKNVTPLSANQKSL 281
Db |||||
Qy 236 IARLVWYQEGYEQPSSEDLKRVTTQWLESEEEETDMPFRQITENTILTVQLIVEFAK 295
Db |||||
Qy 282 IARLVWYQEGYEQPSSEDLKRVTTQWLESEEEETDMPFRQITENTILTVQLIVEFAK 341
Db |||||
Qy 296 LPGAFTKISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYV 355
Db |||||
Qy 342 LPGAFTKISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYV 401
Db |||||
Qy 356 IEDLLHFCRCWMSMDNVHYALLTAIVIPSDRPGLEQPLLVVEEIQRYLKTIRVYILNQ 415
Db |||||

DB 402 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVETIQRYYLKLRLVYILNQ 461

QY 416 HSASPRCAVLFGKILGVLTSLTGTQNSNMCISLKNRKLPPPLEEINWDAEVSSTKL 475

DB 462 HSASPRCAVLFGKILGVLTSLTGTQNSNMCISLKNRKLPPPLEEINWDAEVSSTKL 521

QY 476 APPTDVSIGDELHLDGEDVANAHAADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDNAD 535

DB 522 APPTDVSIGDELHLDGEDVANAHAADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDNAD 581

QY 536 FEFEQMFDTALGIDEYGG 553

DB 582 FEFEQMFDTALGIDEYGG 599

RESULT 6

ADF49199

ID ADF49199 standard; protein; 599 AA.

XX

AC ADF49199;

XX

DT 12-FEB-2004 (first entry)

XX

DE Ecdysone receptor/VP16 transactivation domain seq id 127.

XX

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain; hinge domain; ecdysone receptor; EcR; ligand binding domain; activation domain; transgenic seed; transgenic plant; plant line; herbicide; pesticide; chimeric ecdysone receptor; EcR; yeast GAL4 DNA binding domain; VP16 transactivation domain.

XX

OS Synthetic.

OS Ostrinia nubilalis.

OS Ascomycota.

OS Manduca sexta.

OS Herpes simplex virus unknown type.

XX

PN US2003154509-A1.

XX

PD 14-AUG-2003.

XX

PF 24-OCT-2001; 2001US-00087167.

XX

PR 24-OCT-2001; 2001US-00087167.

XX

PA (PASC/) PASCAL B. J.

PA (VALE/) VALENTINE S. A.

PA (BROW/) BROWN J. A.

PA (COCK/) COCKRELL A. S.

PA (JOHN/) JOHNSON B. D.

XX

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX

DR WPI; 2003-897756/82.

DR N-PSDB; ADF49198.

XX

PT New receptor cassette encoding a chimeric receptor polypeptide, useful for regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands.

XX

PS Example 23; SEQ ID NO 127; 186pp; English.

XX

CC The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding (B) domain that is heterologous with respect to the B domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants can be used for the breeding of improved plant lines that, for e.g., increase the effectiveness of conventional methods such as herbicide or pesticide treatment. This is the amino acid sequence of an ecdysone receptor-VP16 transactivation domain fusion protein.

XX SQ Sequence 599 AA;

Query Match 97.6%; Score 2786.5; DB 7; Length 599;

Best Local Similarity 96.8%; Pred. No. 5.9e-223;

Matches 540; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 1 MKLSSIEQAQCDICRLKCLKSKPKCAKCLKNWECRYSPKTKRSPKTRSLTRAHLTEVSR 60

DB 42 MKLSSIEQAQCDICRLKCLKSKPKCAKCLKNWECRYSPKTKRSPKTRSLTRAHLTEVSR 101

QY 61 LERLEQLFLIFPPREDLMDILKMSLDQIKALLTGLFVQDNNVNDKDAVTRDLASVETDPL 120

DB 102 LERLEQLFLIFPPREDLMDILKMSLDQIKALLTGLFVQDNNVNDKDAVTRDLASVETDPL 161

QY 121 TLQRHRSATSSSESSNKGQRLTVSTRMPECVVPESTCKNRKEAQAQREKDKLPVS 180

DB 162 TLQRHRSATSSSESSNKGQRLTVSTRMPECVVPESTCKNRKEAQAQREKDKLPVS 221

QY 181 TTTVDHMPAIMQCDDPPPPPEAARI-----HEVVPRFLTEKLMQNRLKNVTPLSANQSL 235

DB 222 TTTVDHMPAIMQCDDPPPPPEAARI-----HEVVPRFLTEKLMQNRLKNVTPLSANQSL 281

QY 236 IARLVWYQEGYEQSEEDLKRVTQTWLEEESEETDMPFRQITEMTILTVQLIYEFAG 295

DB 282 IARLVWYQEGYEQSEEDLKRVTQTWLEEESEETDMPFRQITEMTILTVQLIYEFAG 341

QY 296 LPGFSKISQSDQITLLKASSSEVMMLRVARYDAATSVLFANNQAYTRDNYRKAGMSYV 355

DB 342 LPGFSKISQSDQITLLKASSSEVMMLRVARYDAATSVLFANNQAYTRDNYRKAGMSYV 401

QY 356 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVETIQRYYLKLRLVYILNQ 415

DB 402 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVETIQRYYLKLRLVYILNQ 461

QY 416 HSASPRCAVLFGKILGVLTSLTGTQNSNMCISLKNRKLPPPLEEINWDAEVSSTKL 475

DB 462 HSASPRCAVLFGKILGVLTSLTGTQNSNMCISLKNRKLPPPLEEINWDAEVSSTKL 521

QY 476 APPTDVSIGDELHLDGEDVANAHAADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDNAD 535

DB 522 APPTDVSIGDELHLDGEDVANAHAADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDNAD 581

QY 536 FEFEQMFDTALGIDEYGG 553

DB 582 FEFEQMFDTALGIDEYGG 599

RESULT 7

ABJ05372

ID ABJ05372 standard; protein; 591 AA.

AC ABJ05372;

XX 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 119.

KW Plant; gene expression control; insect; hormone receptor; fertility;

KW ecdysone receptor.

XX Manduca sexta.

XX Agrotis ipsilon.

XX Chimeric.

XX WO200261102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

QY 121 TLQHRISATSSSESSNGKQRLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVS 180
DB 162 TLQHRISATSSSESSNGKQRLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVS 221
QY 181 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 240
DB 222 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQGYEQPSSEDLKRVTTQWLESEEEEDTMDPRQITMTILTVQLIVFAKGLPGFS 300
DB 282 WYQGYEQPSSEDLKRVTTQW-SPEDESESDMPERQITMTILTVQLIVFAKGLPGFA 340
QY 301 KISQSDQITLLKACSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
DB 341 KISQSDQITLLKACSEVMMLRVARRYDAATDSVLFANNQAYSRDNRKAGMSYVIEDLL 400
QY 361 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNQHSASP 420
DB 401 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNQHSASP 460
QY 421 RCVLFGKILGVLTELRTLGTONSNMCI SLKLNKRLPPFLEEIWDVAEVSSTKLAPPTD 480
DB 461 RCPVVFALIGLTELRTLGTONSNMCI SLKLNKRLPPFLEEIWDVE--SRGKLAPPTD 518
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEPEQ 540
DB 519 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEPEQ 578
QY 541 MFTDALGIDEYGG 553
DB 579 MFTDALGIDEYGG 591

RESULT 9

ABJ05373
ID AB05373 standard; protein; 588 AA.

AC ABJ05373;

DT 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 121.

DE Plant; gene expression control; insect; hormone receptor; fertility;

KW ecdysone receptor.

XX Manduca sexta.

OS Ostrinia nubilalis.

OS Chimeric.

XX WO200261102-A2.

PN 08-AUG-2002.

PD 24-OCT-2001; 2001WO-US051417.

PF 24-OCT-2000; 2000US-0242969P.

PR (SYGN) SYNGENTA PARTICIPATIONS AG.

PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

PI WPI: 2002-612959/66.

DR N-PSDB; ABT07367.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX Claim 6; Page 273-275; 319pp; English.
PS The present invention relates to a receptor cassette encoding a chimeric
XX

CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a protein described in the exemplification of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 588 AA;

Query Match 95.6%; Score 2731; DB 5; Length 588;

Best Local Similarity 95.3%; Pred. No. 2.4e-218;

Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

QY 1 MKLLSSIEQACDLCRLKXKCKEKPCKAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
DB 42 MKLLSSIEQACDLCRLKXKCKEKPCKAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIFPREDLMDILKMSLODIKALLTGLFVQDNNVNDKDAVTDRLASVETDML 120
DB 102 LERLEQLFLIFPREDLMDILKMSLODIKALLTGLFVQDNNVNDKDAVTDRLASVETDML 161
QY 121 TLQHRISATSSSESSNGKQRLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVS 180
DB 162 TLQHRISATSSSESSNGKQRLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVS 221
QY 181 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 240
DB 222 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQGYEQPSSEDLKRVTTQWLESEEEEDTMDPRQITMTILTVQLIVFAKGLPGFS 300
DB 282 WYQGYEQPSSEDLKRVTTQWQSADEDESDMPERQITMTILTVQLIVFAKGLPGFS 341
QY 301 KISQSDQITLLKACSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
DB 342 KISQSDQITLLKACSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
QY 361 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNQHSASP 420
DB 402 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNQHSASP 461
QY 421 RCVLFGKILGVLTELRTLGTONSNMCI SLKLNKRLPPFLEEIWDVAEVSSTKLAPPTD 480
DB 462 RCVIYAKILSVLTELRTLGTONSNMCI SLKLNKRLPPFLEEIWDV-----KLAPPTD 515
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEPEQ 540
DB 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEPEQ 575
QY 541 MFTDALGIDEYGG 553
DB 576 MFTDALGIDEYGG 588

RESULT 10

ADF49193

ID ADF49193 standard; protein; 588 AA.

AC ADF49193;

XX ADF49193;

DT 12-FEB-2004 (first entry)

XX Ecdysone receptor/VP16 transactivation domain seq id 121.

DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain.

XX OS Synthetic.
OS OS Manduca sexta.
OS OS Ascomycota.
OS OS Ostrinia nubilalis.
OS OS Herpes simplex virus unknown type.
XX XX US2003154509-A1.
XX XX 14-AUG-2003.
XX XX 24-OCT-2001; 2001US-00087167.
XX XX 24-OCT-2001; 2001US-00087167.
XX XX (PASC/) PASCAL E J.
XX XX (VALE/) VALENTINE S A.
XX XX (BROW/) BROWN J A.
XX XX (COCK/) COCKRELL A S.
XX XX (JOHN/) JOHNSON B D.
XX XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX XX WPI; 2003-897756/82.
XX XX N-PSDB; ADF49192.
XX XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX XX for regulating the expression of target polypeptides in plants in the
XX XX presence of appropriate chemical ligands.
XX XX Example 23; SEQ ID NO 121; 186pp; English.
XX XX The invention describes a receptor cassette encoding a chimeric receptor
XX XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX XX (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX XX (E) domain that is heterologous with respect to the D domain, and an
XX XX activation domain. The receptor cassette and method are useful in
XX XX regulating the expression of target polypeptides in plants in the
XX XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX XX can be used for the breeding of improved plant lines that, for e.g.,
XX XX increase the effectiveness of conventional methods such as herbicide or
XX XX pesticide treatment. This is the amino acid sequence of an ecdysone
XX XX receptor-VP16 transactivation domain fusion protein.
XX XX Sequence 588 AA;
XX XX
XX XX Query Match 95.6%; Score 2731; DB 7; Length 588;
XX XX Best Local Similarity 95.3%; Pred. No. 2.4e-218;
XX XX Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;
QY 1 MKLLSSISQACDICELKXKCKSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
DB 42 MKLLSSISQACDICELKXKCKSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLLIPPRDLMLKMDLSLQIKALLTGLFQVDNVNKAQVTRDLASVETDML 120
DB 102 LERLEQLFLLIPPRDLMLKMDLSLQIKALLTGLFQVDNVNKAQVTRDLASVETDML 161
QY 121 TLQRHRIATSSSESSNGRQLTVSTRMPECVVPESTCKNKRREKAEQKDLPV 180
DB 162 TLQRHRIATSSSESSNGRQLTVSTRMPECVVPESTCKNKRREKAEQKDLPV 221
QY 181 TTTVDHHPAQMOCPPPEAARIHEVVPFRFTEKLMQNRLKNVTPISANQKSLIARLV 240
DB 222 TTTVDHHPAQMOCPPPEAARIHEVVPFRFTEKLMQNRLKNVTPISANQKSLIARLV 281
QY 241 WYQEGVEQPSDDLKRVVTQTWLEEEETDMPFRQITEMTLTVQLIVFAKGLPGFS 300
DB 282 WYQEGVEQPSDDLKRVVTQTWQSADEDESDMPFRQITEMTLTVQLIVFAKGLPGFS 341
QY 301 KISQSDQITLLKASSEVMMLVARRYDAATDVLVFNQATYTRNRYKAGMAYVIEDLL 360
DB 342 KISQSDQITLLKACSEVMMLVARRYDAVSDSVLFANNQATYTRNRYKAGMAYVIEDLL 401

361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYLKTRLVILNHSASP 420
DB 402 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYLKTRLVILNHSASP 461
QY 421 RCAVLFGKILGLVLTGLTQNSMNCISILKLNKRLPPFLEEIWDVAEVSSTTKLAPPTD 480
DB 462 RCAVIYAKILSVLTGLTQNSMNCISILKLNKRLPPFLEEIWDV-----KLAPPTD 515
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSGPGFTPHDSAPYCALDMADFEFEQ 540
DB 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSGPGFTPHDSAPYCALDMADFEFEQ 575
QY 541 MFTDALGIDEYGG 553
DB 576 MFTDALGIDEYGG 588

RESULT 11
ABJ05375
ID ABJ05375 standard; protein; 593 AA.
XX AC ABJ05375;
XX DT 29-AUG-2003 (revised)
XX DT 07-NOV-2002 (first entry)
XX XX Chimeric ecdysone receptor SEQ ID NO: 125.
XX XX Plant; gene expression control; insect; hormone receptor; fertility;
XX XX ecdysone receptor.
XX OS Ostrinia nubilalis.
XX OS Ostrinia nubilalis.
XX OS Chimeric.
XX XX WO200261102-A2.
XX PD 08-AUG-2002.
XX XX 24-OCT-2001; 2001WO-US051417.
XX PF 24-OCT-2000; 2000US-0242969P.
XX PR (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX PI WPI; 2002-619259/66.
XX XX N-PSDB; ABT07369.
XX XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX XX regulating expression of target polypeptides in plants in the presence of
XX XX appropriate ligands that may be used in controlling plant fertility.
XX XX Example 23; Page 283-285; 319pp; English.
XX XX The present invention relates to a receptor cassette encoding a chimeric
XX XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX XX domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX XX domain of an insect EcR, where the ligand binding domain is heterologous
XX XX with respect to the hinge domain and an activation domain. The chimeric
XX XX insect hormone receptors and receptor cassettes are useful in regulating
XX XX expression of target polypeptides in plants in the presence of
XX XX appropriate ligands that may be used in controlling plant fertility. The
XX XX method is useful for decreasing or increasing plant gene expression. The
XX XX present sequence is a protein described in the exemplification of the
XX XX invention. (Updated on 29-AUG-2003 to standardise OS field)
XX XX Sequence 593 AA;
XX XX
XX XX Query Match 93.2%; Score 2661.5; DB 5; Length 593;
XX XX Best Local Similarity 92.1%; Pred. No. 1.9e-212;

Matches 514; Conservative 17; Mismatches 16; Indels 11; Gaps 2;	
Qy	1 MKLLSSIEQACDICRLKXKCSKEPKCAKCLKNWECRYSPKTKRSPKTRAHLEVEFSR 60
Db	
Qy	42 MKLLSSIEQACDICRLKXKCSKEPKCAKCLKNWECRYSPKTKRSPKTRAHLEVEFSR 101
Db	
Qy	61 LERLEQLFLIIPREDLMDILKMSLQDIKALLTGLFVQDNVKNDAVTRDLASVETDML 120
Db	
Qy	121 TLQHRISATSSSESSNKGORQLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 180
Db	
Qy	162 TLQHRISATSSSESSNKGORQLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 221
Db	
Qy	181 TTTVDHMPAINQCDPPPEAARI-----HEVVPRLTEKLMQNRKLNVTPLSANQKSL 235
Db	
Qy	236 IARLVWYQGYEQPSEEDLKRVTQTWQLEEEBETDMPFRQITMTILTVQLIVEFAKG 295
Db	
Qy	282 IARLVWYQGYEQPSEEDLKRVTQTWQSADEDESDMPFRQITMTILTVQLIVEFAKG 341
Db	
Qy	296 LPGFSGKISQSDQITLLKACSSSEVMMLRVARRYDAATSDVLFANNOAYTRDNRKAGMAYV 355
Db	
Qy	342 LPGFSGKISQSDQITLLKACSSSEVMMLRVARRYDAVSDVLFANNOAYTRDNRKAGMAYV 401
Db	
Qy	356 IEDLLHFCRCMYSMNDNVHVALTAVIFSDRPGLEQPLVVEEIQRYVLTLYVILNQ 415
Db	
Qy	402 IEDLLHFCRCMYSMNDNVHVALTAVIFSDRPGLEQPLVVEEIQRYVLTLYVILNQ 461
Db	
Qy	416 HSASPRCAVLFGKILGVLTGLTQNSNMCSISLKNRKLPPPLEIWDVAEVSSTKL 475
Db	
Qy	462 HSASPRCAVIYAKILSVLTGLTQNSNMCSISLKNRKLPPPLEIWDV-----KL 515
Db	
Qy	476 APPTDVSUGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSPGPGTTPHDSAPYGALDMAD 535
Db	
Qy	516 APPTDVSUGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSPGPGTTPHDSAPYGALDMAD 575
Db	
Qy	536 FEFEQMFTDALGIDEYGG 553
Db	
Qy	576 FEFEQMFTDALGIDEYGG 593
Db	
RESULT 12	
ID	ADF49197
AD	ADF49197 standard; protein; 593 AA.
AC	ADF49197;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Ecdysone receptor/VP16 transactivation domain seq id 125.
XX	
KW	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW	hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW	activation domain; transgenic seed; transgenic plant; plant line;
KW	herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW	yeast GAL4 DNA binding domain; VP16 transactivation domain.
XX	
OS	Synthetic.
OS	Ostrinia nubilalis.
OS	Ascomycota.
OS	Herpes simplex virus unknown type.
XX	
PN	US2003154509-A1.
XX	
PD	14-AUG-2003.
XX	
PF	24-OCT-2001; 2001US-00087167.
XX	
PR	24-OCT-2001; 2001US-00087167.
XX	
PA	(PASC/) PASCAL E J.

PA	(VALE/) VALENTINE S A.
PA	(BROW/) BROWN J A.
PA	(COCK/) COCKRELL A S.
PA	(JOHN/) JOHNSON B D.
XX	
PI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	
DR	WPI; 2003-897756/82.
DR	N-PSDB; ADF49196.
XX	
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful
PT	for regulating the expression of target polypeptides in plants in the
PT	presence of appropriate chemical ligands.
XX	
PS	Example 23; SEQ ID NO 125; 186pp; English.
XX	
CC	The invention describes a receptor cassette encoding a chimeric receptor
CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC	(D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC	(E) domain that is heterologous with respect to the D domain, and an
CC	activation domain. The receptor cassette and method are useful in
CC	regulating the expression of target polypeptides in plants in the
CC	presence of appropriate chemical ligands. The transgenic seeds and plants
CC	can be used for the breeding of improved plant lines that, for e.g.
CC	increase the effectiveness of conventional methods such as herbicide or
CC	pesticide treatment. This is the amino acid sequence of an ecdysone
CC	receptor-VP16 transactivation domain fusion protein.
XX	
Qy	Sequence 593 AA;
Query Match	93.2%; Score 2661.5; DB 7; Length 593;
Best Local Similarity	92.1%; Pred. No. 1.5e-212;
Matches 514; Conservative 17; Mismatches 16; Indels 11; Gaps 2;	
Qy	1 MKLLSSIEQACDICRLKXKCSKEPKCAKCLKNWECRYSPKTKRSPKTRAHLEVEFSR 60
Db	
Qy	42 MKLLSSIEQACDICRLKXKCSKEPKCAKCLKNWECRYSPKTKRSPKTRAHLEVEFSR 101
Db	
Qy	61 LERLEQLFLIIPREDLMDILKMSLQDIKALLTGLFVQDNVKNDAVTRDLASVETDML 120
Db	
Qy	102 LERLEQLFLIIPREDLMDILKMSLQDIKALLTGLFVQDNVKNDAVTRDLASVETDML 161
Db	
Qy	121 TLQHRISATSSSESSNKGORQLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 180
Db	
Qy	162 TLQHRISATSSSESSNKGORQLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 221
Db	
Qy	181 TTTVDHMPAINQCDPPPEAARI-----HEVVPRLTEKLMQNRKLNVTPLSANQKSL 235
Db	
Qy	236 IARLVWYQGYEQPSEEDLKRVTQTWQLEEEBETDMPFRQITMTILTVQLIVEFAKG 295
Db	
Qy	282 IARLVWYQGYEQPSEEDLKRVTQTWQSADEDESDMPFRQITMTILTVQLIVEFAKG 341
Db	
Qy	296 LPGFSGKISQSDQITLLKACSSSEVMMLRVARRYDAATSDVLFANNOAYTRDNRKAGMAYV 355
Db	
Qy	342 LPGFSGKISQSDQITLLKACSSSEVMMLRVARRYDAVSDVLFANNOAYTRDNRKAGMAYV 401
Db	
Qy	356 IEDLLHFCRCMYSMNDNVHVALTAVIFSDRPGLEQPLVVEEIQRYVLTLYVILNQ 415
Db	
Qy	402 IEDLLHFCRCMYSMNDNVHVALTAVIFSDRPGLEQPLVVEEIQRYVLTLYVILNQ 461
Db	
Qy	416 HSASPRCAVLFGKILGVLTGLTQNSNMCSISLKNRKLPPPLEIWDVAEVSSTKL 475
Db	
Qy	462 HSASPRCAVIYAKILSVLTGLTQNSNMCSISLKNRKLPPPLEIWDV-----KL 515
Db	
Qy	476 APPTDVSUGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSPGPGTTPHDSAPYGALDMAD 535
Db	
Qy	516 APPTDVSUGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSPGPGTTPHDSAPYGALDMAD 575
Db	
Qy	536 FEFEQMFTDALGIDEYGG 553
Db	
Qy	576 FEFEQMFTDALGIDEYGG 593
Db	

```

RESULT 13
ABJ05378
ID ABJ05378 standard; protein; 615 AA.
XX
AC ABJ05378;
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
Chimeric ecdysone receptor SEQ ID NO: 135.
XX
KW Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.
XX
OS Manduca sexta.
OS Os
OS Chimeric.
XX
PN WO200261102-A2.
XX
PD 08-AUG-2002.
XX
PF 24-OCT-2001; 2001WO-US051417.
XX
PR 24-OCT-2000; 2000US-0242969P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI; 2002-619259/66.
DR N-PSDB; ABT07376.
XX
New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX
Example 25; Page 299-301; 319pp; English.
XX
The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
CC domain of an insect EcR, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a protein described in the exemplification of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 615 AA;
Query Match 85.5%; Score 2442.5; DB 5; Length 615;
Best Local Similarity 94.0%; Pred. No. 2.7e-194;
Matches 486; Conservative 1; Mismatches 25; Indels 5; Gaps 2;
Oy 1 MKLLSSIEQACDICRLKKLKCSEKPKCAKCLKNNWECRYSPKTKRSPPLTRAHLTEVESR 60
Db 42 MKLLSSIEQACDICRLKKLKCSEKPKCAKCLKNNWECRYSPKTKRSPPLTRAHLTEVESR 101
Oy 61 LERLEQLFLIPREDLDMILKMSLQDIKALLTGLFVQDNVNVKDAVTDRLASVETDMLP 120
Db 102 LERLEQLFLIPREDLDMILKMSLQDIKALLTGLFVQDNVNVKDAVTDRLASVETDMLP 161
Oy 121 TLQHRISATSSSESSNKGORQLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 180
Db 162 TLQHRISATSSSESSNKGORQLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 221
Oy 181 TTTVDHMPAIMQCDPPPEAARIEHVVPRLTEKLMEQNRLKNVTPLSANQKSLIARLV 240

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Db 222 TTTVDHMPAIMQCDPPPEAARIEHVVPRLTEKLMEQNRLKNVTPLSANQKSLIARLV 281
Oy 241 WYQEGYEQPSEEDLKRVTQTWOLEEESEETDMPFROITEMTILTVOIIVEFAKGLPGFS 300
Db 282 WYQEGYEQPSEEDLKRVTQTWOLEEESEETDMPFROITEMTILTVOIIVEFAKGLPGFS 341
Oy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
Db 342 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 401
Oy 361 HFRCMYSMGMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYILNQHSASP 420
Db 402 HFRCMYSMGMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYILNQHSASP 461
Oy 421 RCVLFQKILGVLTGLTGTQNSNMCISLKNRKLPPFLEEIWDVAEIVSTTKLAPTD 480
Db 462 RCVLFQKILGVLTGLTGTQNSNMCISLKNRKLPPFLEEIWDVAEIVSTTKLAPTD 519
Oy 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGDSGP 517
Db 520 VRCTGGLFFHRDTPPAHA---GETATPMAGGGGGGG 553

RESULT 14
ADF49207
ID ADF49207 standard; protein; 615 AA.
XX
AC ADF49207;
XX
DT 12-FEB-2004 (first entry)
DE Ecdysone receptor/CI transactivation domain seq id 135.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; EcR; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; EcR;
KW yeast GAL4 DNA binding domain; CI transactivation domain.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Zea mays.
XX
PN US2003154509-A1.
PD 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.
XX
PR 24-OCT-2001; 2001US-00087167.
XX
PA (PASC/) PASCAL E J.
PA (VALE/) VALENTINE S A.
PA (BROW/) BROWN J A.
PA (COCK/) COCKRELL A S.
PA (JOHN/) JOHNSON B D.
XX
PI Pascal EU, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI; 2003-897756/82.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful
PT for regulating the expression of target polypeptides in plants in the
PT presence of appropriate chemical ligands.
XX
PS Example 25; SEQ ID NO 135; 186pp; English.
XX
The invention describes a receptor cassette encoding a chimeric receptor
CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding
CC (E) domain that is heterologous with respect to the D domain, and an
CC activation domain. The receptor cassette and method are useful in

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CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-C1 transactivation domain fusion protein.
 XX
 SQ Sequence 615 AA;

Query Match 85.5%; Score 2442.5; DB 7; Length 615;
 Best Local Similarity 94.0%; Pred. No. 2.7e-194;
 Matches 486; Conservative 1; Mismatches 25; Indels 5; Gaps 2;
 QY 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVER 60
 DB 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVER 101
 QY 61 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
 DB 102 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
 QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 180
 DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 221
 QY 181 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
 DB 222 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 281
 QY 241 WYQEGYEQPSEEDLKRVTOTWOLEEEEEETDMPROITMTILTVOILVFAKGLPGFS 300
 DB 282 WYQEGYEQPSEEDLKRVTOTWOLEEEEEETDMPROITMTILTVOILVFAKGLPGFS 341
 QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 DB 342 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
 QY 361 HFRCMYSMDNVHVALLTAVIFSDRPGLEQPLLVVEEIQRYYLKTLRVYLINQHSASP 420
 DB 402 HFRCMYSMDNVHVALLTAVIFSDRPGLEQPLLVVEEIQRYYLKTLRVYLINQHSASP 461
 QY 421 RCVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLEEIWDVAEVSSTTKLAPPTD 480
 DB 462 RCVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLEEIWDVAEVSSTTKLAPPTD 519
 QY 481 VSLGDELHLDGEDVAMAHADALDDDFDMLGDGSPG 517
 DB 520 VRTGGLFFHRTDTPAHA---GETATPMAGGGGGG 553

RESULT 15
 ABJ05379
 ID ABJ05379 standard; protein; 620 AA.
 XX
 AC ABJ05379;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 XX Chimeric ecdysone receptor SEQ ID NO: 137.
 DE Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor.
 XX
 OS Manduca sexta.
 OS Manduca sexta.
 OS Chimeric.
 XX
 PN WO200261102-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI WPI; 2002-619259/66.
 XX N-PSDB; ABT07377.
 DR
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 PS Example 25; Page 304-306; 319pp; English.
 XX
 CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 620 AA;

Query Match 85.4%; Score 2440; DB 5; Length 620;
 Best Local Similarity 88.3%; Pred. No. 4.4e-194;
 Matches 492; Conservative 7; Mismatches 34; Indels 24; Gaps 4;
 QY 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVER 60
 DB 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVER 101
 QY 61 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
 DB 102 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
 QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 180
 DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 221
 QY 181 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
 DB 222 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 281
 QY 241 WYQEGYEQPSEEDLKRVTOTWOLEEEEEETDMPROITMTILTVOILVFAKGLPGFS 300
 DB 282 WYQEGYEQPSEEDLKRVTOTWOLEEEEEETDMPROITMTILTVOILVFAKGLPGFS 341
 QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 DB 342 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
 QY 361 HFRCMYSMDNVHVALLTAVIFSDRPGLEQPLLVVEEIQRYYLKTLRVYLINQHSASP 420
 DB 402 HFRCMYSMDNVHVALLTAVIFSDRPGLEQPLLVVEEIQRYYLKTLRVYLINQHSASP 461
 QY 421 RCVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLEEIWDVAEVSSTTKLAPPTD 480
 DB 462 RCVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLEEIWDVAEVSSTTKLAPPTD 521
 QY 481 VSLGDELHLDGEDVAMAHADALDDDFDMLGDG---DPSGPGFT 521
 DB 522 ADPGKATATTTTSTSEITTTGALSDSLAHLLOQGTEDAEVALGLSLDPSAGKA 581
 QY 522 PHDSA-----PYGALDM 533
 DB 582 VLDDSDSFVWPAASFD 598

Search completed: April 14, 2005, 12:23:32
Job time : 175 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 48 Seconds
(without alignments)
1108.497 Million cell updates/sec

Title: US-10-087-167-105
Perfect score: 2856
Sequence: 1 MKLSSIEQACDICKLKKL.....ADFBEQMTDGLGIDYGG 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Piri: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	36.0	536	2 A56590	ecdysteroid recept
2	986.5	34.5	878	2 A41055	ecdysone receptor
3	764.5	26.8	881	1 RGEYGA	regulatory protein
4	452.5	15.8	447	2 I38975	nuclear orphan rec
5	451.5	15.8	445	2 A56043	steroid hormone re
6	438	15.3	446	2 I49021	retinoid X recepto
7	436	15.3	446	2 I59354	orphan nuclear rec
8	423	14.8	479	1 IXBELF	alpha trans-induci
9	423	14.8	490	1 IYBEL7	alpha trans-induci
10	419	14.7	461	2 JC4014	steroid hormone-nu
11	320.5	11.2	484	2 I49018	retinoid X recepto
12	312	10.9	469	2 A56918	farneesoid x-activa
13	302.5	10.6	490	1 IYBE33	alpha trans-induci
14	302.5	10.6	490	2 I59689	vitron protein 16
15	290	10.2	448	2 A43786	retinoic acid rece
16	287.5	10.1	452	2 S74841	retinoic acid rece
17	287.5	10.1	458	2 S06123	retinoic acid rece
18	287	10.0	448	2 B56558	retinoic acid rece
19	287	10.0	455	2 S13512	retinoic acid rece
20	286.5	10.0	459	2 A41977	retinoic acid rece
21	286.5	10.0	464	2 A56558	retinoic acid rece
22	285.5	10.0	448	2 S02827	retinoic acid rece
23	285	10.0	448	2 S05051	retinoic acid rece
24	284	9.9	462	1 A29491	retinoic acid rece
25	284	9.9	955	4 C40045	probable transcrip
26	283	9.9	453	2 I50674	retinoic acid rece
27	282	9.9	462	2 S05050	retinoic acid nucl
28	279.5	9.8	454	2 S06124	retinoic acid rece
29	276	9.7	447	2 B34714	retinoic acid rece

30	274.5	9.6	444	2 I51256	retinoic acid rece
31	274.5	9.6	576	2 A57048	nuclear receptor R
32	274	9.6	458	2 A34714	retinoic acid rece
33	273	9.6	443	1 C35991	retinoic acid rece
34	273	9.6	454	1 A33903	retinoic acid rece
35	271.5	9.5	476	2 B41977	retinoic acid rece
36	269.5	9.4	442	2 A38592	retinoic acid rece
37	267.5	9.4	499	2 I51257	retinoic acid rece
38	261.5	9.2	578	2 S52913	nuclear receptor R
39	257.5	9.0	373	2 C36067	thyroid hormone re
40	257.5	9.0	373	2 D36067	thyroid hormone re
41	255	8.9	508	2 A30226	thyroid/steroid ho
42	254	8.9	388	2 JC7510	benzoate X recepto
43	251.5	8.8	579	2 A57057	orphan nuclear hor
44	251	8.8	373	2 I51165	gene c-erba-beta p
45	248	8.7	386	2 S41497	thyroid hormone re

ALIGNMENTS

RESULT 1

A56590
ecdysteroid receptor homolog cEcRH - midge (Chironomus tentans)
C:Species: Chironomus tentans
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56590
R:Imhof, M.O.; Rusconi, S.; Lezzi, M.
Insect Biochem. Mol. Biol. 23, 115-124, 1993
A:Title: Cloning of a Chironomus tentans cDNA encoding a protein (cEcRH) homologous to
A:Reference number: A56590; MUID:93250857; PMID:8485513
A:Accession: A56590
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-536 <IMH>
A:Cross-references: UNIPROT:P49882; GB:S60739; NID:g385893; PIDN:AAC60500.1; PID:g385894
A:Note: sequence extracted from NCBI backbone (NCBIN:132124, NCBI:P132127)
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; steroid hormone receptor; zinc finger
F:113-432/Domain: erba transforming protein homology <ERBA>

Query Match 36.0%; Score 1029; DB 2; Length 536;
Best Local Similarity 52.0%; Pred. No. 2.5e-61;
Matches 210; Conservative 67; Mismatches 83; Indels 44; Gaps 5;

Qy	97	FVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNKGORQLTVSTRMRPECVV	156
Db	138	FRRSVTKNAVYCKFGHECDMTMRR-----KQCEKRLKCLAVGMRPECVV	186
Qy	157	PESTCKNKRREKAQREKDKLP-----VSTTVT-----DDHMPAIM	192
Db	187	PENQCAIKRKEKKAQKEDKVPYGVSGNTSSSSLLNQSLNGLKNLEISYREELLEQLM	246
Qy	193	QCDPPPEAARIHEVVPFRLTEKLEQNRKNVTPLSANQKSLIARLVWYQEGYQPSSEE	252
Db	247	KCDPPP-----HPMQQLPEKLMENRAGTQTQLTANQAVAVIKLIWYQDGYQPSSEE	299
Qy	253	DLKVTQTQWLEEESEETDMPFQITMTILTQVIVFAKGLPGESKISOSDOITLLK	312
Db	300	DLKRIIT--ELEEEDEQHEANFRYTEVITLTQVIVFAKGLPAFTIKIPOEDQITLLK	357
Qy	313	ASSEVVMMLRVARYDAATDSVLFPANQAVTRDNYRKAGMSYVIEDLHFCRCMYSMSMD	372
Db	358	ACSEVVMMLRVARYDHDSDSILFANNTAYTKQYQLAGMBETIDDLHFCRCMYALSID	417
Qy	373	NVHALLTAIVIFSDRPGLEQPLVBEIQRYYLTKTLRVYILNQHSASPRCAVLFGKILGV	432
Db	418	NVEYALLTAIVIFSDRPGLEKAEWVDIIQSYTTETLKYIVNRRHGSRCSVQPAKLAGI	477
Qy	433	LTELRTGTQNSNWCISLKLNRKLPFLEIWDVAEVSITKLA	476
Db	478	LTELRTGKNKSNCEMFCFLKLRNRKLPFLEEVWDVGDVNNQTTA	521

nuclear orphan receptor LXR-alpha - human

C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 16-Aug-2004
C:Accession: I38975
R:Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
Genes Dev. 9, 1033-1045, 1995
A>Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
A:Reference number: I38975; MUID:95262897; PMID:7744246
A:Accession: I38975
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-447 <RES>
A:CROSS-references: UNIPROT:Q13133; EMBL:U22662; NID:g726512; PIDN:AAA85856.1; PID:g7265
C:Superfamily: erba transforming protein homology
C:Keywords: zinc finger
F:96-367/Domain: erba transforming protein homology <ERBA>

Query Match 15.8%; Score 452.5; DB 2; Length 447;
Best Local Similarity 34.0%; Pred. No. 8e-23;
Matches 111; Conservative 60; Mismatches 108; Indels 47; Gaps 9;

QY 150 MRPECVPESTCKNK--RREKAQREKDKLPVSTTTVDHMPAIMQCDDPPPEAARIHEV 207
DB 163 MREECVLEEQLRLKKLRQEEQAHATSLPPRRS-----PP-----QI 202
QY 208 VPRFTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--EE 265
DB 203 LPQ-----LSPEQLGMIEKLVAAQOCNRRSFSDRLRVTPWMPADP 244
QY 266 EEEETDMPFRQITMTILTVQILVIFAKLPGFSKISQSDQITLLKASSEVMMLRVAR 325
DB 245 HSREARQORFAHFTELAIYSQVEIVDFAKLPGFLQSLREDQIALKTSIEVMLLETSR 304
QY 326 RYDAATDSVLFANNOAYTDRNRYKAGMSY-VIEDLLHFCRCMYSMNDNVHYALLTAIVI 384
DB 305 RYNGPESITFLKDFSYNRDEFKAGLQVEFINPIFEFSRAMELQNDASFALLIAISIF 364
QY 385 FS-DRPGLQEPQLVEEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLGTON 443
DB 365 FSADRPNVQDQLOVERLQHTYVEALHAYVSIH---PHDRLMFPRLMKLVSLRTLSVH 421
QY 444 SNMCISLKLKNRKLPPFLEEIWDVAE 469
DB 422 SEQVFAIRLQDKKLPPLLSEIWDVHE 447

RESULT 5

A56043
steroid hormone receptor-like protein RLD-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A56043
R:Apfel, R.; Benbrook, D.; Lernhardt, B.; Ortiz, M.A.; Salbert, G.; Pfahl, M.
Mol. Cell. Biol. 14, 7025-7035, 1994
A>Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive ele
A:Reference number: A56043; MUID:95021230; PMID:7935418
A:Accession: A56043
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <APP>
A:CROSS-references: UNIPROT:Q62685; GB:U11685; NID:G555751; PIDN:AAA53633.1; PID:G555752
A>Note: authors translated the codon GAG for residue 73 as Ser
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: steroid hormone receptor; zinc finger
F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 15.8%; Score 451.5; DB 2; Length 445;
Best Local Similarity 33.3%; Pred. No. 9.3e-23;
Matches 108; Conservative 62; Mismatches 111; Indels 43; Gaps 7;

QY 150 MRPECVPESTCKNKREKAQREKDKLPVSTTTVDHMPAIMQCDDPPPEAARIHEVVP 209
DB 161 MREECVLEEQLRLKKLRQEEQAHATSVS-----PRVSSPPQVLP 202

QY 210 RFLTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--EBEE 267
DB 203 Q-----LSPEQLGMIEKLVAAQOCNRRSFSDRLRVTPWPIADPQS 244
QY 266 EEEETDMPFRQITMTILTVQILVIFAKLPGFSKISQSDQITLLKASSEVMMLRVAR 327
DB 245 REARQORFAHFTELAIYSQVEIVDFAKLPGFLQSLREDQIALKTSIAEVMMLLETSSRY 304
QY 328 DAATDSVLFANNOAYTDRNRYKAGMSY-VIEDLLHFCRCMYSMNDNVHYALLTAIVIFS 386
DB 305 NPGSESITFLKDFSYNRDEFKAGLQVEFINPIFEFSRAMELQNDASFALLIAISIF 364
QY 387 -DRPGLQEPQLVEEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLGTON 445
DB 365 ADRPNVQDQLOVERLQHTYVEALHAYVSIH---PHDRLMFPRLMKLVSLRTLSVHSE 421
QY 446 MCISLKLKNRKLPPFLEEIWDVAE 469
DB 422 QVFAIRLQDKKLPPLLSEIWDVHE 445

RESULT 6

I49021
retinoid X receptor interacting protein No.15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49021
R:Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-85, 1995
A>Title: Isolation of proteins that interact specifically with the retinoid X receptor:
A:Reference number: A57664; MUID:95280959; PMID:7760852
A:Accession: I49021
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-446 <RES>
A:CROSS-references: UNIPROT:Q60644; EMBL:U09419; NID:G691713; PIDN:AAC52164.1; PID:G6917
C:Genetics: R1P15
C:Superfamily: erba transforming protein homology
C:Keywords: zinc finger
F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 15.3%; Score 438; DB 2; Length 446;
Best Local Similarity 33.6%; Pred. No. 7.5e-22;
Matches 110; Conservative 62; Mismatches 123; Indels 32; Gaps 7;

QY 150 MRPECVPESTCKNKREKAQREKDKLPVSTTTVDHMPAIMQCDDPPPEAARIHEVVP 209
DB 145 MRECVLSEEQIRKKRIKQKQKQ-----PPPESEPAASSSGRP 183
QY 210 RF---LTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--E 264
DB 184 AASPTSEASSQSGEGEGEIGLTAAQELMIQOLVAAQLQCNKRSFSDQPKVT-PMPLGAD 242
QY 265 EEEETDMPFRQITMTILTVQILVIFAKLPGFSKISQSDQITLLKASSEVMMLRVA 324
DB 243 PQSDARQORFAHFTELAIYSQVEIVDFAKVPGFLQGRDQIALKASTIEIMLETA 302
QY 325 RRYDAATDSVLFANNOAYTDRNRYKAGMSY-VIEDLLHFCRCMYSMNDNVHYALLTAIV 383
DB 303 RRYNHETECITFLKDFSYNRDEFKAGLQVEFINPIFEFSRAMELQNDASFALLIAIN 362
QY 384 IFS-DRPGLQEPQLVEEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLTGTQ 442
DB 363 IFSADRPNVQEPSRVEALQQPYVEALLSY---TRIKRPDQQLRFPRLMKLVSLRTLSV 419
QY 443 NSNWCISLKLKNRKLPPFLEEIWDVAE 469
DB 420 HSEQVFAIRLQDKKLPPLLSEIWDVHE 446

RESULT 7

A:Molecule type: mRNA
A:Residues: 1-461 <SH1>
A:Cross-references: UNIPROT:P55055; GB:U07132; NID:G641961; PIDN:AAA61783.1; PID:G641962
A:Experimental source: osteosarcoma cells SAOS-2/B10
C:Genetics:
A:Gene: GDB:UNR

A:Cross-references: GDB:389570; OMIM:600380

A:Map position: 19q13.3-19q13.3

C:Superfamily: erba transforming protein homology

C:Keywords: steroid hormone receptor

F:85-381/Domain: erba transforming protein homology <ERBA>

F:87-154/Domain: DNA binding #status predicted <BIN>

Query Match 14.7%; Score 419; DB 2; Length 461;

Best Local Similarity 33.0%; Pred. No. 1.5e-20;

Matches 108; Conservative 63; Mismatches 130; Indels 26; Gaps 7;

QY 150 MRPECVPESTCKNKRKEAQEKDLPVSTTTVDHMPALMQCDPPPPPEAAARHVEVP 209

DB 154 MREQCVLSEQIRKKIRKQQQESQSQS-----PVGPGSSSSASGP 198

QY 210 RFL---TEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOL--E 264

DB 199 GASPGEAGSGSGEGEVQTAQELMIQQLVAQAQCNKRFSFSDQPKVT-PMPLGAD 257

QY 265 EEEBETDMPFRQITTEMTILTVQILVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRV 324

DB 258 PQSDARQORFAHFTELAIISVQEIYDFAKVQPGFQLGREGDQIALKASTIEIMLETA 317

QY 325 RYDAATOSVLFANNQAYTRDNYRKAGMSY-VIEDLLHFCRCMYSMDNVHYALLTAIV 383

DB 318 RRYNHETECITELKQFTYKSKDFHRAQLQVEFINPIFEFSRAMRLGLDDAEYALLI 377

QY 384 IFS-DRPGLQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTSLTGTQ 442

DB 378 IFSADRPNVQEPGRVEALQOPVEALLSY---TRIKRPQDQLRFPRLMKLVSLRTLSSV 434

QY 443 NSNMICISLKNRKLPPPLEEIDWVAE 469

DB 435 HSEQVFLRLQDKLPPPLSEIWDVHE 461

RESULT 11
I49018
retinoid X receptor interacting protein No.6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49018
R:Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-85, 1995
A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:
A:Reference number: A57664; MUID:95280959; PMID:7760852
A:Accession: I49018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-484 <RES>
A:Cross-references: UNIPROT:Q60641; EMBL:U09416; NID:G691707; PIDN:AAC53066.1; PID:G69171

Query Match 11.2%; Score 320.5; DB 2; Length 484;

Best Local Similarity 31.7%; Pred. No. 6.2e-14;

Matches 102; Conservative 46; Mismatches 129; Indels 45; Gaps 10;

QY 150 MRPECVPESTCKNKRKEAQEKDLPVSTTTVDHMPALMQCDPPPPPEAAARHVEV 207

DB 203 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

QY 208 VPRFLTEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOLEBEE 267

Query Match 11.2%; Score 320.5; DB 2; Length 484;

Best Local Similarity 31.7%; Pred. No. 6.2e-14;

Matches 102; Conservative 46; Mismatches 129; Indels 45; Gaps 10;

QY 150 MRPECVPESTCKNKRKEAQEKDLPVSTTTVDHMPALMQCDPPPPPEAAARHVEV 207

DB 203 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

QY 208 VPRFLTEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOLEBEE 267

DB 203 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

QY 208 VPRFLTEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOLEBEE 267

DB 203 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

QY 208 VPRFLTEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOLEBEE 267

DB 203 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

DB 247 TTKFCREK-----TELTADQOTLLDYIMDSYNKQRMPOE-----ITNKILKEEFS 291

QY 268 BEETDMPFRQITTEMTILTVQILVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRY 327

DB 292 AEEN---FLILTEMATSHVOILVEFTKKLPQFQTLHDHEDQIALKGSVAEMFLRSAEIF 348

QY 328 DAATDSVLFANNQAYTRDNYRKAGMS-YVIEDLLHFCRCMYSMDNVHYALLTAIVTFS 386

DB 349 ----NKKLPAGHADLLERIRKSGISDEYITPMFSFYKSVGELKMTQEBEYALLTAIVLS 404

QY 387 -DRPGLQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTSLTGTQSN 445

DB 405 PDRQYIKDREAVEKLEPLDVLQKCKMYQENPQ---HFACLLGLRTELTFTFNHHA 461

QY 446 MCISLKNRKLPPPLEEIDWV 467

DB 462 MLMSRWVNDHKFTPLLCIWDV 483

RESULT 12
A56918
farnesoid x-activated receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56918
R:Forman, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Perlmann, T.; Noonan, D.J.
Cell 81, 687-695, 1995
A:Title: Identification of a nuclear receptor that is activated by farnesol metabolites
A:Reference number: A56918; MUID:95292336; PMID:7774010
A:Accession: A56918
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-469 <FOR>
A:Cross-references: UNIPROT:Q62735; GB:U18374; NID:G868031; PIDN:AAC52205.1; PID:G868032
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; nucleus; zinc finger
F:122-390/Domain: erba transforming protein homology <ERBA>

Query Match 10.9%; Score 312; DB 2; Length 469;

Best Local Similarity 31.2%; Pred. No. 2.2e-13;

Matches 101; Conservative 47; Mismatches 126; Indels 50; Gaps 11;

QY 150 MRPECVPESTCKNKRKEAQEKDLPVSTTTVDHMPALMQCDPPPPPEAAARHVEVP 209

DB 189 MIAECLELTIQCKSKRLKRVKQHADQ-----TVNE-----DSEGRDLRQVTS 231

QY 210 RFLTEKLMQNRLKNVTPLSANQSLIARLVMYQEGYEQPSBEDLKRVTQTWOLEBEE 269

DB 232 ---TTKLCREK-----TELTVDQOTLLDYIMDSYSKQRMPOE-----ITNKILKEEFS 278

QY 270 ETDMPFRQITTEMTILTVQILVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 329

DB 279 EN---FLILTEMATSHVOILVEFTKKLPQFQTLHDHEDQIALKGSVAEMFLRSAEIF-- 333

QY 330 ATDSVLFANNQAYTRDNYRKAGMS-YVIEDLLHFCRCMYSMDNVHYALLTAIVTFS-D 387

DB 334 --NKKLPAGHADLLERIRKSGISDEYITPMFSFYKSVGELKMTQEBEYALLTAIVLSPD 391

QY 388 RPLGLEQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTSLTGTQSN 443

DB 392 RQYIKDREAVEKLEPLDVLQKCKMYQENPQ---HFACLLGLRTELTFTFNHHA 444

QY 444 SNMISLKNRKLPPPLEEIDWV 467

DB 445 AEMLSMRVNDHKFTPLLCIWDV 468

RESULT 13

IXBE33

alpha trans-inducing protein - human herpesvirus 2 (strain 333)

N:Alternate names: virion transactivator protein Vmw65

C:Species: human herpesvirus 2

A>Note: host Homo sapiens (man)

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C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Feb-1997
C/Accession: A41562
R/Creaves, R.F.; O'Hare, P.
J. Virol. 65, 6705-6713, 1991
A>Title: Sequence, function, and regulation of the Vmw65 gene of herpes simplex virus ty
A/Reference number: A41562; MUID:92046332; PMID:1658370
A/Accession: A41562
A/Molecule type: DNA
A/Residues: 1-490 <GRE>
A/Cross-references: GB:M75098
C/Superfamily: herpesvirus alpha trans-inducing protein
C/Keywords: DNA binding; trans-inducing protein; transcription

Query Match      10.6%; Score 302.5; DB 1; Length 490;
Best Local Similarity 72.6%; Pred. No. 1e-12;
Matches 61; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 470 VSTTKLAPPTDVSGLDELHLDCGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYG 529
Db 410 LSTT--APITDVSGLDELRLDGEVDVMTPADALDDFDLEMLGDVESPSFGMT-HDPVSYG 466

QY 530 ALDMADFEFEQMTDALGIDYGG 553
Db 467 ALDVEDDFEQMTDAMGIDDFGG 490

RESULT 14
JS0689
varion protein 16 - human herpesvirus 2
C/Species: human herpesvirus 2
C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 26-Aug-1999
C/Accession: JS0689
R/Croass, A.; Triebenberg, S.J.
Gene 103, 235-238, 1991
A>Title: Nucleotide and deduced amino acid sequences of the gene encoding virion protein
A/Reference number: JS0689; MUID:91365250; PMID:1653757
A/Accession: JS0689
A/Molecule type: DNA
A/Residues: 1-490 <CRE>
A/Cross-references: GB:M60050; NID:g330317; PIDN:AAA45863.1; PID:g330318
A/Experimental source: strain HG52
C/Superfamily: herpesvirus alpha trans-inducing protein
C/Keywords: DNA binding; transcription regulation

Query Match      10.6%; Score 302.5; DB 2; Length 490;
Best Local Similarity 72.6%; Pred. No. 1e-12;
Matches 61; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 470 VSTTKLAPPTDVSGLDELHLDCGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYG 529
Db 410 LSTT--APITDVSGLDELRLDGEVDVMTPADALDDFDLEMLGDVESPSFGMT-HDPVSYG 466

QY 530 ALDMADFEFEQMTDALGIDYGG 553
Db 467 ALDVEDDFEQMTDAMGIDDFGG 490

RESULT 15
A43786
retinoic acid receptor beta-4 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 11-Dec-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C/Accession: A43786; S14291; A60129; S17072; S16243
R/Smith, S.M.; Eichele, G.
Development 111, 245-252, 1991
A>Title: Temporal and regional differences in the expression pattern of distinct retinoi
A/Reference number: A43786; MUID:91199956; PMID:1849811
A/Accession: A43786
A/Molecule type: mRNA
A/Residues: 1-448 <SM1>
A/Cross-references: UNIPROT:P22448; GB:X59473; NID:g63753; PIDN:CAA42077.1; PID:g63754
A/Note: the authors translated the codon ACT for residue 96 as Ser, TCC for residue 167
R/Noji, S.; Nohno, T.; Koyama, E.; Muto, K.; Ohya, K.; Aoki, Y.; Tamura, K.; Ohnogi, M.

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Nature 350, 83-86, 1991
A>Title: Retinoic acid induces polarizing activity but is unlikely to be a morphogen in
A/Reference number: S14291; MUID:91163640; PMID:1848357
A/Accession: S14291
A/Molecule type: mRNA
A/Residues: 1-95, 'S', '97-448 <NOJ>
A/Cross-references: EMBL:X57340; NID:g62976; PIDN:CAA40616.1; PID:g62977
R/Rowe, A.; Richman, J.M.; Brickell, P.M.
Development 111, 1007-1016, 1991
A>Title: Retinoic acid treatment alters the distribution of retinoic acid receptor-beta
A/Reference number: A60129; MUID:91347912; PMID:1652423
A/Accession: A60129
A/Molecule type: mRNA
A/Residues: 23-24, 26-95, 'S', '97-165, 'D', '167-448 <ROW>
A/Cross-references: GB:S63196; NID:g234370; PIDN:AAB19628.1; PID:g234371
R/Nohno, T.
submitted to the EMBL Data Library, January 1991
A/Reference number: S17072
A/Accession: S17072
A/Molecule type: mRNA
A/Residues: 15-95, 'S', '97-434 <NOH1>
A/Cross-references: EMBL:X57339
R/Nohno, T.; Muto, K.; Noji, S.; Saito, T.; Taniguchi, S.
Biochim. Biophys. Acta 1089, 273-275, 1991
A>Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
A/Reference number: S16243; MUID:91274365; PMID:1647216
A/Accession: S16243
A/Molecule type: mRNA
A/Residues: 15-60 <NOH2>
A/Cross-references: EMBL:X57339
C/Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C/Keywords: alternative splicing; DNA binding; zinc finger
F:79-330/Domain: erba transforming protein homology <ERBA>
F:81-101/Region: zinc finger
F:117-141/Region: zinc finger

Query Match      10.2%; Score 290; DB 2; Length 448;
Best Local Similarity 22.2%; Pred. No. 6.2e-12;
Matches 11; Conservative 86; Mismatches 157; Indels 166; Gaps 19;

QY 69 LLIFPREDLMDLKMDS---LQD--IKALTGLFVQDNVNKDAVTDRLASVETDMLTLR 123
Db 8 LAVSPAQMDFYTAASPSSCMLQEKALKACFSGL-----AQTEW----- 45

QY 124 QHRISAT$-----SSE$-----SSN-----KG-- 140
Db 46 QHRHSAQSVETQSTSSSELPSPPLPPRVYKPCFVCQDKSGYHYGTACGCKGFF 105

QY 141 ----QRLTVSTRMRPCVVPEST-----C-----KNKRKEAQR 172
Db 106 RRSIQKNNVYTCRDKNVCVINKVTRNCQYCRLOKCEVGMSKESVNRDRNKKKKEPTKQ 165

QY 173 EKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEWVPRFLTEKLMQNRLKNVTPLSANQ 232
Db 166 ESTENYEMTAELDD-----LTKIRKA----- 187

QY 233 KSLIARLVWYQEGYEQSPSEEDLKRVTOTWGLEBEEETDMPFRQITEMILTTLVQLIVEP 292
Db 188 -----HQETF--PSCQLGKYTTNSSADHRVRLDLGL-WDKFSELATKCIKIIVEF 235

QY 293 AKGLPGFSKISQSDQITLLKASVSSEVMRLVARYDAATDSVLFANNOAVTRDNYRAGM 352
Db 236 AKLPGFTSITADQITLLKAAACLDILILICITRYTPEQDTWTFSDGLTNRTQHNAGP 295

QY 353 SYVIEDLLHFCRCMYMSMDNVHVALTAT-VIFSDRPGLEQPLLVEEIQRYLKTIRVY 411
Db 296 GPLTDLVFTFANQLLPLEMDDTETGLLSAICLCIGDRQDLDEEPKVDKLEPLLEALKIY 355

QY 412 ILNQHGASPRCAVLFGKILGVLTRELTLGTQNSNMCI$K$K-NRKLPPPLEEWDVAEV 470
Db 356 IRKRPRNPKR---MFPKILMKITDLRSISAKGAERVITL$K$EIPGSMPPPIQEMLENSEG 412
QY 471 STTKLAPPTDVSGLDELHLDCGEDVAMAHADALDDFDLMDLGDGSP 516

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Db 413 H----EPLTPTSGN-----TAHSPSISPSSVDNSSVSQSP 445

Search completed: April 14, 2005, 12:20:32
Job time : 50 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 184 Seconds
(without alignments)
1539.021 Million cell updates/sec

Title: US-10-087-167-105

Perfect score: 2856

Sequence: 1 MKLSSISQACIDRLKXK.....ADFFEQMTDALGIDYGG 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1673	58.6	556	1 ECR_MANSE	P49883 manduca sex
2	1518.5	53.2	518	2 Q8MYA7	Q8mya7 chilo suppr
3	1518.5	53.2	547	2 Q8MYA6	Q8mya6 chilo suppr
4	1497	52.4	541	2 Q6RVD3	Q6rvd3 plodia inte
5	1488.5	52.1	576	1 ECR_HBLVI	O18473 heliothis v
6	1458	51.1	339	2 Q9U0R9	Q9u0r9 junonia coe
7	1437	50.3	606	1 ECR_BOMMO	P49881 bombyx mori
8	1430	50.1	513	2 Q77240	O77240 choristoneu
9	1430	50.1	541	2 Q77255	O77255 choristoneu
10	1381	48.4	346	2 Q9U3U4	Q9u3u4 bicyclus an
11	1116	39.1	680	2 Q9U3Y4	Q9u3y4 aedes alboop
12	1113	39.0	675	1 ECR_ASDAE	P49880 aedes aegypt
13	1113	39.0	776	2 Q6VA69	Q6va69 aedes aegypt
14	1029	36.0	536	1 ECR_CHITE	P49882 chironomus
15	1011	35.4	757	1 ECR_LUCCU	O18531 lucilia cup
16	1007	35.3	784	2 Q9GPH1	Q9gph1 calliphora
17	992	34.7	673	2 Q76827	Q76827 ceratitis c
18	986.5	34.5	878	1 ECR_DROME	P34021 drosophila
19	983	34.4	520	2 Q7FVB2	Q7fwb2 anopheles g
20	849.5	29.7	541	2 Q70795	Q70795 locusta mig
21	838.5	29.4	491	2 O02035	O02035 tenebrio mo
22	764.5	26.8	881	1 GAL4_YEAST	P04386 saccharomyc
23	764.5	26.8	881	2 Q76NW9	Q76nw9 drosophila
24	748.5	26.2	518	2 Q76246	Q76246 uca pugilat
25	739	25.9	444	2 O44336	O44336 amblyomma a
26	739	25.9	560	2 O44337	O44337 amblyomma a
27	739	25.9	570	2 O44338	O44338 amblyomma a
28	711	24.9	336	2 Q6RIB4	Q6rib4 carcinus ma
29	683	23.9	403	2 Q8MRW2	Q8mrw2 scodoptera
30	651	22.8	212	2 Q8MWR0	Q8mwr0 trichoplusi
31	481	16.8	182	2 Q8NGU6	Q8ngu6 sarcophaga

32	479	16.8	181	2	Q75ZW2	Q75zw2 lucilia ser
33	456.5	16.0	402	2	Q8IW13	Q8iw13 homo sapien
34	456.5	16.0	447	1	NRH3_HUMAN	Q13133 homo sapien
35	456	16.0	207	2	Q9XYR8	Q9xyr8 bradyaia hy
36	453.5	15.9	445	2	Q91X41	Q91x41 mus musculu
37	452.5	15.8	445	1	NRH3_MOUSE	Q950y9 mus musculu
38	451.5	15.8	445	1	NRH3_RAT	Q62685 ratus norv
39	438	15.3	443	2	Q8BP65	Q8bp65 mus musculu
40	438	15.3	446	1	NRH2_MOUSE	Q60644 mus musculu
41	436	15.3	446	1	NRH2_RAT	Q62755 ratus norv
42	434.5	15.2	409	2	Q8THU1	Q8thul gallus gall
43	431.5	15.1	409	2	Q8AXU8	Q8axus gallus gall
44	428	15.0	441	2	Q6GMA2	Q6gma2 xenopus lae
45	423	14.8	479	1	ATIN_HHVIF	P04486 human herpe

ALIGNMENTS

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RESULT 1
ECR_MANSE
ID ECR MANSE STANDARD; PRT; 556 AA.
AC P49883;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor).
DS Name=ECR; Synonyms=NRH1;
GN Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95360028; PubMed=7633469; DOI=10.1016/0965-1748(95)00023-O;
RA Fujiwara H., Jindra M., Newitt R., Palli S.R., Hiruma K.,
RA Riddiford L.M.;
RT "Cloning of an ecdysone receptor homolog from Manduca sexta and the
RT developmental profile of its mRNA in wings.";
RL Insect Biochem. Mol. Biol. 25:845-856(1995).
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: It is found in both larval wing disks and
CC pupal wings and in prothoracic glands.
CC -!- DEVELOPMENTAL STAGE: In the wing disks levels increase on day 2
CC sharply on day 6. In the prothoracic glands levels increase
CC sharply on day 6. Then remain high throughout the larval-pupal
CC transformation and after pupal ecdysis.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U19812; AAA86699.1; -.
CC HSSP; P20393; 1A6Y.
CC InterPro; IPR000536; Hrmn_recept_lig.
CC InterPro; IPR001723; Stdhrmn_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; Hormone_recep; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.

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DR ProDom: PD000035; Znf_C4steroid; 1.
DR PROSITE, PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW zinc-finger.
FT FT DOMAIN 1 146 Modulating (Potential).
FT FT DNA_BIND 147 212 Nuclear receptor-type.
FT FT ZN_FING 147 167 C4-type.
FT FT ZN_FING 183 207 C4-type.
FT FT DOMAIN 305 528 Hormone-binding (Potential).
FT FT DOMAIN 75 84 Poly-Gln.
FT FT DOMAIN 258 261 Poly-Pro.
FT FT DOMAIN 326 332 Poly-Glu.
SQ SEQUENCE 556 AA; 62830 MW; 9AF83AA33D551EB1 CRC64;

Query Match 58.6%; Score 1673; DB 1; Length 556;
Best Local Similarity 99.1%; Pred. No. 1.7e-97;
Matches 325; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 150 MRPECVVPSTCKNKRREKEAQREKDKLPVSTTTVDDHMPAIMQCDDPPPPPEAARIHEVVP 209
DB 212 MRPECVVPSTCKNKRREKEAQREKDKLPVSTTTVDDHMPAIMQCDDPPPPPEAARIHEVVP 271
QY 210 RFLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE 269
DB 272 RFLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE 331
QY 270 ETDMPFROIEMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 329
DB 332 ETDMPFROIEMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 391
QY 330 ATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 389
DB 392 ATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 451
QY 390 GLEQPLLVVEEIQRYLYKTLRLVILNQHSASPRCAVLFGKILGLVLTGLTQNSNMCIS 449
DB 452 GLEQPLLVVEEIQRYLYKTLRLVILNQHSASPRCAVLFGKILGLVLTGLTQNSNMCIS 511
QY 450 LKLNKRLPPPLEEINWDVAEVSTTKLAP 477
DB 512 LKLNKRLPPPLEEINWDVAEVSTTKLAP 539

RESULT 2
Q8MYA7 PRELIMINARY; PRT; 518 AA.
AC Q8MYA7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor A isoform.
GN Name=C8Ecr-A;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RX MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
RT two ecdysone receptor isoforms from the rice stem borer Chilo
RT suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB067811; BAC11713.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 518 AA; 58320 MW; 5E757803E248E118 CRC64;

Query Match 53.2%; Score 1518.5; DB 2; Length 518;
Best Local Similarity 86.7%; Pred. No. 9e-88;
Matches 293; Conservative 19; Mismatches 21; Indels 5; Gaps 1;

QY 150 MRPECVVPSTCKNKRREKEAQREKDKLPVSTTTVDDHMPAIMQCDDPPPPPEAARI----- 204
DB 178 MRPECVVPSTCKNKRREKEAQREKDKLPVSTTTVDDHMPAIMQCDDPPPPPEAARIIECLQ 237
QY 205 HEVVPFRLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLE 264
DB 238 HEVVPFRLSEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQSN 297
QY 265 EEEEEETDMPFROIEMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324
DB 298 EDEEETDLPFROIEMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKACSSSEVMMLRVA 357
QY 325 RRYDAATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 384
DB 358 RRYDAASDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 417
QY 385 FSDRPGLEQPLLVVEEIQRYLYKTLRLVILNQHSASPRCAVLFGKILGLVLTGLTQNS 444
DB 418 FSDRPGLEQPLLVVEEIQRYLYKTLRLVILNQHSASPRCAVLFGKILGLVLTGLTQNS 477
QY 445 NMCISLKNRKLPPPLEEINWDVAEVSTTKLAPPTDVS 482
DB 478 NMCISLKNRKLPPPLEEINWDVADVSAAQAPAIMDVA 515

RESULT 3
Q8MYA6 PRELIMINARY; PRT; 547 AA.
AC Q8MYA6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor B1 isoform.
GN Name=C8Ecr-B1;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RX MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
RT two ecdysone receptor isoforms from the rice stem borer Chilo
RT suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB067811; BAC11713.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.

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DR EMBL; AB067812; BAC11714.1; -.
 DR HSSP; P34021; IR00.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdystd receptor.
 DR InterPro; IPR001723; Stdhrmn recept lig.
 DR InterPro; IPR008946; Str ncl receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 547 AA; 61815 MW; 335528572066256E CRC64;

Query Match 53.2%; Score 1518.5; DB 2; Length 547;
 Best Local Similarity 86.7%; Pred. No. 9.7e-88;
 Matches 293; Conservative 19; Mismatches 21; Indels 5; Gaps 1;

QY 150 MRPCVVPESCTCKNKRREKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARI----- 204
 DB 207 MRPCVVPETCAIKRKEKKAQREKDKLPVSTTTVDHMPPTMQCDPPPPPEAARILECLQ 266

QY 205 HEVPRFTEKLMQNRKNVPLSANOKSLIARLVWYQGYEQPSEEDLKRVTOTWOLE 264
 DB 267 HEVPRFSEKLMQNRKNVPLSANOKSLIARLVWYQGYEQPSEEDLKRVTOTWOSN 326

QY 265 EEEETDMPFRQITTEMTILTTLVQVIFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324
 DB 327 EDEEETDLPFRQITTEMTILTTLVQVIFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 386

QY 325 RYDAATSVLFPANNOQTRDNYRKAGMSYVIEDLLHFCRCMYSMNDVHYALLTAIVI 384
 DB 387 RYDAASDVLFPANNOQTRDNYRKAGMAYVIEDLLHFCRCMYSLMDVHYALLTAVVI 446

QY 385 FSDRGLQPLQVIEIORVYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONS 444
 DB 447 FSDRGLQPLQVIEIORVYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONS 506

QY 445 NNCISLKLNRKLPPLFEEIWDVAEVSTTKLAPPTDVS 482
 DB 507 NNCISLKLNRKLPPLFEEIWDVAEVSTTKLAPPTDVS 544

RESULT 4
 Q6RVD3
 ID Q6RVD3 PRELIMINARY; PRT; 541 AA.
 AC Q6RVD3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ecdysone receptor.
 OS Plodia interpunctella (Indianmeal moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Phycitinae; Plodia.
 OX NCBI_TaxID=58824;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slausat D., Debernard S., Bozzolan F., Queguiner I., Porcheron P.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY489269; AAR84611.1; -.
 DR HSSP; P20393; IAGY.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdystd receptor.
 DR InterPro; IPR001723; Stdhrmn recept lig.
 DR InterPro; IPR008946; Str ncl receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 541 AA; 61030 MW; 145588BE2EFA07AD CRC64;

Query Match 52.4%; Score 1497; DB 2; Length 541;
 Best Local Similarity 87.0%; Pred. No. 2.2e-86;
 Matches 288; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

QY 150 MRPCVVPESCTCKNKRREKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARIHEVVP 209
 DB 208 MRPCVVPETCAIKRKEKKAQREKDKLPVSTTTVDHMPPTMQCDPPPPPEAARIHEVVP 267

QY 210 RFLTEKLMQNRKNVPLSANOKSLIARLVWYQGYEQPSEEDLKRVTOTWOLESEEE 269
 DB 268 RFLSKLMQNRKNVPLSANOKSLIARLVWYQGYEQPSEEDLKRVTOTWQPTDEDD 327

QY 270 ETDMPFRQITTEMTILTTLVQVIFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 329
 DB 328 --DMPFRQITTEMTILTTLVQVIFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 385

QY 330 ATDSVLFANNOQTRDNYRKAGMSYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 389
 DB 386 ATDSVLFANNOQTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 445

QY 390 GLEOPLVEETQRYLKLTVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 449
 DB 446 GLEOPLVEETQRYLKLTVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 505

QY 450 LKLNKRLPPLFEEIWDVAEVSTTKLAPPTD 480
 DB 506 LKLNKRLPPLFEEIWDVAEVSTTKLAPPTD 536

RESULT 5
 ECR_HELVI
 ID ECR_HELVI STANDARD; PRT; 576 AA.
 AC 018473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ecdysone receptor (Ecdysteroicd receptor) (20-hydroxy-ecdysone receptor) (20E receptor) (HvEcR).
 OS Name=ECR; Synonyms=NR1H1;
 OS Heliothis virescens (Noctuid moth) (Owlet moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Heliothis.
 OX NCBI_TaxID=7102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRC;
 RX MEDLINE=99457718; PubMed=10528411; DOI=10.1016/S0965-1748(99)00067-3;

RA Martinez A., Scanlon D., Gross B., Perara S.C., Palli S.R.,
 RA Greenland A.J., Windass J., Pongs O., Broad P., Jepson I.;
 RT "Transcriptional activation of the cloned Heliothis virescens
 RT (Lepidoptera) ecdysone receptor (HVECR) by muristeroneA";
 RL Insect Biochem. Mol. Biol. 29:915-930(1999).
 CC -|- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
 CC elements (ECRES) (By similarity).
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; Y09009; CAAY70212.1; -.
 DR PDB; 1R1K; X-ray; D:288-550.
 DR InterPro; IPR005336; Hrmn_recept_lig.
 DR InterPro; IPR001723; Stchrnm_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRODOM; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1_1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR 3D-structure; DNA-binding; Nuclear protein; Receptor;
 KW Transcription regulation; Zinc-finger.
 FT DOMAIN 1 162 Modulating (Potential).
 FT DNA_BIND 163 228 Nuclear receptor-type.
 FT ZN_FING 163 183 C4-type.
 FT ZN_FING 199 223 C4-type.
 FT DOMAIN 326 545 Hormone-binding (Potential).
 SQ SEQUENCE 576 AA; 64638 MW; D13EF787BF263A8 CRC64;

Query Match 52.1%; Score 1488.5; DB 1; Length 576;
 Best Local Similarity 88.1%; Pred. No. 8.2e-86;
 Matches 290; Conservative 19; Mismatches 11; Indels 9; Gaps 2;

Qy 150 MRPECVPESTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDDPPPEAAARI----- 204
 Db 228 MRPECVPEVQCAMKREKAEQKDKLPVSTTTVDHMPPIMQCDPPPEAAARILECVQ 287

Qy 205 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGVEQSEEDLKRVTQTWOLE 264
 Db 288 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGVEQSEEDLKRVTQS----- 343

Qy 265 EEEETDMPFRQITEMITLTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVA 324
 Db 344 DEDSDSDMPFRQITEMITLTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVA 403

Qy 325 RYDAATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVI 384
 Db 404 RYDAATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVI 463

Qy 385 FSDRGLQPLVBEIQRYLTKLTVLYLNQHSASPRCAVLFGKILGVLTELRTLTGTONS 444
 Db 464 FSDRGLQPLVBEIQRYLTKLTVLYLNQHSASPRCAVLFGKILGVLTELRTLTGTONS 523

Qy 445 NNCISLKNRKLPPFLEBEIWDVAEVSST 473
 Db 524 NNCISLKNRKLPPFLEBEIWDVAEVSST 552

RESULT 6
 Q9U0R9

ID Q9U0R9 PRELIMINARY; PRT; 339 AA.
 AC Q9U0R9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Ecdysteroid receptor (Fragment).
 GN Name:ecr;
 OS Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
 OX NCBI_TaxID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Wing;
 RA Reinhardt R.K., Weber P., Koch P.B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.
 DR EMBL; AJ251809; CAB63485.1; -.
 DR HSP; P34021; IR00.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003065; Ecdystd_receptor.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Stchrnm_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR SMART; SM00430; HOL1; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39363 MW; 3EC1C7AD294782EB CRC64;

Query Match 51.1%; Score 1458; DB 2; Length 339;
 Best Local Similarity 87.7%; Pred. No. 3.4e-84;
 Matches 277; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Qy 150 MRPECVPESTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDDPPPEAAARIHEVVP 209
 Db 24 MRPECVPEVQCAMKREKAEQKDKLPVSTTTVDHMPPIMQCDPPPEAAARIHEVVP 83

Qy 210 RLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGVEQSEEDLKRVTQTWOLEEEEE 269
 Db 84 RLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGVEQSEEDLKRVTQTWOLESDDE 143

Qy 270 ETDMPPFRQITEMITLTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDA 329
 Db 144 ESDLPPFRQITEMITLTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDA 203

Qy 330 ATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVIFSDRP 389
 Db 204 TDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVIFSDRP 263

Qy 390 GLEOPLAVEIQRYLTKLTVLYLNQHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 449
 Db 264 GLEOPLAVEIQRYLTKLTVLYLNQHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 323

Qy 450 LKLNKRLPPFLEBEIW 465
 Db 324 LKLNKRLPPFLEBEIW 339

RESULT 7
 ECR_BOMMO

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ID ECR_BOMMO STANDARD; PRT; 606 AA.
AC P49881;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor).
GN Name=ECR; Synonyms=NR1H1;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Myse; TISSUE=Ovary;
RX MEDLINE=95360029; PubMed=7633470; DOI=10.1016/0965-1748(95)00024-P;
RA Swevers L., Drevet J.R., Lunke M.D., Iatrou K.;
RT "The silkmoth homolog of the Drosophila ecdysone receptor (B1
RT isoform): cloning and analysis of expression during follicular cell
RT differentiation.";
RL Insect Biochem. Mol. Biol. 25:857-866(1995).
RN [2]
RP SEQUENCE OF 61-606 FROM N.A.
RC STRAIN=Kinshu X Showa; TISSUE=Fat body;
RA Kamimura M., Tomita S., Fujiwara H.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES). May play a role in the implementation of the
CC chorionic program at the end of vitellogenesis.
CC -!- SUBUNIT: Heterodimer of ECR and Cr1 (potential).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=P49881-1; Sequences=Displayed;
CC Name=2;
CC IsoId=P49881-2; Sequences=VSP 003663;
CC -!- DEVELOPMENTAL STAGE: It is present in constant amounts in
CC follicular cells throughout vitellogenesis but disappears
CC transiently at the onset of chorionogenesis and reappears during the
CC later stages of chorionogenesis.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-61 is the initiator.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L35266; AAA87341.1; -
CC EMBL; L35266; AAA87340.1; -
CC EMBL; D43943; BAA07890.1; -
CC HSSP; P20393; IAGY.
CC InterPro; IPR000536; Hrmn_recept_lig.
CC InterPro; IPR001723; Strdhm_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; Hormone_recep; 1.
CC Pfam; PF00105; Zf-C4; 1.
CC PRINTS; PR00398; STRDHOMER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Alternative splicing; DNA-binding; Nuclear protein; Receptor;
Transcription regulation; Zinc-finger.
FT DOMAIN 1 206 Modulating (Potential).
FT DNA_BIND 207 272 Nuclear receptor-type.
FT ZN_FING 207 227 C4-type.

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FT ZN_FING 243 267 C4-type.
FT DOMAIN 364 586 Hormone-binding (Potential).
FT DOMAIN 134 142 Poly-Gln.
FT DOMAIN 317 320 Poly-Pro.
FT VARSPLIC 380 382 Missing (in isoform 2).
FT CONFLICT 67 67 /FTID=VSP_003663.
FT CONFLICT 81 81 N -> D (in Ref. 2).
FT CONFLICT 108 108 S -> T (in Ref. 2).
FT CONFLICT 469 470 R -> G (in Ref. 2).
FT CONFLICT 591 591 QG -> KA (in Ref. 2).
FT CONFLICT 591 591 A -> P (in Ref. 2).
SQ SEQUENCE 606 AA; 68201 MW; 960EBB9A1E4F2202 CRC64;

Query Match 50.3%; Score 1437; DB 1; Length 606;
Best Local Similarity 83.3%; Pred. No. 1.6e-82;
Matches 280; Conservative 31; Mismatches 15; Indels 10; Gaps 5;

QY 150 MRPCVVPSTCKKREKEAQRKDK---LPVSTTTVDHMPALMQCDPPPPPEAARIHE 206
DB 272 MRPCVTPQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPPPEAARIHE 327
QY 207 VVPRFLTEKLMQNRKLNKVTPLSANOKSLIARLVYQSGYEQPSDEDLKRVTTQTWQLEE 266
DB 328 VVPRFLSEKLMQNRKLNKVTPLSANOKSLIARLVYQSGYEQPSDEDLKRVTTQTWQ--SDE 386
QY 267 EEBETDMPFRQITMTILTQLIVEFAKGLPGFKSKISQSDQITLLKASSSEVMMLRVARR 326
DB 387 EDESDLPFRQITMTILTQLIVEFAKGLPGFKSKISQSDQITLLKASSSEVMMLRVARR 446
QY 327 YDAATSDVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFS 386
DB 447 YDAASDSVLFANNAKAYTRDNYRQGMAYVIEDLLHFCRCMFAMGNDNVHFALLTAIVIFS 506
QY 387 DRPGLEOPLAVEIQRYYLKTLLRVYILNOHSASPRCAVLFGKILGLVLTGLTQNSNM 446
DB 507 DRPGLEOPLVEEIQRYYLNTLRIYIINQNSASRCAYIYGRILSVLTGLTQNSNM 566
QY 447 CISLKLNNRKLPPFLEEIWDVAEVSTT--KLAPPTD 480
DB 567 CISLKLNNRKLPPFLEEIWDVAEVATHTPTVLPPTN 602

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RESULT 8

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O77240
ID O77240 PRELIMINARY; PRT; 513 AA.
AC O77240;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor isoform A.
GN Name=ECR;
OS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricinae; Choristoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99359183; PubMed=10432225; DOI=10.1016/S0303-7207(99)00058-1;
RA Perera S.C., Ladd T.R., Dhaddiala T.S., Krell P.J., Sohli S.S.,
RA Retnakaran A., Palli S.R.;
RT "Studies on two ecdysone receptor isoforms of the spruce budworm,
RT Choristoneura fumiferana.";
RL Mol. Cell. Endocrinol. 152:73-84(1999).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF092030; AAC61596.2; -
DR HSSP; P34021; 1R0O.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

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DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR000536; Hmon_recept_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 513 AA; 57622 MW; F110540A3030E602 CRC64;

Query Match 50.1%; Score 1430; DB 2; Length 513;
Best Local Similarity 80.4%; Pred. No. 3.5e-82;
Matches 270; Conservative 36; Mismatches 26; Indels 4; Gaps 1;

QY 150 MRPECVPESTCKNKRREKAEQKDLPVSTTTVDHHPAIMQCDPPPPPEAARIHEVVP 209
DB 178 MRPECVPESTCKNKRREKAEQKDLPVSTTTVDHHPAIMQCDPPPPPEAARIHEVVP 237
QY 210 RFLTEKLEMEQRLKNVTPLSANOKSLIARLVYQEGYQEPSEEDLKRVTQTWOLEEEEE 269
DB 238 RFLSKLLETRQKNIPQLTANQQLIARLIWYQGYEQSPDEDLKRITQTWQADDENE 297
QY 270 ETDMPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 329
DB 298 ESDTFRQITEMTILTVQLIVEFAKGLPGFAKISQPDQITLLKACSEVMMLRVARYDA 357
QY 330 ATDSVLFPANQAYTRDNRKAGMSVIEDLLHFRCRCMYSMNDVHYALLTAIVIFSDRP 389
DB 358 ASDSVLPANQAYTRDNRKAGMAYVIEDLLHFRCRCMYSMALDNIHYALLTAIVIFSDRP 417
QY 390 GLEQPLLVETORYYKTLRVYILNQHSAPRCVLFGLKILGVLTGLTGTQNSNMCI 449
DB 418 GLEQPLLVETORYYKTLRVYILNQHSAPRCVLFGLKILGVLTGLTGTQNSNMCI 477
QY 450 LKLNKRLPPFLEEIWDVAEVSSTTKLAP----PTDV 481
DB 478 LKLNKRLPPFLEEIWDVADMSHTQPPPLESPTNL 513

RESULT 9
O77255 PRELIMINARY; PRT; 541 AA.
AC O77255;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysteroide receptor Ecr-B.
OS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Choristoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96191152; PubMed=8641050;
RA Kothapalli R., Palli S.R., Ladd T.R., Sohi S.S., Cress D.,
RA Dhadialla T.S., Izertznis G., Retnakaran A.;
RT "Cloning and developmental expression of the ecdysone receptor gene
RT from the spruce budworm, Choristoneura fumiferana.";
RL Dev. Genet. 17:319-330(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kothapalli R., Palli S.R., Ladd T., Retnakaran A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
```



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[1]
RN RP SEQUENCE FROM N.A.
RC RX MEDLINE=20112665; PubMed=10644973;
RA Reinhardt R.K., Weber P., Koch P.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -l- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -l- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AJ251810; CAB63236.1; -.
DR HSSP; P34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR InterPro; IPR003355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR PRINTS; PR01283; ECDYSTERO1DR.
DR PRINTS; PR00398; STRDHMONER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 346
SQ SEQUENCE 346 AA; 40036 MW; 04323E79C2D055D2 CRC64;

Query Match 48.4%; Score 1381; DB 2; Length 346;
Best Local Similarity 82.4%; Pred. No. 2.6e-79;
Matches 266; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

Qy 150 MRPECVPESTCKNKRKEAQRKDLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 204
Db 24 MRPECVPESTCKNKRKEAQRKDLPVSTTTVDHMPAIMQCDPPPPPEAARILECLQ 83

Qy 205 HEVPRFTEKLMQNRKLVNTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWOLE 264
Db 84 HEVPRFTEKLMQNRKLVNTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWOLE 143

Qy 265 EEE--EEETDMPFRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLRV 323
Db 144 TEEIGEASDLPRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLRV 203

Qy 324 ARRYDAATDSVLFANNQAYTRDNRYKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIV 383
Db 204 SRRYDMSTDSVMFANNQAYTREIYNKAGFGYVYIENLLHFCRCMYSMDNVHYALLTAIV 263

Qy 384 IFSDRPGLEQPLVVEEIQRYVYKTLRVYILNQHSASPCAVLFGKILGVLTELRTLGTON 443
Db 264 IFSDRPGLENQPLVVEEIQRYVYKTLRVYILNQHSASPCAVLFGKILGVLTELRTLGTON 323

Qy 444 SNMCSISLKLKNRKLPFPFLEEIWD 466
Db 324 SNMCSISLKLKNRKLPFPFLEEIWD 346

RESULT 11
Q9U3Y4 PRELIMINARY; PRT; 680 AA.
ID Q9U3Y4
AC Q9U3Y4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysteroid receptor.
GN Name=Ecd;
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7160;
RN [1]

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SEQUENCE FROM N.A.
RX DOI=10.1002/(SICI)1520-6327(200002)43:2<87::AID-ARCH5>3.0.CO;2-0;
RA Javachandran G., Fallon A.M.;
RT "Evidence for expression of EcR and USP components of the 20-
hydroxyecdysone receptor by a mosquito cell line.";
RL Arch. Insect Biochem. Physiol. 43:87-96(2000).
CC -l- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -l- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF210733; AAF19032.1; -.
DR HSSP; P34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR PRINTS; PR01283; ECDYSTERO1DR.
DR PRINTS; PR00398; STRDHMONER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 680 AA; 74924 MW; 272C8E6AB1021C98 CRC64;

Query Match 39.1%; Score 1116; DB 2; Length 680;
Best Local Similarity 58.9%; Pred. No. 3.7e-62;
Matches 226; Conservative 59; Mismatches 71; Indels 28; Gaps 8;

Qy 150 MRPECVPESTCKNKRKEAQRKDL-----PVSTTTV-----DDHMPAIMQCDPPPPPEAA 202
Db 255 MRPECVPESTCKNKRKEAQRKDL-----PVSTTTV-----DDHMPAIMQCDPPPPPEAA 310

Qy 203 RIHEVPRFTEKLMQNRKLVNTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWQ 262
Db 311 --HQAIIP--LLPEKLLQENLRNLNIPLLTANQMAVYIKLIWYQDGYEQSPSEDLKRI--MIG 365

Qy 263 LEEEEEETDMPFRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLR 322
Db 366 SPNEEDQDHDVHFPHITTEITLTVQLIVFAKGLPFAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNQAYTRDNRYKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAI 382
Db 426 MARRYDAATDSVLFANNQAYTRDSYRMAGMADTIEDLLHFCRCMFSLTDVNDVYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEEIQRYVYKTLRVYILNQHSASPCAVLFGKILGVLTELRTLTGTQ 442
Db 486 VIFSDRPGLEQAEVVEHIQSYVIDTLRIYILNRHAGDPKCSVIPAKLLSILTLRTLTGNQ 545

Qy 443 NSNMCSISLKLKNRKLPFPFLEEIWDVAVSTTKLAPPTDVSIGDELHLDG---EDVAMAH 499
Db 546 NSEMCFSKLKNRKLPFPFLEEIWDVQDI-----PP---SMQAQWHSHTGTPQSSSSSSSS 596

Qy 500 DALDDFDLMDLGDGSDPGPGFTPH 523
Db 597 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 620

RESULT 12
ECR_AEDAE STANDARD; PRT; 675 AA.
ID ECR_AEDAE
AC P49880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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311 --HQAIP-LPEKLLQNRUNRLEPLLTAQNAVYIKLIWYQDGYEQPSEBDLKRI--MIG 366

263 LEEEBEETDMPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLR 322

366 SPNEEDQHDVHFRHTEITILTVQLIVEFAKGLPAFTKIPQEQITLLKACSSSEVMMLR 425

323 VARRYDAATOSVLFANNOAVTRDNYRKAHGSYVIEDLLHFCRCMYKSMQNDVHYALLTAI 382

426 MARRYDAATOSILFANNRSYTRDSYRMAGMADTTIEDLLHFCRQMFSLTVDNVYALLTAI 485

383 VIFSDRGLRQPLLVERIQRYLKTARVYLINQHSASPRCAVLFGKILGVLTSLRTLTGQ 442

486 VIFSDRGLRQAEVHEHISQSYIDTLRIYILNRHAGDPKCSVIFAKLLSIITELRTLGQ 545

443 NSNMCSLKLNKRLKPLPFLIEINDVAEVSTTKLAPPTDVSLGDELHLHDGEDVAMAHADAL 502

546 NSEMCFSLKLNKRLKPLPFLIEINDVQDI-----PP---SMAQVHSHGTQSSSSSSSS 596

503 DFDLMDLMDGSDSPGPGFTPHDSAPYG 529

597 SS-----SSNGSGNGSSNSNSQHG 618

RESULT 13

Q6VA69 PRELIMINARY; PRT; 776 AA.

ID Q6VA69 PRELIMINARY; PRT; 776 AA.

AC Q6VA69;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE EGRA.

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

OX NCBI_TaxID=1159;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=2227472; PubMed=12385823; DOI=10.1016/S0303-7207(02)00225-3;

RA Wang S.F., Li C., Sun G., Zhu J., Raikhel A.S.;

RA "Differential expression and regulation by 20-hydroxycydysone of

RT mosquito ecdysteroid receptor isoforms A and B.;"

RL Mol. Cell. Endocrinol. 196:29-42(2002).

RN [2]

RP SEQUENCE FROM N.A.

RP Wang S.F., Sun G., Raikhel A.S.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY345989; AAQ23183.1; -.

DR HSP; P20393; IAGY

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.

DR GO; GO:0005496; F:steroid binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPRO031069; Rcdyscd receptor.

DR InterPro; IPRO00536; Hrmomn receptor.

DR InterPro; IPRO01723; Stdhrmn_receptor.

DR InterPro; IPRO08946; Str_ncl_receptor.

DR InterPro; IPRO01628; Znf_C4steroid.

DR Pfam; PF00104; Hormone recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR01283; ECDYSTEROIDS.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

SW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 776 AA; 83645 MW; C9B1E893C08E0CAC CRC64;

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Query Match          39.0%; Score 1113; DB 2; Length 776;
Best Local Similarity 58.1%; Pred. No. 6.9e-62;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

QY 150 MRPECVVPESTCKNKRREKEAQEKDLP-----PVSTTTV---DDHMPAIMQCDDPPPEAA 202
DB 356 MRPECVVPESTCKNKRREKEAQEKDLP-----PVSTTTV---DDHMPAIMQCDDPPPEAA 411
QY 203 RIHEVVPRLTEKLMONRLKNVTPLSANQKSLIARLVWYQGYQPSSEDLKRVTTQW 262
DB 412 --HQAIP--LLPEKLLQENLRNIPLLTANQMAVIVKLIWYQGYQPSSEDLKRI--MIG 466
QY 263 LEEEEEEDMDPRQITENTILTVQIVFAKGLGFCFSKISQSDQITILKASSSEVMMLR 322
DB 467 SNEEEDQHDVFRHHTITILTVQIVFAKGLGFCFSKISQSDQITILKASSSEVMMLR 526
QY 323 VARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSDNVHYALLTAI 382
DB 527 MARRYDAATSDVLFANNSYTRDSYRMAGMATIEDLLHFCRCMYSMSDNVHYALLTAI 586
QY 383 VIFSDRPGLEQPLVEEIQRYVYKTRVYILNQHSASPRCAVLFGKILGVLTFLTGQ 442
DB 587 VIFSDRPGLEQPLVEEIQRYVYKTRVYILNQHSASPRCAVLFGKILGVLTFLTGQ 646
QY 443 NSNMCLISLKNRKLPPFLEEDWDVAEVSITKLAPPTDVLGDELHLDGEDVMAHADAL 502
DB 647 NSNMCLISLKNRKLPPFLEEDWDVAEVSITKLAPPTDVLGDELHLDGEDVMAHADAL 502
QY 503 DFDLDMLGDDGSPGPGFTPHDSAPVG 529
DB 698 SS-----SSNGSSNGSSNSNSSQHG 719

RESULT 14
ID ECR CHITE STANDARD; PRT; 536 AA.
AC P49882;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor) (ECRH).
GN Name=ECR; Synonyms=NRH1;
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93250857; PubMed=8485513; DOI=10.1016/0965-1748(93)90089-B;
RA Imhof M.O., Rusconi S., Lezzi M.;
RT "Cloning of a Chironomus tentans cDNA encoding a protein (cECRH)
RT homologous to the Drosophila melanogaster ecdysteroid receptor
RT (dECR).";
RL Insect Biochem. Mol. Biol. 23:115-124 (1993).
CC -!- FUNCTION: Receptor for ecdysone..Binds to ecdysone response
CC elements (ECRES).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.

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or send an email to license@isb-sib.ch).

EMBL; S60739; AAC60500.1; -
PIR; A56590; A56590.
HSP; P20393; IAGY.
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DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR00536; Hmon_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLJ_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT DOMAIN 1 114 Modulating (Potential).
FT DNA_BIND 115 180 Nuclear receptor-type.
FT ZN_FING 115 135 C4-type.
FT ZN_FING 151 175 C4-type.
FT DOMAIN 290 511 Hormone-binding (Potential).
FT DOMAIN 216 219 Poly-Ser.
FT DOMAIN 307 312 Poly-Glu.
SQ SEQUENCE 536 AA; 61192 MW; 196B0C1CB8048CA7 CRC64;

Query Match          36.0%; Score 1029; DB 1; Length 536;
Best Local Similarity 52.0%; Pred. No. 8.5e-57;
Matches 210; Conservative 67; Mismatches 83; Indels 44; Gaps 5;

QY 97 FVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNKQORQLTVSTRPRPCVV 156
DB 138 FFRSVTKNAVYCKFGHECEMDMYRR-----KQECRLKKCLAVGRPCVV 186
QY 157 PESTCKNKRREKEAQEKDLP-----VSTTTV-----DDHMPAIM 192
DB 187 PENQCAIKRKEKKAQEKDLP-----VSTTTV-----DDHMPAIM 246
QY 193 QCDPPPPPEAARIHEVVPRLTEKLMONRLKNVTPLSANQKSLIARLVWYQGYQPSSE 252
DB 247 KCDPPP-----HPMQQLLPKLLMENRAKGTPLTANQVAVIVKLIWYQGYQPSSE 299
QY 253 DLKRVTTQWLEEEEEEDMDPRQITENTILTVQIVFAKGLGFCFSKISQSDQITILK 312
DB 300 DLKRVTTQWLEEEEEEDMDPRQITENTILTVQIVFAKGLGFCFSKISQSDQITILK 357
QY 313 ASSEVVMKLVARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSMD 372
DB 358 ACSEVVMKLVARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSMD 417
QY 373 NVHYALLTAIVIFSDRPGLEQPLVEEIQRYVYKTRVYILNQHSASPRCAVLFGKILGV 432
DB 418 NVEYALLTAIVIFSDRPGLEQPLVEEIQRYVYKTRVYILNQHSASPRCAVLFGKILGV 477
QY 433 LTELRTGTGNSNMCLISLKNRKLPPFLEEDWDVAEVSITKLAPPTDVLGDELHLDGEDV 476
DB 478 LTELRTGTGNSNMCLISLKNRKLPPFLEEDWDVAEVSITKLAPPTDVLGDELHLDGEDV 521

RESULT 15
ID ECR LUCCU STANDARD; PRT; 757 AA.
AC O18531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor).
GN Name=ECR; Synonyms=NRH1;
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
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Job time : 187 secs

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RP SEQUENCE FROM N.A.
RX MEDLINE=97449774; PubMed=9304790; DOI=10.1016/S0965-1748(97)00019-2;
RA Hannan G.N., Hill R.J.;
RT "Cloning and characterization of LcEGR: a functional ecdysone receptor
RL from the sheep blowfly Lucilia cuprina.";
RL Insect Biochem. Mol. Biol. 27:479-488(1997).
CC 1- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES) (By similarity).
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U75355; AAB81130.1; -.
DR HSP; P20393; IAGY.
DR InterPro; IPR005336; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW zinc-finger.
FT DOMAIN 1 300 Modulating (Potential).
FT DNA_BIND 301 366 Nuclear receptor-type.
FT ZN_FING 301 321 C4-type.
FT ZN_FING 337 361 C4-type.
FT DOMAIN 454 674 Hormone-binding (Potential).
SQ SEQUENCE 757 AA; 83075 MW; C1511452ED37D359 CRC64;

Query Match 35.4%; Score 1011; DB 1; Length 757;
Best Local Similarity 60.8%; Pred. No. 1.9e-55;
Matches 202; Conservative 43; Mismatches 69; Indels 18; Gaps 5;

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QY 208 VPRFLTEKLMQNRUKNVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQWLEBEE 267
DQ 420 CP--LLPEDILAKCOARNIPPLSYNQLAVIYKLIWYQGYQPSSEDLKRIMSS---PDEN 475

QY 268 BEETDMPFROITEMILTQVLIVEFAKGLPGFSKISQSDQITLKASSEVMMLRVARRY 327
DQ 476 ESQHDASFHTEITILTQVLIVEFAKGLPAFTKIPQEDQITLLKACSEVMMLRMARRY 535

QY 328 DAATDSVLFPANQAYTRDNYRKAGMSYVIEDLLHFCRCMYGMSMDNVHYALLTAIVFSD 387
DQ 536 DHNSDSIFPANNRSYTRDSYKMGADNIEDLLHFCRCMYGMSKMDNVEYALLTAIVFSD 595

QY 388 RGLSQPLLVIEIQRYLKLRYILNQHSAPRCVLFGLKILGVLTELRTLTGTONSMC 447
DQ 596 RGLSEAEALVIAIQSYIIDTLRIYILNRHCGDPSMLVFFAKLLSLTELRTLTGNAEMC 655

QY 448 ISLKLNRKLPPLFSEIWDVAEVSATKLAAPT 479
DQ 656 FSLKLNKRLPKFLEIWDVHAI-----PPS 681
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:39 ; Search time 44 Seconds
(without alignments)
938.203 Million cell updates/sec

Title: US-10-087-167-105
Perfect score: 2856
Sequence: 1 MKLSSIEQACDICKLKLK.....ADFFEQMTDALGIDEYGG 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661	58.2	556	US-09-564-418-11	Sequence 11, Appl
2	1650.5	57.8	557	US-08-653-648A-12	Sequence 12, Appl
3	1507	52.8	546	US-09-393-839-2	Sequence 2, Appl
4	1479.5	51.8	575	US-08-653-648A-5	Sequence 5, Appl
5	1479.5	51.8	575	US-09-564-418-5	Sequence 5, Appl
6	1446	50.6	319	US-08-653-648A-7	Sequence 7, Appl
7	1446	50.6	319	US-09-564-418-13	Sequence 13, Appl
8	1437	50.3	606	US-08-891-298-3	Sequence 3, Appl
9	1425	49.9	606	US-08-653-648A-11	Sequence 11, Appl
10	1425	49.9	606	US-09-564-418-10	Sequence 10, Appl
11	1412.5	49.5	314	US-08-653-648A-16	Sequence 16, Appl
12	1412.5	49.5	314	US-09-564-418-7	Sequence 7, Appl
13	1113	39.0	674	US-08-653-648A-14	Sequence 14, Appl
14	1113	39.0	675	US-09-564-418-12	Sequence 12, Appl
15	1112.5	39.0	560	US-09-435-019-6	Sequence 6, Appl
16	1112.5	39.0	560	US-09-435-019-9	Sequence 9, Appl
17	1112.5	39.0	560	US-10-065-200A-6	Sequence 6, Appl
18	1112.5	39.0	560	US-10-065-200A-9	Sequence 9, Appl
19	1112.5	39.0	561	US-09-435-019-14	Sequence 14, Appl
20	1112.5	39.0	561	US-09-435-019-17	Sequence 17, Appl
21	1112.5	39.0	561	US-10-065-200A-14	Sequence 14, Appl
22	1112.5	39.0	561	US-10-065-200A-17	Sequence 17, Appl
23	1010	35.4	536	US-08-653-648A-13	Sequence 13, Appl
24	1010	35.4	536	US-09-564-418-9	Sequence 9, Appl
25	1000.5	35.0	226	US-09-133-321-2	Sequence 2, Appl
26	988.5	34.6	746	US-09-042-488B-5	Sequence 5, Appl
27	986.5	34.5	550	US-08-659-188-18	Sequence 18, Appl

28	986.5	34.5	550	3	US-08-655-227-18	Sequence 18, Appl
29	986.5	34.5	550	3	US-08-655-241-18	Sequence 18, Appl
30	986.5	34.5	550	3	US-09-398-326-18	Sequence 18, Appl
31	986.5	34.5	550	4	US-09-853-450-18	Sequence 18, Appl
32	986.5	34.5	746	4	US-09-042-488B-7	Sequence 7, Appl
33	986.5	34.5	1041	4	US-09-042-488B-9	Sequence 9, Appl
34	986.5	34.4	746	3	US-09-144-759-18	Sequence 18, Appl
35	982.5	34.4	746	4	US-09-570-267-18	Sequence 18, Appl
36	982.5	34.4	764	3	US-09-144-759-20	Sequence 20, Appl
37	982.5	34.4	764	4	US-09-570-267-20	Sequence 20, Appl
38	966	33.8	878	3	US-08-653-648A-15	Sequence 15, Appl
39	966	33.8	878	4	US-09-564-418-8	Sequence 8, Appl
40	876	30.7	231	4	US-09-324-258-20	Sequence 20, Appl
41	827.5	29.0	219	4	US-09-435-019-65	Sequence 65, Appl
42	827.5	29.0	219	4	US-09-435-019-67	Sequence 67, Appl
43	827.5	29.0	219	4	US-10-065-200A-65	Sequence 65, Appl
44	827.5	29.0	219	4	US-10-065-200A-67	Sequence 67, Appl
45	768	26.9	496	4	US-08-840-713-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-564-418-11
; Sequence 11, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martineez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-564-418-11

Query Match	58.2%	Score 1661;	DB 4;	Length 556;
Best Local Similarity	98.8%	Pred. No. 1.1e-138;		
Matches 324;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
QY	150	MRPCVVPPESTCKNKRREKAQREKDKLPVSTTTTVDHMPAIMOCDDPPPPPEAARITHEVVP	209	
Db	212	MRPCVVPPESTCKNKRREKAQREKDKLPVSTTTTVDHMPAIMOCDDPPPPPEAARITHEVVP	271	
QY	210	RFLTEKLEMEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE	269	
Db	272	RFLTEKLEMEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE	331	
QY	270	ETDMPFRQITMTLTVOLIVEPAKGLPGFSGKISQSDQITLLKASSSVMMMLRVARRYDA	329	
Db	332	ETDMPFRQITMTLTVOLIVEPAKGLPGFSGKISQSDQITLLKASSSVMMMLRVARRYDA	391	
QY	330	ATDSVLFPANNQAYTRDNVRKAGMSVYEDLLHFCRCMYSMDNVHVALLTAVIFSDRP	389	
Db	392	ATDSVLFPANNQAYTRDNVRKAGMSVYEDLLHFCRCMYSMDNVHVALLTAVIFSDRP	451	
QY	390	GLEQPLAVEEIQRYLKTLLRVYILNQHSASPRCAVLFGKILGVLTELRTLTGTONSMCIS	449	
Db	452	GLEQPLAVEEIQRYLKTLLRVYILNQHSASPRCAVLFGKILGVLTELRTLTGTONSMCIS	511	
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RESULT 2
US-08-653-648A-12
; Sequence 12, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martine, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Manduca sexta
US-08-653-648A-12

Query Match      57.8%; Score 1650.5; DB 3; Length 557;
Best Local Similarity 98.5%; Pred. No. 9.6e-138; Indels 1; Gaps 1;
Matches 324; Conservative 1; Mismatches 3;

Qy 150 MRPECVVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARIHEVVP 209
Db 212 MRPECVVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARIHEVVP 271

Qy 210 RPLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLEBEE 268
Db 272 RPLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLEBEE 331

Qy 269 EBTDMPPFQITMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYD 328
Db 332 EBTDMPPFQITMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYD 391

Qy 329 AATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDR 388
Db 392 AATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDR 451

Qy 389 PGLEQPLLVVEEIQRYLYKTLRVYILNOHSASPRCAVLFCKILGVLTLELTGTONSMCI 448
Db 452 PGLEQPLLVVEEIQRYLYKTLRVYILNOHSASPRCAVLFCKILGVLTLELTGTONSMCI 511

Qy 449 SLKLNKRLKLPPLLEEIWDVAEVSTTKLAP 477
Db 512 SLKLNKRLKLPPLLEEIWDVAEVSTTKLAP 540

RESULT 3
US-09-393-839-2
; Sequence 2, Application US/09393839
; Patent No. 6504082
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooker, Catherine D.
; APPLICANT: Garnaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/09/393,839
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-09-393-839-2

Query Match      52.8%; Score 1507; DB 4; Length 546;
Best Local Similarity 87.4%; Pred. No. 4.9e-125; Indels 6; Gaps 2;
Matches 291; Conservative 19; Mismatches 17;

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Db 206 MRPECVVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARILECLQ 265

Qy 205 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 264
Db 266 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 325

Qy 265 EBEETDMPPFQITMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324
Db 326 DEEDSDMPFQITMTILTVQLIVVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 385

Qy 325 RRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 384
Db 386 RRYDAVSDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 445

Qy 385 FSDRPGLEQPLLVVEEIQRYLYKTLRVYILNOHSASPRCAVLFCKILGVLTLELTGTONS 444
Db 446 FSDRPGLEQPLLVVEEIQRYLYKTLRVYILNOHSASPRCAVLFCKILGVLTLELTGTONS 505

Qy 445 NMCISLKNKRLKLPPLLEEIWDVAEVSTTKLAP 477
Db 506 NMCISLKNKRLKLPPLLEEIWDVAEVSTTKLAP 537

RESULT 4
US-08-653-648A-5
; Sequence 5, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martine, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-08-653-648A-5

Query Match      51.8%; Score 1479.5; DB 3; Length 575;
Best Local Similarity 87.5%; Pred. No. 1.5e-122; Indels 9; Gaps 2;
Matches 288; Conservative 20; Mismatches 12;

Qy 150 MRPECVVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARI----- 204
Db 228 MRPECVVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARILECVQ 287

Qy 205 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 264
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Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS----- 343
Qy 265 EEEBETDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVA 324
Db 344 DEDDSDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKACSEVMMLRVA 403
Qy 325 RYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 384
Db 404 RYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 463
Qy 385 FSDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 444
Db 464 FSDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 523
Qy 445 NNCISLKLKRNKLPPLFLEIMDVAVSTT 473
Db 524 NNCISLKLKRNKLPPLFLEIMDVAVT 552

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RESULT 5

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US-09-564-418-5
; Sequence 5, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-5

```

```

Query Match 51.8%; Score 1479.5; DB 4; Length 575;
Best Local Similarity 87.5%; Pred. No. 1.5e-122;
Matches 288; Conservative 20; Mismatches 12; Indels 9; Gaps 2;

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Qy 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 204
Db 228 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 287
Qy 205 HEVPRFLTEKLMQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 264
Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS----- 343
Qy 265 EEEBETDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVA 324
Db 344 DEDDSDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKACSEVMMLRVA 403
Qy 325 RYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 384
Db 404 RYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 463
Qy 385 FSDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 444
Db 464 FSDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 523
Qy 445 NNCISLKLKRNKLPPLFLEIMDVAVSTT 473
Db 524 NNCISLKLKRNKLPPLFLEIMDVAVT 552

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RESULT 6

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US-08-653-648A-7
; Sequence 7, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-7

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Query Match 50.6%; Score 1446; DB 3; Length 319;
Best Local Similarity 87.9%; Pred. No. 5.8e-120;
Matches 284; Conservative 17; Mismatches 12; Indels 10; Gaps 3;

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Qy 151 RPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI-----H 205
Db 1 RPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI-----H 205
Qy 206 EVPRFLTEKLMQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 265
Db 61 EVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS-----D 116
Qy 266 EEEBETDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVAR 325
Db 117 EDESDMPFRQITTEMILTTLVQVEFAKGLPGFSGKISQSDQITLLKACSEVMMLRVAR 176
Qy 326 RYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 385
Db 177 RYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 236
Qy 386 SDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 445
Db 237 SDRGLQPLVBEIQRYLKTLYILNQHSASPRCAVLFKGLVLTGLTGTQNS 296
Qy 446 MCISLKLKRNKLPPLFLEI-WDV 467
Db 297 MCISLKLKRNKLPPLFLEI-WDV 319

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RESULT 7

```

US-09-564-418-13
; Sequence 13, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0

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; SEQ ID NO 13
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-13

Query Match      50.6%; Score 1446; DB 4; Length 319;
Best Local Similarity 87.9%; Pred. No. 5.8e-120; Indels 10; Gaps 3;
Matches 284; Conservative 17; Mismatches 12;

Qy 151 RPECVVPSTCKNKRREKAQREKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI-----H 205
Db 1 RPECVVPENQCAMKEKKAQREKDKLPVSTTTVDHMPPIMQCDPPPPPEAARILECVQH 60

Qy 206 EVVPRFLTEKLMQNRNLKNTPLSANQKSLIARLVVYQEGYEQSEEDLKRVTQTWOLEE 265
Db 61 EVVPRFLNEKLMQNRNLKNTPLSANQKSLIARLVVYQEGYEQSEEDLKRVTQS----D 116

Qy 266 EEEETDMPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 325
Db 117 EDEEDSDMPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 176

Qy 326 RYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIF 385
Db 177 RYDAATDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIF 236

Qy 386 SDRPGLQPLVVEIQRYLYKTLRVYILNQHSASPRCAVLFGKILGVLTUETLRTLTGTONSN 445
Db 237 SDRPGLQPLVVEIQRYLYKTLRVYILNQHSASPRGAVIFGEILGILTEIRTLGMSQNSN 296

Qy 446 MCISLKLKRNKLPPLPLEEII-WDV 467
Db 297 MCISLKLKRNKLPPLPLEEIDWDV 319

RESULT 8
US-08-891-298-3
; Sequence 3, Application US/08891298
; Patent No. 6300488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; APPLICANT: Suhr, Steven T.
; TITLE OF INVENTION: Modified Lepidopteran Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.00
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TBLEX:
```

```
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-891-298-3

Query Match      50.3%; Score 1437; DB 3; Length 606;
Best Local Similarity 83.3%; Pred. No. 9.3e-119;
Matches 280; Conservative 31; Mismatches 15; Indels 10; Gaps 5;

Qy 150 MRPECVVPSTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDPPPPPEAARIHE 206
Db 272 MRPECVQEPS-KYKDRQHQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPPPEAARIHE 327

Qy 207 VVPRFLTEKLMQNRNLKNTPLSANQKSLIARLVVYQEGYEQSEEDLKRVTQTWOLEE 266
Db 328 VVPRYISEKLMQNRQKNIPPLSANQKSLIARLVVYQEGYEQSEEDLKRVTQTWQ--SDE 386

Qy 267 EEEETDMPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARR 326
Db 387 EDESDLPFRQITEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARR 446

Qy 327 YDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFS 386
Db 447 YDAATDSVLFANNOAYTRDNYRQGGMAYVIEDLLHFCRCMFMGMNDNVHYALLTAIVIFS 506

Qy 387 DRPGLQPLVVEIQRYLYKTLRVYILNQHSASPRCAVLFGKILGVLTUETLRTLTGTONSNM 446
Db 507 DRPGLQPLVVEIQRYLYKTLRVYILNQHSASPRCAVIYGRILSVLTUETLRTLTGTONSNM 566

Qy 447 CISLKLKRNKLPPLPLEEIMDVAEVSTT--KLAPPTD 480
Db 567 CISLKLKRNKLPPLPLEEIMDVAEVATHTPTVLPPTN 602

RESULT 9
US-08-653-648A-11
; Sequence 11, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-08-653-648A-11

Query Match      49.9%; Score 1425; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 1.1e-117;
Matches 278; Conservative 31; Mismatches 17; Indels 10; Gaps 5;

Qy 150 MRPECVVPSTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDPPPPPEAARIHE 206
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Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPEAARIHE 327
Qy 207 VVPRFLEKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQLEEE 266
Db 328 VVPRYLSKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQ-SDE 386
Qy 267 EEEETDMPFRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 326
Db 387 EDEESDLPRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 446
Qy 327 YDAATDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 386
Db 447 YDAASDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 506
Qy 387 DRPGLQEPQLVEEIQRYVLTNRVYILNQHSASPRCAVLFKGLVLTTELRTLTGQNSNM 446
Db 507 DRPGLQEPQLVEEIQRYVLTNRVYILNQHSASPRCAVYIGRILSVLTTELRTLTGQNSNM 566
Qy 447 CISLKLNRKLPPLFLEEIWDVAEVS--TKLAPPTD 480
Db 567 CISLKLNRKLPPLFLEEIWDVAEVARRHPTVLPPTN 602

RESULT 10
US-09-564-418-10
; Sequence 10, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-09-564-418-10

Query Match 49.9%; Score 1425; DB 4; Length 606;
Best Local Similarity 82.7%; Pred. No. 1.1e-117;
Matches 278; Conservative 31; Mismatches 17; Indels 10; Gaps 5;

Qy 150 MRPECVPESTCKNRKEKQREKDK--LPVSTTTVDHMPPIMQCDPPPEAARIHE 206
Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPEAARIHE 327
Qy 207 VVPRFLEKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQLEEE 266
Db 328 VVPRYLSKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQ-SDE 386
Qy 267 EEEETDMPFRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 326
Db 387 EDEESDLPRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 446
Qy 327 YDAATDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 386
Db 447 YDAASDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 506
Qy 387 DRPGLQEPQLVEEIQRYVLTNRVYILNQHSASPRCAVLFKGLVLTTELRTLTGQNSNM 446
Db 507 DRPGLQEPQLVEEIQRYVLTNRVYILNQHSASPRCAVYIGRILSVLTTELRTLTGQNSNM 566
Qy 447 CISLKLNRKLPPLFLEEIWDVAEVS--TKLAPPTD 480
Db 567 CISLKLNRKLPPLFLEEIWDVAEVARRHPTVLPPTN 602

RESULT 11
US-08-653-648A-16
; Sequence 16, Application US/08653648A
; Patent No. 6379345
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; APPLICANT: A Gene Switch
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-16

Query Match 49.5%; Score 1412.5; DB 3; Length 314;
Best Local Similarity 86.5%; Pred. No. 5.3e-117;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 151 RPECVPESTCKNRKEKQREKDKLPVSTTTVDHMPPIMQCDPPPEAARIHEVVP 210
Db 1 RPECVPESTCKNRKEKQREKDKLPVSTTTVDHMPPIMQCDPPPEAARIHEVVP 60
Qy 211 FLTEKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQLEEE 270
Db 61 FLTEKLMQNRKKNVTPLSANQKSLIARLVVYQEGYQPSDEDLKRVTTQTWQ-SDE 116
Qy 271 TDMPEFRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAA 330
Db 117 SDMPFRQITTEMILTTLVQIVFPAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAA 176
Qy 331 TDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 390
Db 177 TDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMTSMNDNVHYALLTAIVIFS 236
Qy 391 LEQPLLVVEEIQRYVLTNRVYILNQHSASPRCAVLFKGLVLTTELRTLTGQNSNM 450
Db 237 LEUTLLVVEEIQRYVLTNRVYILNQHSASPRCAVYIGRILSVLTTELRTLTGQNSNM 296
Qy 451 KLKRNKLPPLFLEEIWDV 467
Db 297 KLKRNKLPPLFLEEIWDV 314

RESULT 12
US-09-564-418-7
; Sequence 7, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418

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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-09-564-418-7

Query Match          49.5%; Score 1412.5; DB 4; Length 314;
Best Local Similarity 86.5%; Pred. No. 5.3e-117;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 151 RPECVPESTCKNKRREKAEQKDLVSTTTVDHHPALMOCDPPPEAARTHEVVPR 210
Db 1 RPECVVPENQCAIKRREKAEQKDLVSTTTVDHHPALMOCDPPPEAARTHEVVPR 60

Qy 211 FLTEKLMQENRLKNVTPLSANQKSLIARLVMYQEGYQPSSEDLKRVTTQWQLBEEBEE 270
Db 61 FLNEKLMERTLRNVPLITANQKSLIARLVMYQEGYQPSSEDLKRVTTQWQLBEEBEE 116

Qy 271 TDMFPRQITMTILTVQILVFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDAA 330
Db 117 SDMPFPRQITMTILTVQILVFAKGLPAFAKISQSDQITLLKASSEVMMLRVARRYDAA 176

Qy 331 TDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 390
Db 177 TDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 236

Qy 391 LEQPLLVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQNSNMCISL 450
Db 237 LELTLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQNSNMCISL 296

Qy 451 KLRKRLPPFLVEEIMDV 467
Db 297 KLRNRVPPFEDIDMV 314

RESULT 13
US-08-653-648A-14
; Sequence 14, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; PRIOR FILING DATE: 1996-05-24
; PRIOR FILING DATE: 1995-05-26
; PRIOR FILING DATE: 1995-05-26
; PRIOR FILING DATE: 1996-03-18
; PRIOR FILING DATE: 1995-07-07
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-08-653-648A-14

Query Match          39.0%; Score 1113; DB 3; Length 674;
Best Local Similarity 58.1%; Pred. No. 5.9e-90;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

Qy 150 MRPECVPESTCKNKRREKAEQKDL-----PVSTTTV---DDHMPAIMQCDPPPEAA 202
Db 255 MRPECVVPENQCAIKRREKAEQKDLKQVQTNATVSTTNSYRSEILFILMKCDPPP----- 310

Qy 203 RIHEVVPRFLTEKLMQENRLKNVTPLSANQKSLIARLVMYQEGYQPSSEDLKRVTTQW 262
Db 311 --HQAIPL--LPEKQLQENRLNIPLTANQMAVIYKLIWYQDGYEQPSSEDLKRI--MIG 365

Qy 263 LEEEBEETDMPFPRQITMTILTVQILVFAKGLPGFSKISQSDQITLLKASSEVMMLR 322
Db 366 SPNEEDQHDVHFRHTEITILTVQILVFAKGLPAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAI 382
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMYSMNDNVHYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQ 442
Db 486 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQ 545

; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-09-564-418-7

Query Match          49.5%; Score 1412.5; DB 4; Length 314;
Best Local Similarity 86.5%; Pred. No. 5.3e-117;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 151 RPECVPESTCKNKRREKAEQKDLVSTTTVDHHPALMOCDPPPEAARTHEVVPR 210
Db 1 RPECVVPENQCAIKRREKAEQKDLVSTTTVDHHPALMOCDPPPEAARTHEVVPR 60

Qy 211 FLTEKLMQENRLKNVTPLSANQKSLIARLVMYQEGYQPSSEDLKRVTTQWQLBEEBEE 270
Db 61 FLNEKLMERTLRNVPLITANQKSLIARLVMYQEGYQPSSEDLKRVTTQWQLBEEBEE 116

Qy 271 TDMFPRQITMTILTVQILVFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDAA 330
Db 117 SDMPFPRQITMTILTVQILVFAKGLPAFAKISQSDQITLLKASSEVMMLRVARRYDAA 176

Qy 331 TDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 390
Db 177 TDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 236

Qy 391 LEQPLLVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQNSNMCISL 450
Db 237 LELTLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQNSNMCISL 296

Qy 451 KLRKRLPPFLVEEIMDV 467
Db 297 KLRNRVPPFEDIDMV 314

RESULT 14
US-09-564-418-12
; Sequence 12, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-09-564-418-12

Query Match          39.0%; Score 1113; DB 4; Length 675;
Best Local Similarity 58.1%; Pred. No. 5.9e-90;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

Qy 150 MRPECVPESTCKNKRREKAEQKDL-----PVSTTTV---DDHMPAIMQCDPPPEAA 202
Db 255 MRPECVVPENQCAIKRREKAEQKDLKQVQTNATVSTTNSYRSEILFILMKCDPPP----- 310

Qy 203 RIHEVVPRFLTEKLMQENRLKNVTPLSANQKSLIARLVMYQEGYQPSSEDLKRVTTQW 262
Db 311 --HQAIPL--LPEKQLQENRLNIPLTANQMAVIYKLIWYQDGYEQPSSEDLKRI--MIG 365

Qy 263 LEEEBEETDMPFPRQITMTILTVQILVFAKGLPGFSKISQSDQITLLKASSEVMMLR 322
Db 366 SPNEEDQHDVHFRHTEITILTVQILVFAKGLPAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNOAYTRDNYRKAGSVYVIEDLLHFCRCMYSMNDNVHYALLTAI 382
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMYSMNDNVHYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQ 442
Db 486 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVILNQHSGASPRCAVLFGKILGLVLTTELRTLTGQ 545
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RESULT 15
US-09-435-019-6
; Sequence 6, Application US/09435019
; Patent No. 6489140
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Becher, Anna M.
; APPLICANT: Jarvis, Eric
; TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPIRACLE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-4
; CURRENT APPLICATION NUMBER: US/09/435,019
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 60/107,559
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Ctеноcephalides felis
US-09-435-019-6

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Search completed: April 14, 2005, 12:27:32
Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:39 ; Search time 137 Seconds
(without alignments)
1341.613 Million cell updates/sec

Title: US-10-087-167-105

Perfect score: 2856

Sequence: 1 MKLSSIEQACDICRLKCLK.....ADPFEQMTDALGIDYGG 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 312370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2856	100.0	553	14 US-10-087-167-105	Sequence 105, App
2	2803	98.1	588	14 US-10-087-167-123	Sequence 123, App
3	2786.5	97.6	599	14 US-10-087-167-127	Sequence 127, App
4	2738.5	95.9	591	14 US-10-087-167-119	Sequence 119, App
5	2731	95.6	588	14 US-10-087-167-121	Sequence 121, App
6	2661.5	93.2	593	14 US-10-087-167-125	Sequence 125, App
7	2442.5	85.5	615	14 US-10-087-167-135	Sequence 135, App
8	2440	85.4	620	14 US-10-087-167-137	Sequence 137, App
9	2433	85.2	475	14 US-10-087-167-129	Sequence 129, App
10	2428	85.0	602	14 US-10-087-167-143	Sequence 143, App
11	2381.5	83.4	599	14 US-10-087-167-148	Sequence 148, App
12	2100	73.5	505	14 US-10-087-167-94	Sequence 94, Appl
13	2047	71.7	499	14 US-10-087-167-70	Sequence 70, Appl

14	2030.5	71.1	510	14	US-10-087-167-80	Sequence 80, Appl
15	1982.5	69.4	502	14	US-10-087-167-66	Sequence 66, Appl
16	1975	69.2	499	14	US-10-087-167-68	Sequence 68, Appl
17	1913	67.0	507	14	US-10-087-167-78	Sequence 78, Appl
18	1905.5	66.7	504	14	US-10-087-167-76	Sequence 76, Appl
19	1816	63.6	521	14	US-10-087-167-90	Sequence 90, Appl
20	1791.5	62.7	516	14	US-10-087-167-72	Sequence 72, Appl
21	1763	61.7	487	14	US-10-087-167-84	Sequence 84, Appl
22	1725.5	60.4	500	14	US-10-087-167-92	Sequence 92, Appl
23	1712	59.9	501	14	US-10-087-167-64	Sequence 64, Appl
24	1674	58.6	513	14	US-10-087-167-74	Sequence 74, Appl
25	1673	58.6	556	14	US-10-083-842A-7	Sequence 7, Appl
26	1673	58.6	556	14	US-10-087-167-2	Sequence 2, Appl
27	1661	58.6	556	15	US-10-606-060A-11	Sequence 11, Appl
28	1617.5	56.2	496	14	US-10-087-167-86	Sequence 86, Appl
29	1507	52.8	546	14	US-10-295-370-2	Sequence 2, Appl
30	1507	52.8	546	14	US-10-292-356-2	Sequence 2, Appl
31	1507	52.8	546	14	US-10-292-324-2	Sequence 2, Appl
32	1479.5	51.8	575	15	US-10-606-060A-5	Sequence 5, Appl
33	1446	50.6	319	15	US-10-606-060A-13	Sequence 13, Appl
34	1441.5	50.5	516	14	US-10-087-167-88	Sequence 88, Appl
35	1437	50.3	606	9	US-09-952-559-3	Sequence 3, Appl
36	1430	50.1	401	15	US-10-468-199-70	Sequence 70, Appl
37	1430	50.1	412	9	US-09-985-703-11	Sequence 11, Appl
38	1430	50.1	412	9	US-09-985-703-12	Sequence 12, Appl
39	1430	50.1	412	15	US-10-239-134-11	Sequence 11, Appl
40	1430	50.1	412	15	US-10-239-134-12	Sequence 12, Appl
41	1430	50.1	440	9	US-09-965-703-71	Sequence 71, Appl
42	1430	50.1	440	15	US-10-239-134-63	Sequence 63, Appl
43	1430	50.1	513	9	US-09-985-703-59	Sequence 59, Appl
44	1430	50.1	513	15	US-10-239-134-50	Sequence 50, Appl
45	1425	49.9	606	15	US-10-606-060A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-087-167-105
; Sequence 105, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 105
; LENGTH: 553
; TYPE: PRT
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3972)
; OTHER INFORMATION: GAL4-Manduca ECR-VP16 fragment in pCGS202
US-10-087-167-105

Query Match 100.0%; Score 2856; DB 14; Length 553;
Best Local Similarity 100.0%; Pred. No. 2e-229;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSSIEQACDICRLKCLKSKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVSSR 60
DB 1 MKLSSIEQACDICRLKCLKSKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVSSR 60

Qy 61 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
 Db 61 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
 Qy 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 180
 Db 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 180
 Qy 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPFLTEKLMQNRKLNKVTPLSANQKSLIARLV 240
 Db 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPFLTEKLMQNRKLNKVTPLSANQKSLIARLV 240
 Qy 241 WYQEGYQPSSEDLKRVYQWLESEEEETDMPFRQITTEMILTTLVQIIVFAKGLPGFS 300
 Db 241 WYQEGYQPSSEDLKRVYQWLESEEEETDMPFRQITTEMILTTLVQIIVFAKGLPGFS 300
 Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 Db 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 Qy 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYYLKTLRVYILNQHSASP 420
 Db 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYYLKTLRVYILNQHSASP 420
 Qy 421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
 Db 421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
 Qy 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
 Db 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
 Qy 541 MFTDALGIDEGG 553
 Db 541 MFTDALGIDEGG 553

RESULT 2

US-10-087-167-123
 ; Sequence 123, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 123
 ; LENGTH: 588
 ; TYPE: PRT
 ; ORGANISM: Synthetic Construct
 US-10-087-167-123

Query Match 98.1%; Score 2803; DB 14; Length 588;
 Best Local Similarity 98.6%; Pred. No. 5,9e-225;
 Matches 545; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
 Qy 1 MKLLSSIEQACDICRLKCLKSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
 Db 42 MKLLSSIEQACDICRLKCLKSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
 Qy 61 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
 Db 102 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161

Qy 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 180
 Db 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 221
 Qy 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPFLTEKLMQNRKLNKVTPLSANQKSLIARLV 240
 Db 221 TTTVDDHMPAIMQCDPPPEAAARHEVVPFLTEKLMQNRKLNKVTPLSANQKSLIARLV 281
 Qy 241 WYQEGYQPSSEDLKRVYQWLESEEEETDMPFRQITTEMILTTLVQIIVFAKGLPGFS 300
 Db 281 WYQEGYQPSSEDLKRVYQWLESEEEETDMPFRQITTEMILTTLVQIIVFAKGLPGFS 341
 Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 Db 341 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
 Qy 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYYLKTLRVYILNQHSASP 420
 Db 401 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYYLKTLRVYILNQHSASP 461
 Qy 421 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
 Db 461 RC AVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDV-----KLAPPTD 515
 Qy 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
 Db 515 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 575
 Qy 541 MFTDALGIDEGG 553
 Db 575 MFTDALGIDEGG 588

RESULT 3

US-10-087-167-127
 ; Sequence 127, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 127
 ; LENGTH: 599
 ; TYPE: PRT
 ; ORGANISM: Synthetic Construct
 US-10-087-167-127

Query Match 97.6%; Score 2786.5; DB 14; Length 599;
 Best Local Similarity 96.8%; Pred. No. 1.5e-223;
 Matches 540; Conservative 7; Mismatches 6; Indels 5; Gaps 1;
 Qy 1 MKLLSSIEQACDICRLKCLKSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
 Db 42 MKLLSSIEQACDICRLKCLKSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
 Qy 61 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
 Db 102 LERLEQLFLIIFPREDLDMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
 Qy 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 180
 Db 162 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRREKEAQREKDKLPVS 221

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QY 181 TTTVDHMPAIMQCDDPPPEAAARI-----HEVVPRFLTEKMEQNRLKNVTPLSANQKSL 235
Db 222 TTTVDHMPPIQCDDPPPEAAARILECLQHEVVPRFLSEKLEQNRLKNIPPLTANQQPL 281
QY 236 IARLVYQSGYQPSSEEDLKRVTTQWLEEEEEEEDMPFRQITENTILTVQLIIVEFAK 295
Db 282 IARLVYQSGYQPSSEEDLKRVTTQWLEEEEEEEDMPFRQITENTILTVQLIIVEFAK 341
QY 296 LFGFSKISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYTRDNYRKAGMSV 355
Db 342 LFGFSKISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYTRDNYRKAGMSV 401
QY 356 IEDLHFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQRYYLKTLRVYILNQ 415
Db 402 IEDLHFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQRYYLKTLRVYILNQ 461
QY 416 HSASPRCAVLFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKL 475
Db 462 HSASPRCAVLFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKL 521
QY 476 APPTDVSGLDELHLDGEDVAMAHADALDDFDLMDLGDGSDSGPGFTPHDSAPYGALDMAD 535
Db 522 APPTDVSGLDELHLDGEDVAMAHADALDDFDLMDLGDGSDSGPGFTPHDSAPYGALDMAD 581
QY 536 PFEQMFDTALGIDEYGG 553
Db 582 PFEQMFDTALGIDEYGG 599
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RESULT 4

US-10-087-167-119

; Sequence 119, Application US/10087167

; Publication No. US20030154509A1

; GENERAL INFORMATION:

; APPLICANT: Pascal, Erica

; APPLICANT: Valentine, Scott

; APPLICANT: Brown, Jeffrey

; APPLICANT: Cockrell, Adam

; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS

; CURRENT APPLICATION NUMBER: US/10/087,167

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 60/242,969

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 119

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Synthetic Construct

US-10-087-167-119

Query Match

Best Local Similarity 95.9%; Score 2738.5; DB 14; Length 591;

Matches 532; Conservative 8; Mismatches 10; Indels 3; Gaps 2;

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Db 42 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
QY 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS 180
Db 162 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS 221
QY 181 TTTVDHMPAIMQCDDPPPEAAARIHEVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPAIMQCDDPPPEAAARIHEVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLV 281
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QY 241 WYQEGYQPSSEEDLKRVTTQWLEEEEEEEDMPFRQITENTILTVQLIIVEFAKGLPGFS 300
Db 282 WYQEGYQPSSEEDLKRVTTQW-SDEDEESDMPFRQITENTILTVQLIIVEFAKGLPGFA 340
QY 301 KISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLL 360
Db 341 KISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYSRDNYRKAGMSYVIEDLL 400
QY 361 HFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQRYYLKTLRVYILNQHASP 420
Db 401 HFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQRYYLKTLRVYILNQHASP 460
QY 421 RCAVLFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKLAPPTD 480
Db 461 RCPVVFAKILGILTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVE--SRGKLAPPTD 518
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSGPGFTPHDSAPYGALDMADPFEQ 540
Db 519 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSDSGPGFTPHDSAPYGALDMADPFEQ 578
QY 541 MFTDALGIDEYGG 553
Db 579 MFTDALGIDEYGG 591
```

RESULT 5

US-10-087-167-121

; Sequence 121, Application US/10087167

; Publication No. US20030154509A1

; GENERAL INFORMATION:

; APPLICANT: Pascal, Erica

; APPLICANT: Valentine, Scott

; APPLICANT: Brown, Jeffrey

; APPLICANT: Cockrell, Adam

; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS

; FILE REFERENCE: 50018A

; CURRENT APPLICATION NUMBER: US/10/087,167

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 60/242,969

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 121

; LENGTH: 588

; TYPE: PRT

; ORGANISM: Synthetic Construct

US-10-087-167-121

Query Match

Best Local Similarity 95.6%; Score 2731; DB 14; Length 588;

Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

```
QY 1 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 60
Db 42 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
QY 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS 180
Db 162 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS 221
QY 181 TTTVDHMPAIMQCDDPPPEAAARIHEVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPAIMQCDDPPPEAAARIHEVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQEGYQPSSEEDLKRVTTQWLEEEEEEEDMPFRQITENTILTVQLIIVEFAKGLPGFS 300
Db 282 WYQEGYQPSSEEDLKRVTTQWQSADEEDEDMPFRQITENTILTVQLIIVEFAKGLPGFS 341
```

Qy	301	KI	QSQSDQITLLKASSEVWMLRVARRDYDA	ATDSVLFANNQAYTRDNYRKAGMSYVIEDLL	360
Db	342	KI	QSQSDQITLLKACSEVWMLRVARRDYDA	VSDFSVLFANNQAYTRDNYRKAGMAYVIEDLL	401
Qy	361	HF	CRWYMSMDNVHYALLTAIVIFSDRPGLEQ	PLLVVEEQRYLYLKTLRVYILNQHSA	420
Db	402	HF	CRWYMSMDNVHYALLTAIVIFSDRPGLEQ	PQLVVEEQRYLYLNTLRVYIMNQHSA	461
Qy	421	RC	AVFUGKILGVLTERTLTGTONSMCISLKL	KNRKLPPFLEEIMDVAEVSTTKLAPPTD	480
Db	462	RC	AVIYAKILSVLTERTLTGMQNSMCI	SLKLKNRKLPPFLEEIMDV	515
Qy	481	VS	IGDELHLDGSDVAMAHADALDDFDL	DMLGDGSPGPGTTPHDSAPYGALDMA	540
Db	516	VS	IGDELHLDGSDVAMAHADALDDFDL	DMLGDGSPGPGTTPHDSAPYGALDMA	575
Qy	541	MFT	DALGIDEXGG	553	
Db	576	MFT	DALGIDEXGG	588	
RESULT 6					
US-10-087-167-125					
; Sequence 125, Application US/10087167					
; Publication No. US20030154509A1					
; GENERAL INFORMATION:					
; APPLICANT: Pascal, Erica					
; APPLICANT: Valentine, Scott					
; APPLICANT: Brown, Jeffrey					
; APPLICANT: Cockrell, Adam					
; APPLICANT: Johnson, Brian					
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS					
; FILE REFERENCE: 50018A					
; CURRENT APPLICATION NUMBER: US/10/087,167					
; CURRENT FILING DATE: 2002-03-01					
; PRIOR APPLICATION NUMBER: US 60/242,969					
; PRIOR FILING DATE: 2000-10-24					
; NUMBER OF SEQ ID NOS: 148					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 125					
; LENGTH: 593					
; TYPE: PRT					
; ORGANISM: Synthetic Construct					
US-10-087-167-125					

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356 QY IEDLLHFCRCWYMSMDNVHYALLTAIVIFSDRFGLEQPLLVEBIQRYLYAKTLRVYILNQ 415
402 Db IEDLLHFCRCWYMSMDNVHYALLTAIVIFSDRFGLEQPLLVEBIQRYLYAKTLRVYIMNQ 461
416 QY HSASPRCAVLFGKTLGLVLT,ELRTLGTGTONSNMCISLKLKNRKLPPFLBBIWDVAEYSTTKL 475
462 Db HSASPRCAVIYAKLTSLVLT,ELRTLGTGTONSNMCISLKLKNRKLPPFLBBIWDV-----KL 515
476 QY APPTDVSIGDELHLJDGEDVAMAHADALDDFDLMDLGDGDSFGPGFTPHDSAPYGALDMAD 535
516 Db APPTDVSIGDELHLJDGEDVAMAHADALDDFDLMDLGDGDSFGPGFTPHDSAPYGALDMAD 575
536 QY FEFEQMFETDALGIDEYGG 553
576 Db FEFEQMFETDALGIDEYGG 593

RESULT 7
US-10-087-167-135
; Sequence 135, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 135
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-135

```

Qy 421 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKLAPPTD 480
Db 462 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKL--PKA 519
Qy 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLMDGDSFG 517
Db 520 VRCCTGGLFFHRRDTPAH--GETATPMAGGGGGG 553

RESULT 8

US-10-087-167-137
; Sequence 137, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-137

Query Match 85.4%; Score 2440; DB 14; Length 620;
Best Local Similarity 88.3%; Pred. No. 1.3e-194;
Matches 492; Conservative 7; Mismatches 34; Indels 24; Gaps 4;

Qy 1 MKLSSIEQACDICRLKCLKSKEPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 42 MKLSSIEQACDICRLKCLKSKEPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESR 101
Qy 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVDNVDNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVDNVDNDAVTDRLASVETDML 161
Qy 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAREKDKLPVS 180
Db 162 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAREKDKLPVS 221
Qy 181 TTTVDHMPALMQCDPPPEAARIEHVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPALMQCDPPPEAARIEHVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 281
Qy 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
Db 282 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 341
Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNYRKAGSVYIEDLL 360
Db 342 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNYRKAGSVYIEDLL 401
Qy 361 HFCRCWMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYRYLKTURVILNQHSA 420
Db 402 HFCRCWMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYRYLKTURVILNQHSA 461
Qy 421 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKLAPPTD 480
Db 462 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKLELATA 521
Qy 481 VSLGDEL-----HLGDGEDVAMAHADAL-----DPPDLMDLGDG--DSPGPGFT 521
Db 522 ADPGKATATTTTTTSEITETGALESDSLAHLQLQPGTDEAAVALGLGLSDPFSAGKA 581

Qy 522 PHDSA-----PYGALDM 533
Db 582 VLDDDESFVWPAASFD 598

RESULT 9

US-10-087-167-129
; Sequence 129, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-129

Query Match 85.2%; Score 2433; DB 14; Length 475;
Best Local Similarity 100.0%; Pred. No. 3.3e-194;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSSIEQACDICRLKCLKSKEPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 1 MKLSSIEQACDICRLKCLKSKEPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESR 60
Qy 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVDNVDNDAVTDRLASVETDML 120
Db 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVDNVDNDAVTDRLASVETDML 120
Qy 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAREKDKLPVS 180
Db 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAREKDKLPVS 180
Qy 181 TTTVDHMPALMQCDPPPEAARIEHVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
Db 181 TTTVDHMPALMQCDPPPEAARIEHVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
Qy 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
Db 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNYRKAGSVYIEDLL 360
Db 301 KISQSDQITLLKASSSEVMMLRVARRYDAATSDSVLFANNQAYTRDNYRKAGSVYIEDLL 360
Qy 361 HFCRCWMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYRYLKTURVILNQHSA 420
Db 361 HFCRCWMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYRYLKTURVILNQHSA 420
Qy 421 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKL 475
Db 421 RCACVFGKILGVLTLRTLTGTONSNMCISLKLKNNKLPFFLEEIWDVAEVSTTKL 475

RESULT 10

US-10-087-167-143
; Sequence 143, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott

```
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 143
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-143

Query Match      85.0%; Score 2428; DB 14; Length 602;
Best Local Similarity 100.0%; Pred. No. 1.2e-193;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRL 61
Db 129 KLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRL 188
Qy  62 ERLEQLFLLIFPREDLDMILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLPT 121
Db 189 ERLEQLFLLIFPREDLDMILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLPT 248
Qy 122 LRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 181
Db 249 LRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 308
Qy 182 TTVDHMPAIIWQCDPPPEAARIHEVVPFTEKLMQENRUKNTVPLSANQKSLIARLW 241
Db 309 TTVDHMPAIIWQCDPPPEAARIHEVVPFTEKLMQENRUKNTVPLSANQKSLIARLW 368
Qy 242 YQEGYEQSEEDLKRVTQWOLEEBEETDMPFQITEMTILTVQLIVEPAKGLPGFSK 301
Db 369 YQEGYEQSEEDLKRVTQWOLEEBEETDMPFQITEMTILTVQLIVEPAKGLPGFSK 428
Qy 302 ISQSDQITLLKASSSEVMMLVARRYDAATDSVLFANNQATRDNRKAGMSYVIEDLLH 361
Db 429 ISQSDQITLLKASSSEVMMLVARRYDAATDSVLFANNQATRDNRKAGMSYVIEDLLH 488
Qy 362 FCRCMYSMDNVHAYALLTAIVIFSDRPGLEQPLLVIEIQRYLKTLRVYILNQHSASPR 421
Db 489 FCRCMYSMDNVHAYALLTAIVIFSDRPGLEQPLLVIEIQRYLKTLRVYILNQHSASPR 548
Qy 422 CAVLFGKILGVLTRELTLGTQNSNMCIISLKNRKLPPFLEEIWDVAEVSTTKL 475
Db 549 CAVLFGKILGVLTRELTLGTQNSNMCIISLKNRKLPPFLEEIWDVAEVSTTKL 602

RESULT 11
US-10-087-167-148
; Sequence 148, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 148

; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 148

; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-148

Query Match      83.4%; Score 2381.5; DB 14; Length 599;
Best Local Similarity 85.1%; Pred. No. 9.3e-190;
Matches 475; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

Qy  1 MKLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db  42 MKLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
Qy  61 LERLEQLFLLIFPREDLDMILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLLIFPREDLDMILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 159
Db 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 221
Qy 160 ----- 159
Db 222 DVAMAHADALDDPDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQMFDTALGIDEYG 281
Qy 160 --TCKNKRKEAQAQREKDKLPVSTTTTVDHMPAIIWQCDPPPEAARIHEVVPFTEKLM 217
Db 282 GNTCKNKRKEAQAQREKDKLPVSTTTTVDHMPAIIWQCDPPPEAARIHEVVPFTEKLM 341
Qy 218 EQNRLKNVTPLSANQKSLIARLVMYQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQ 277
Db 342 EQNRLKNVTPLSANQKSLIARLVMYQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQ 401
Qy 278 ITEMILTITVQLIVEPAKGLPGFSKISQSDQITLLKASSSEVMMLVARRYDAATDSVLFA 337
Db 402 ITEMILTITVQLIVEPAKGLPGFSKISQSDQITLLKASSSEVMMLVARRYDAATDSVLFA 461
Qy 338 NNQAYTRDNRKAGMSYVIEDLLHFCRCMYSMDNVHAYALLTAIVIFSDRPGLEQPLLV 397
Db 462 NNQAYTRDNRKAGMSYVIEDLLHFCRCMYSMDNVHAYALLTAIVIFSDRPGLEQPLLV 521
Qy 398 EEIQRYLKTLRVYILNQHSASPRCAVLFGKILGVLTRELTLGTQNSNMCIISLKNRKL 457
Db 522 EEIQRYLKTLRVYILNQHSASPRCAVLFGKILGVLTRELTLGTQNSNMCIISLKNRKL 581
Qy 458 PPFLLEEIWDVAEVSTTKL 475
Db 582 PPFLLEEIWDVAEVSTTKL 599

RESULT 12
US-10-087-167-94
; Sequence 94, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 94
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-94
```

```
Query Match      73.5%; Score 2100; DB 14; Length 505;
Best Local Similarity 100.0%; Pred. No. 2.3e-166;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARIHEVVP 209
Db 102 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARIHEVVP 161

Qy 210 RFLTEKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEES 269
Db 162 RFLTEKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEES 221

Qy 270 ETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 329
Db 222 ETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 281

Qy 330 ATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMSMDNVHYALLTAIVIFSDRP 389
Db 282 ATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMSMDNVHYALLTAIVIFSDRP 341

Qy 390 GLEOPLLVEEIQRYLTKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNSNMCIS 449
Db 342 GLEOPLLVEEIQRYLTKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNSNMCIS 401

Qy 450 LKLNKRLPPLLEIWDVAEYSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLDM 509
Db 402 LKLNKRLPPLLEIWDVAEYSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLDM 455

Qy 510 LGDGSPPGPTPHDSAPYAGALDMADFEFEQMTDALGIDEYGG 553
Db 456 LGDGSPPGPTPHDSAPYAGALDMADFEFEQMTDALGIDEYGG 499

RESULT 14
US-10-087-167-80
; Sequence 80, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-80

Query Match      71.1%; Score 2030.5; DB 14; Length 510;
Best Local Similarity 95.6%; Pred. No. 1.5e-160;
Matches 391; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

Qy 150 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARI----- 204
Db 102 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARI----- 161

Qy 205 HEVVPREFLTKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLE 264
Db 162 HEVVPREFLTKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLE 221

Qy 265 EEEEEEDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVA 324
Db 222 EEEEEEDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVA 281

Qy 325 RRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMSMDNVHYALLTAIVI 384
Db 282 RRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMSMDNVHYALLTAIVI 341

Qy 385 PSDRPGLLEQPLLEIQRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNS 444
Db 342 PSDRPGLLEQPLLEIQRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNS 401

Qy 445 NMCISLKLKLRKLPPLLEIWDVAEYSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDD 504
Db 402 NMCISLKLKLRKLPPLLEIWDVAEYSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDD 461

Qy 505 FDLMLGDGSPGPGFTPHDSAPYAGALDMADFEFEQMTDALGIDEYGG 553
Db 462 FDLMLGDGSPGPGFTPHDSAPYAGALDMADFEFEQMTDALGIDEYGG 510

Query Match      71.7%; Score 2047; DB 14; Length 499;
Best Local Similarity 98.0%; Pred. No. 5.9e-162;
Matches 396; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

Qy 150 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARIHEVVP 209
Db 102 MRPCVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPAAARIHEVVP 161

Qy 210 RFLTEKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEES 269
Db 162 RFLTEKLEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEES 221

Qy 270 ETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 329
Db 222 ETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 281
```



```
RESULT 15
US-10-087-167-66
; Sequence 66, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-66

Query Match      69.4%; Score 1982.5; DB 14; Length 502;
Best Local Similarity 94.8%; Pred. No. 1.5e-156;
Matches 383; Conservative 8; Mismatches 10; Indels 3; Gaps 2;

QY 150 MRPECVPESTCKNKRREKEAQREKDLPSVSTTTVDDHMPAIMQCDDPPPEAAARIHEVVP 209
Db 102 MRPECVPESTCKNKRREKEAQREKDLPSVSTTTVDDHMPAIMQCDDPPPEAAARIHEVVP 161

QY 210 RPLTEKLEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSSEEDLKRVTTQTWQLEEEEEE 269
Db 162 RPLTEKLEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSSEEDLKRVTTQTWQ-SDEDEE 220

QY 270 ETDMPFRQITETIITLVQIIVFEFAGLPGFSGKISQSDQITLLKASSSEVMMLRVARRYDA 329
Db 221 ESDMPFRQITETIITLVQIIVFEFAGLPGFSGKISQSDQITLLKACSEVMMLRVARRYDA 280

QY 330 ATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 389
Db 281 ATDSVLFANNQAYSRDNYRKAGMSYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRP 340

QY 390 GLEQPLLVEEIORYLKLTVYILNQHSASPRCAVLFGKILGLVLTGLTGTQNSNMCIS 449
Db 341 GLEQPLLVEEIORYYLVNTLRVYILNQHSASPRCPVYFAKILGLTGLTGTQNSNMCIS 400

QY 450 LKLNKRLPPPLEETDVAEYSTTKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLDM 509
Db 401 LKLNKRLPPPLEETDVAEYSTTKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLDM 458

QY 510 LGDGDSPGPGFTPHDAPYGLDMADDFEQMFTDALGIDEYGG 553
Db 459 LGDGDSPGPGFTPHDAPYGLDMADDFEQMFTDALGIDEYGG 502
```

Search completed: April 14, 2005, 12:29:56
Job time : 139 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:55 ; Search time 79 Seconds
(without alignments)
2878.672 Million cell updates/sec

Title: US-10-087-167-121

Perfect score: 3072

Sequence: 1 MQQLYVDFSPAFIRYLPFW.....ADFFEQMTDALGIDEYGG 588

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980a:*
- 2: Geneseqp1990a:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001a:*
- 5: Geneseqp2002a:*
- 6: Geneseqp2003a:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3072	100.0	588	5	Abj05373 Chimeric
2	3072	100.0	588	7	Adf49193 Ecdysone
3	3002.5	97.7	593	5	Abj05375 Chimeric
4	3002.5	97.7	593	7	Adf49197 Ecdysone
5	2968.5	96.6	591	5	Abj05372 Chimeric
6	2968.5	96.6	591	7	Adf49191 Ecdysone
7	2965	96.5	588	5	Abj05374 Chimeric
8	2965	96.5	588	7	Adf49195 Ecdysone
9	2895.5	94.3	599	5	Abj05376 Chimeric
10	2895.5	94.3	599	7	Adf49199 Ecdysone
11	2731	88.9	553	5	Abj05371 Ecdysone
12	2731	88.9	553	7	Adf49177 Ecdysone
13	2552	83.1	620	5	Abj05379 Chimeric
14	2552	83.1	620	7	Adf49209 Ecdysone
15	2551.5	83.1	615	5	Abj05378 Chimeric
16	2551.5	83.1	615	7	Adf49207 Ecdysone
17	2494.5	81.2	599	5	Abj05381 Chimeric
18	2494.5	81.2	599	7	Adf49220 Ecdysone
19	2493	81.2	602	5	Abj05380 Chimeric
20	2493	81.2	602	7	Adf49215 Ecdysone
21	2312	75.3	475	5	Abj05377 Chimeric
22	2312	75.3	475	7	Adf49201 Ecdysone
23	2082	67.8	499	5	Abj05356 Chimeric
24	2082	67.8	499	7	Adf49140 Ecdysone
25	2012.5	65.5	504	5	Abj05360 Chimeric

26	2012.5	65.5	504	7	Adf49148 Ecdysone
27	1978.5	64.4	502	5	Abj05355 Chimeric
28	1978.5	64.4	502	7	Adf49138 Ecdysone
29	1975	64.3	499	5	Abj05357 Chimeric
30	1975	64.3	499	7	Adf49142 Ecdysone
31	1975	64.3	505	5	Abj05369 Chimeric
32	1975	64.3	505	7	Adf49166 Ecdysone
33	1909	62.1	507	5	Abj05361 Chimeric
34	1909	62.1	507	7	Adf49150 Ecdysone
35	1905.5	62.0	510	5	Abj05362 Chimeric
36	1905.5	62.0	510	7	Adf49152 Ecdysone
37	1741	56.7	501	5	Abj05354 Chimeric
38	1741	56.7	501	7	Adf49136 Ecdysone
39	1716.5	55.9	500	5	Abj05368 Chimeric
40	1716.5	55.9	500	7	Adf49164 Ecdysone
41	1691	55.0	521	5	Abj05367 Chimeric
42	1691	55.0	521	7	Adf49162 Ecdysone
43	1670	54.4	513	5	Abj05359 Chimeric
44	1670	54.4	513	7	Adf49146 Ecdysone
45	1666.5	54.2	516	5	Abj05358 Chimeric

ALIGNMENTS

RESULT 1

ABJ05373
ID ABJ05373 standard; protein; 588 AA.
XX
AC ABJ05373;
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
DE Chimeric ecdysone receptor SEQ ID NO: 121.
XX
KW Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.
XX
OS Manduca sexta.
OS Ostrinia nubilalis.
OS Chimeric.
XX
PN WO200261102-A2.
XX
PD 08-AUG-2002.
XX
PF 24-OCT-2001; 2001WO-US051417.
XX
PR 24-OCT-2000; 2000US-0242969P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI: 2002-619259/66.
XX
N-PSDB; ABT07367.

New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

Claim 6; Page 273-275; 319pp; English.

The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect EcR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The

```
CC present sequence is a protein described in the exemplification of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 588 AA;

Query Match      100.0%; Score 3072; DB 5; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.6e-250;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFAWYCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLYVDFSPAFIRYLFAWYCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLLIPREDLM 120
DB 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLLIPREDLM 120

QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPITLQHRISATSSSEESNK 180
DB 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPITLQHRISATSSSEESNK 180

QY 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARIEHVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQ 300
DB 241 EAARIEHVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQ 300

QY 301 TQWQADEDESDMPFRQITMTILTQVLI VEFKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TQWQADEDESDMPFRQITMTILTQVLI VEFKGLPGFSKISQPDQITLLKACSEVM 360

QY 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHALL 420
DB 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHALL 420

QY 421 TAIIVFSDRPGLEQPOLVEIQRYLNTLRVYIMNQHSPRCAVIYAKILSVLTETRL 480
DB 421 TAIIVFSDRPGLEQPOLVEIQRYLNTLRVYIMNQHSPRCAVIYAKILSVLTETRL 480

QY 481 GNQNSNMICISLKNRKLPPFLBEIWDVKLAPPTDVSIGDELHLDGEDVAMAHADALDDF 540
DB 481 GNQNSNMICISLKNRKLPPFLBEIWDVKLAPPTDVSIGDELHLDGEDVAMAHADALDDF 540

QY 541 DLDMLGDSGSPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588
DB 541 DLDMLGDSGSPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588

RESULT 2
ADF49193
ID ADF49193 standard; protein; 588 AA.
XX
AC ADF49193;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/VP16 transactivation domain seq id 121.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Ostrinia nubilalis.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
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XX 14-AUG-2003.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX (PASC/) PASCAL E J.
XX (VALE/) VALENTINE S A.
XX (BROW/) BROWN J A.
XX (COCK/) COCKRELL A S.
XX (JOHN/) JOHNSON B D.
XX
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX WPI; 2003-897756/82.
XX DR N-PSDB; ADF49192.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX for regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands.
XX
XX Example 23; SEQ ID NO 121; 186pp; English.
XX
XX The invention describes a receptor cassette encoding a chimeric receptor
XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX (E) domain that is heterologous with respect to the D domain, and an
XX activation domain. The receptor cassette and method are useful in
XX regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX can be used for the breeding of improved plant lines that, for e.g.
XX increase the effectiveness of conventional methods such as herbicide or
XX pesticide treatment. This is the amino acid sequence of an ecdysone
XX receptor-VP16 transactivation domain fusion protein.
XX
XX Sequence 588 AA;

Query Match      100.0%; Score 3072; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.6e-250;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFAWYCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLYVDFSPAFIRYLFAWYCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLLIPREDLM 120
DB 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLLIPREDLM 120

QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPITLQHRISATSSSEESNK 180
DB 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPITLQHRISATSSSEESNK 180

QY 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARIEHVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQ 300
DB 241 EAARIEHVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQ 300

QY 301 TQWQADEDESDMPFRQITMTILTQVLI VEFKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TQWQADEDESDMPFRQITMTILTQVLI VEFKGLPGFSKISQPDQITLLKACSEVM 360

QY 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHALL 420
DB 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHALL 420

QY 421 TAIIVFSDRPGLEQPOLVEIQRYLNTLRVYIMNQHSPRCAVIYAKILSVLTETRL 480
DB 421 TAIIVFSDRPGLEQPOLVEIQRYLNTLRVYIMNQHSPRCAVIYAKILSVLTETRL 480
```

61	ALSKENAFKARCLUNNNWELKISFALNASFLIRAGHUIEVESKDEKUEQJUFUULIFFREDUDD	121
Qy	ILKWSLQDIIKALLTGLFVQDNVNKDAVTRLASVETDMPLTLRHRISATSSSESSNK	180
Db	ILKWSLQDIIKALLTGLFVQDNVNKDAVTRLASVETDMPLTLRHRISATSSSESSNK	180
Qy	GORQLTVSTRMBECVVPPESTCKNKRREKEAQRKDKLPVSTTTVVDDHMPAIMQCDPPPP	240
Db	GORQLTVSTRMBECVVPPESTCKNKRREKEAQRKDKLPVSTTTVVDDHMPAIMQCDPPPP	240

Qy	241	EAARI-----HEVVPRFLTEKLMQENRKNVTPISANOKSLIARLWVQDGVEQSEEDL	295
Db	241	EAARILECLQHEVVPRFLSEKLMQENRKNIPPTANQOFLIARLWVQDGVEQSEEDL	300
Qy	296	KRVTQTWQSADEDEDESDMPQRTTEMTILTVQLIVLVEPAKGLPGFSKLSQPDQITLLKAC	355
Db	301	KRVTQTWQSADEDEDESDMPQRTTEMTILTVQLIVLVEPAKGLPGFSKLSQPDQITLLKAC	360
Qy	356	SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNV	415

DU	361	S95VNTLTKVAKKIDAVSDSVLEANNQALLNDNNANNAQTAAIVTEDEJLTF	CACHTI3IMCHINDAV	472
DU	362	SSSSTNLTAKVAKKIDAVSDSVLEANNQALLNDNNANNAQTAAIVTEDEJLTF	CACHTI3IMCHINDAV	473
QV	416	HVALLTALVIFSDRPGLEGEPOLVEEIORVYLLTLRWYINNOHSASPRCAVIYAKILSVLT	475	

421	HYALLTAIVFSDRPGUEQPOLVEEQRYYLNTLRVYIMNOHSASPRCAVIYAKILSVLT	480
476	ELRTLGNQNSMCI ^{SL} LK ^{NR} LK ^{NR} LK ^{NR} LP ^{PF} EEI ^{WD} VKL ^{AP} PTD ^{VS} LGD ^{EL} HL ^{DG} ED ^{VA} NA ^{HA} D	535

db 481 ELRTLGMONSMCISLKLKNRKLPPFLEEIWDVKLAPPTDVSGLGDELHLDGEDVAMAHAD 540

Qv 536 ALDDEPLDMLGDGDSPGPGGTHPDSAPYGALDMDADFEFEOMFTDALGIDVEGG 588

db 541 AI.DDEFI.DMI.GDGDSPGPGFTPHDSPA PYGAI.DMADEFEOMFTDAI.GIDEYGG 593

RESULT 4
ADP49J97

ID ADF49197 standard; protein; 593 AA.
XX

AC ADF49197;
XX

DT 12-FEB-2004 (first entry)

xx	Ecdysone receptor/VP16 transactivation domain seq id 125.
xx	
DE	
xx	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
xx	
kw	

KW activation domain; transgenic seed; transgenic plant; plant line;

[illegible]

24-OC1-2001; 200105-0008/167.
FF
XX

FR
24-UCI-2001; 2001US-0008/167.
XX

PA (PASC//) PASCAL E J.
PA (VALE//) VALENTINE S A.

PA (COCK/) COCKRELL A S.

FA (JOHN//) JOHNSON B D.
XX

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI: 2003-897756/82

DECREE A

ANF49197

ID ADF49197 standard: protein: 593 AA.



AC ADF49197;

XX
DT 12-FEB-2004 (first entry)

XX DE Ecdysone receptor/VP16 transactivation domain seq id 125.

XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain.

OS Synthetic.

OS *Ovulinia nubialis*.
OS *Ascomycota*.

OS Herpes simplex virus unknown type.

XX
PN
US2003154509-A1.

XX
PD
14-AUG-2003.

XX
PF
24-OCT-2001: 2001US-00087167.

XX
PB
24-OCT-2001: 2001US-00087167

XX
PA
(PAGE) PAGE 5 1

PA (VALE//) VALENTINE S A.
PA (PROW//) PROW T A

PA (COCK/) COCKRELL A S.

[illegible]

PT FAVCAT EV, VALENTINE SA, BLOWN UA, COSYGETT AZ, UOHHVON BU,
....

DR WPI: 2003-897756/82.

Db 301 TWQS-DEDEESDMPFRQITMTLTQVLIIVEFAKGLPGFAKISQSDQITLLKACSEVM 359
 Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALL 420
 Db 360 MLRVARRYDAATDSVLFANNOAYSRDNYRKAGMSVIEDLLHFCRCMYSMNDNVHYALL 419
 Qy 421 TAIVIFSDRPGLEOPOLVEEIQRYVYNTLRVYIMNQHSGASPCAVIYAKILSVLTETRL 480
 Db 420 TAIVIFSDRPGLEOPOLVEEIQRYVYNTLRVYIMNQHSGASPCAVIYAKILSVLTETRL 479
 Qy 481 GMQNSNMCSISLKNRKLPPFLEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 536
 Db 480 GMQNSNMCSISLKNRKLPPFLEEIWDVSGKGLAPPTDVSIGDELHLDGEDVAMAHADA 539
 Qy 537 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 588
 Db 540 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 591

RESULT 6
 ID ADF49191 standard; protein; 591 AA.
 XX ADF49191;
 AC ADF49191;
 XX DT 12-FEB-2004 (first entry)
 XX DE Ecdysone receptor/VP16 transactivation domain seq id 119.
 XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
 XX Synthetic.
 OS Manduca sexta.
 OS Ascomycota.
 OS Agrotis ipsilon.
 OS Herpes simplex virus unknown type.
 XX US2003154509-A1.
 PN 14-AUG-2003.
 XX 24-OCT-2001; 2001US-00087167.
 XX 24-OCT-2001; 2001US-00087167.
 XX (PASC/) PASCAL E J.
 PA (VALE/) VALENTINE S A.
 PA (BROW/) BROWN J A.
 PA (COCK/) COCKRELL A S.
 PA (JOHN/) JOHNSON B D.
 PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX WPI, 2003-897756/82.
 DR N-FSDB; ADF49190.
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX Example 23; SEQ ID NO 119; 186pp; English.
 PS The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants

CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-VP16 transactivation domain fusion protein.
 XX Sequence 591 AA;

Query Match 96.6%; Score 2968.5; DB 7; Length 591;
 Best Local Similarity 95.9%; Pred. No. 2e-241;
 Matches 568; Conservative 13; Mismatches 6; Indels 5; Gaps 2;

Qy 1 MQQLIYVDFSPAFIRYLFAMWYCFRCSPCCLVLLQGSATMKLLSSIEQACDCLRLKKL 60
 Db 1 MQQLIYVDFSPAFIRYLFAMWYCFRCSPCCLVLLQGSATMKLLSSIEQACDCLRLKKL 60

Qy 61 KCSKEKPKCAKCLKNWECRYSPKTKSPKRAHLTEVESLERLEQLFLIFPREDLDM 120
 Db 61 KCSKEKPKCAKCLKNWECRYSPKTKSPKRAHLTEVESLERLEQLFLIFPREDLDM 120

Qy 121 ILKMSLDQIKALLTGLFVQDNVKNDAVTRLASVETDMPITLRQHRISATSSSESSNK 180
 Db 121 ILKMSLDQIKALLTGLFVQDNVKNDAVTRLASVETDMPITLRQHRISATSSSESSNK 180

Qy 181 GQRLTVSTRMRPECVVPSTCKNKRKEKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240
 Db 181 GQRLTVSTRMRPECVVPSTCKNKRKEKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Qy 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANOKSLARLVYQDGYQBPSEEDLKRYTQ 300
 Db 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANOKSLARLVYQDGYQBPSEEDLKRYTQ 300

Qy 301 TWQSADBEDSDMPPFRQITMTLTQVLIIVEFAKGLPGFAKISQSDQITLLKACSEVM 360
 Db 301 TWQS-DEDEESDMPFRQITMTLTQVLIIVEFAKGLPGFAKISQSDQITLLKACSEVM 359

Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALL 420
 Db 360 MLRVARRYDAATDSVLFANNOAYSRDNYRKAGMSVIEDLLHFCRCMYSMNDNVHYALL 419

Qy 421 TAIVIFSDRPGLEOPOLVEEIQRYVYNTLRVYIMNQHSGASPCAVIYAKILSVLTETRL 480
 Db 420 TAIVIFSDRPGLEOPOLVEEIQRYVYNTLRVYIMNQHSGASPCAVIYAKILSVLTETRL 479

Qy 481 GMQNSNMCSISLKNRKLPPFLEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 536
 Db 480 GMQNSNMCSISLKNRKLPPFLEEIWDVSGKGLAPPTDVSIGDELHLDGEDVAMAHADA 539

Qy 537 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 588
 Db 540 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 591

RESULT 7
 ID ADF49191 standard; protein; 591 AA.

XX ADF49191;
 AC ADF49191;
 XX DT 29-AUG-2003 (revised)
 XX DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 123.
 XX Plant; gene expression control; insect; hormone receptor; fertility;
 XX ecdysone receptor.

XX Manduca sexta.
 OS Spodoptera frugiperda.
 OS Chimeric.

XX WO200261102-A2.
 XX 08-AUG-2002.

XX PF 24-OCT-2001; 2001WO-US051417.
 XX PR 24-OCT-2000; 2000US-0242969P.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX DR WPI; 2002-619259/66.
 XX DR N-PSDB; ABTO7368.
 XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
 XX PT regulating expression of target polypeptides in plants in the presence of
 XX PT appropriate ligands that may be used in controlling plant fertility.
 XX PS Example 23; Page 278-280; 319pp; English.
 XX CC The present invention relates to a receptor cassette encoding a chimeric
 XX CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 XX CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 XX CC domain of an insect Ecr, where the ligand binding domain is heterologous
 XX CC with respect to the hinge domain and an activation domain. The chimeric
 XX CC insect hormone receptors and receptor cassettes are useful in regulating
 XX CC expression of target polypeptides in plants in the presence of
 XX CC appropriate ligands that may be used in controlling plant fertility. The
 XX CC method is useful for decreasing or increasing plant gene expression. The
 XX CC present sequence is a protein described in the exemplification of the
 XX CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX SQ Sequence 588 AA;

Query Match 96.5%; Score 2965; DB 5; Length 588;
 Best Local Similarity 96.3%; Pred. No. 3.9e-241;
 Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQQLYVDFPFAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
 DB 1 MQQLYVDFPFAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEKPKCAKCKNNWECRYSPKTRSPKTRAHLETVESRLERLEQLFLIFPREDLDM 120
 DB 61 KCSKEKPKCAKCKNNWECRYSPKTRSPKTRAHLETVESRLERLEQLFLIFPREDLDM 120

QY 121 ILKMDSLQDIKALTGLFQDQNVNKAQVTDRLASVETDPLTLQHRISATSSSESSNK 180
 DB 121 ILKMDSLQDIKALTGLFQDQNVNKAQVTDRLASVETDPLTLQHRISATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVPESTCKNKRREKQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240
 DB 181 GORQLTVSTRMRPECVPESTCKNKRREKQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

QY 241 EAARITHEVVPFLTEKLEMEONRLKNVTPLSANQKSLIARLVWYQGYQPSSEEDLKRTQ 300
 DB 241 EAARITHEVVPFLTEKLEMEONRLKNVTPLSANQKSLIARLVWYQGYQPSSEEDLKRTQ 300

QY 301 TWQSADEDESDMPFOITETILTTLVOLIVEFAGKLPFGSKISOPDQITLLKACSSVM 360
 DB 301 TWQSADEDESDMPFOITETILTTLVOLIVEFAGKLPFGSKISOPDQITLLKACSSVM 360

QY 361 MLRVARRYDVSQVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
 DB 361 MLRVARRYDVSQVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420

QY 421 TAIVIFSDRPGLEQPOLVEETORYYNTLRVYIMNQHSPRCVAVIYAKILSVLTELRTL 480
 DB 421 TAIVIFSDRPGLEQPOLVEETORYYNTLRVYIMNQHSPRCVAVIYAKILSVLTELRTL 480

QY 481 GQNSNMCIISLKLKRLKLPPLLEEVDVKLAPPTDVLSDGLHLDGEDVAMAHADALDDF 540
 DB 481 GQNSNMCIISLKLKRLKLPPLLEEVDVKLAPPTDVLSDGLHLDGEDVAMAHADALDDF 540

QY 541 DLDMLGDSGPGFTPHDSAPYGALDMADFEQMFDTALGIDYGG 588

DB 541 DLDMLGDSGPGFTPHDSAPYGALDMADFEQMFDTALGIDYGG 588

RESULT 8
 ADF49195
 ID ADF49195 standard; protein; 588 AA.
 XX AC ADF49195;
 XX DT 12-FEB-2004 (first entry)
 XX DE Ecdysone receptor/VP16 transactivation domain seq id 123.
 XX KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 XX KW hinge domain; ecdysone receptor; ECR; ligand binding domain; a hinge
 XX KW activation domain; transgenic seed; transgenic plant; plant line;
 XX KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 XX KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
 XX OS Synthetic.
 XX OS Manduca sexta.
 XX OS Ascomycota.
 XX OS Spodoptera frugiperda.
 XX OS Herpes simplex virus unknown type.
 XX PN US2003154509-A1.
 XX PD 14-AUG-2003.
 XX PF 24-OCT-2001; 2001US-00087167.
 XX PR 24-OCT-2001; 2001US-00087167.
 XX PA (PASC/) PASCAL E J.
 XX PA (VALE/) VALENTINE S A.
 XX PA (BROW/) BROWN J A.
 XX PA (COCK/) COCKRELL A S.
 XX PA (JOHN/) JOHNSON B D.
 XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX DR WPI; 2003-897756/82.
 XX DR N-PSDB; ADF49194.
 XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful
 XX PT for regulating the expression of target polypeptides in plants in the
 XX PT presence of appropriate chemical ligands.
 XX PS Example 23; SEQ ID NO 123; 186pp; English.
 XX CC The invention describes a receptor cassette encoding a chimeric receptor
 XX CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 XX CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 XX CC (E) domain that is heterologous with respect to the D domain, and an
 XX CC activation domain. The receptor cassette and method are useful in
 XX CC regulating the expression of target polypeptides in plants in the
 XX CC presence of appropriate chemical ligands. The transgenic seeds and plants
 XX CC can be used for the breeding of improved plant lines that, for e.g.,
 XX CC increase the effectiveness of conventional methods such as herbicide or
 XX CC pesticide treatment. This is the amino acid sequence of an ecdysone
 XX CC receptor-VP16 transactivation domain fusion protein.
 XX SQ Sequence 588 AA;

Query Match 96.5%; Score 2965; DB 7; Length 588;
 Best Local Similarity 96.3%; Pred. No. 3.9e-241;
 Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQQLYVDFPFAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
 DB 1 MQQLYVDFPFAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEKPKCAKCLKNNWECRYSPKTRSPKTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
 Db 61 KCSKEKPKCAKCLKNNWECRYSPKTRSPKTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
 QY 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLROHRIASATSSSESSNK 180
 Db 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLROHRIASATSSSESSNK 180
 QY 181 GORQLTVSTRMRPECVPESTCKNRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
 Db 181 GORQLTVSTRMRPECVPESTCKNRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
 QY 241 EAARIHEVVPRFLTEKLMQNRKLNKNTPLSANQKSLIARLVWYQGYQPSEEDLKRVTVQ 300
 Db 241 EAARIHEVVPRFLTEKLMQNRKLNKNTPLSANQKSLIARLVWYQGYQPSEEDLKRVTVQ 300
 QY 301 TWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSSVM 360
 Db 301 TWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSSVM 360
 QY 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
 Db 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
 QY 421 TAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVIYAKILSVLTELRTL 480
 Db 421 TAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVLPGKILSVLTELRTL 480
 QY 481 GQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDVAMAHADALDDF 540
 Db 481 GQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDVAMAHADALDDF 540
 QY 541 DLDMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 588
 Db 541 DLDMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 588

RESULT 9

ABJ05376

ID ABJ05376 standard; protein; 599 AA.

XX ABJ05376;

XX 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 127.

DE Plant; gene expression control; insect; hormone receptor; fertility;

KW ecdysone receptor.

XX Ostrinia nubilalis.

OS Manduca sexta.

OS Chimeric.

XX WO200261102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

XX N-PSDB; ABT07370.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 appropriate ligands that may be used in controlling plant fertility.

XX

PS Example 23; Page 288-291; 319pp; English.

CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
 CC domain of an insect EcR, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 599 AA;

QY Query Match 94.3%; Score 2895.5; DB 5; Length 599;

Db Best Local Similarity 92.7%; Pred. No. 2.9e-235;

QY Matches 555; Conservative 17; Mismatches 16; Indels 11; Gaps 2;

QY 1 MQQYVDFPSPAFIRYLFPAWYCFRCSPCCLVLLQGSATMKLSSIEQACDICRLKKL 60

Db 1 MQQYVDFPSPAFIRYLFPAWYCFRCSPCCLVLLQGSATMKLSSIEQACDICRLKKL 60

QY 61 KCSKEKPKCAKCLKNNWECRYSPKTRSPKTRAHLTEVESRLERLEQLFLIFPPREDLDM 120

Db 61 KCSKEKPKCAKCLKNNWECRYSPKTRSPKTRAHLTEVESRLERLEQLFLIFPPREDLDM 120

QY 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLROHRIASATSSSESSNK 180

Db 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLROHRIASATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVPESTCKNRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

Db 181 GORQLTVSTRMRPECVPESTCKNRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARIHEVVPRFLTEKLMQNRKLNKNTPLSANQKSLIARLVWYQGYQPSEEDL 295

Db 241 EAARIHEVVPRFLTEKLMQNRKLNKNTPLSANQKSLIARLVWYQGYQPSEEDL 295

QY 296 KRVTQWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 355

Db 296 KRVTQWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 355

QY 301 KRVTQWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 360

Db 301 KRVTQWQADEDESDMPFROITMTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 360

QY 356 SSEVMMLRVABRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNV 415

Db 356 SSEVMMLRVABRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNV 415

QY 416 HYALLTAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVIYAKILSVLT 475

Db 416 HYALLTAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVIYAKILSVLT 475

QY 421 HYALLTAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVIYAKILSVLT 480

Db 421 HYALLTAIVFSDRPGLEQPOLVEEIQRYYLNTLRVYIMNQHSAASPRCAVIYAKILSVLT 480

QY 476 ELRTLGQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDV 529

Db 476 ELRTLGQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDV 529

QY 481 ELRTLGQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDV 540

Db 481 ELRTLGQNSNMNCISLKLKNRKLPPLFEEIWDVYKLPAPPTDVSIGDELHLDGEDV 540

QY 530 AMAHADALDDPDLMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 588

Db 530 AMAHADALDDPDLMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 588

QY 541 AMAHADALDDPDLMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 599

Db 541 AMAHADALDDPDLMLGDSGPGGFTPHDSAPYGALDMADPFEQMTDALGIDYGG 599

RESULT 10

ADF49199

ID ADF49199 standard; protein; 599 AA.

XX ADF49199;

XX ADF49199;

XX 12-FEB-2004 (first entry)

XX Ecdysone receptor/vp16 transactivation domain seq id 127.

DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;

XX

KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
 XX
 OS Synthetic.
 OS Ostrinia nubilalis.
 OS Agomycota.
 OS Manduca sexta.
 OS Herpes simplex virus unknown type.
 XX
 XX US2003154509-A1.
 XX
 XX 14-AUG-2003.
 XX
 XX 24-OCT-2001; 2001US-00087167.
 XX
 XX 24-OCT-2001; 2001US-00087167.
 XX
 XX (PASC/) PASCAL E J.
 XX (VALE/) VALENTINE S A.
 XX (BROW/) BROWN J A.
 XX (COCK/) COCKRELL A S.
 XX (JOHN/) JOHNSON B D.
 XX
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX
 XX WPI; 2003-897756/82.
 XX N-PSDB; ADF49198.
 XX
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 XX for regulating the expression of target polypeptides in plants in the
 XX presence of appropriate chemical ligands.
 XX
 XX Example 23; SEQ ID NO 127; 186pp; English.
 XX
 XX The invention describes a receptor cassette encoding a chimeric receptor
 XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 XX (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 XX (E) domain that is heterologous with respect to the D domain, and an
 XX activation domain. The receptor cassette and method are useful in
 XX regulating the expression of target polypeptides in plants in the
 XX presence of appropriate chemical ligands. The transgenic seeds and plants
 XX can be used for the breeding of improved plant lines that, for e.g.
 XX increase the effectiveness of conventional methods such as herbicide or
 XX pesticide treatment. This is the amino acid sequence of an ecdysone
 XX receptor-VP16 transactivation domain fusion protein.
 XX
 XX Sequence 599 AA;
 XX
 Query Match
 Best Local Similarity 94.3%; Score 2895.5; DB 7; Length 599;
 Matches 555; Conservative 17; Mismatches 16; Indels 11; Gaps 2;
 QY 1 MQQLYVDFSPAFIRYLFAMWYCFRCSPCCVLVLLQGSATMKLSSIEQACDLCRLKL 60
 DB 1 MQQLYVDFSPAFIRYLFAMWYCFRCSPCCVLVLLQGSATMKLSSIEQACDLCRLKL 60
 QY 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIPREDLDM 120
 DB 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIPREDLDM 120
 QY 121 ILKMDSLQDIKALLTGLFQDNNVNDKAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
 DB 121 ILKMDSLQDIKALLTGLFQDNNVNDKAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
 QY 181 GORQLTVSTRMPECVPESTCKNREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
 DB 181 GORQLTVSTRMPECVPESTCKNREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
 QY 241 EAARI-----HVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVYQDGEQSEEDL 295
 DB 241 EAARILECLQHEVWVPRFLSEKLEQNRLKNVTPLSANQKSLIARLVYQDGEQSEEDL 300

QY 296 KRVTQWQADERDESDMPFROITMTILTVOIVEFAKGLPGFSKISQPDQITLLKAC 355
 DB 301 KRVTQWQLEEEEBEETDMPFROITMTILTVOIVEFAKGLPGFSKISQSDQITLLKAS 360
 QY 356 SSEVMMLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNV 415
 DB 361 SSEVMMLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNV 420
 QY 416 HYALLTAIVFSDRPGLEQPOLVEETORYVNTLRYVIMNQHSAPRCVAVIYAKILSVLT 475
 DB 421 HYALLTAIVFSDRPGLEQPOLVEETORYVNTLRYVIMNQHSAPRCVAVIYAKILSVLT 480
 QY 476 ELRTLGMQNSMCISLKNRKLPPFLEEIWDV-----KLAPPTDVSGLDELHLGDEV 529
 DB 481 ELRTLGMQNSMCISLKNRKLPPFLEEIWDVAEVSTTKLAPPTDVSGLDELHLGDEV 540
 QY 530 AMAHADALDDFDLMDLGDGSPGPTPHDSAPYGALDMADPFEOMFTDALGIDEYGG 588
 DB 541 AMAHADALDDFDLMDLGDGSPGPTPHDSAPYGALDMADPFEOMFTDALGIDEYGG 599

RESULT 11
 ID ABJ05371 standard; protein; 553 AA.
 AC ABJ05371;
 XX
 XX 07-NOV-2002 (first entry)
 XX
 DE Bcdysone receptor encoded by vector pCGS202 SEQ ID NO: 105.
 XX
 KW Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor.
 XX
 OS Synthetic.
 OS
 XX WO200261102-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 24-OCT-2001; 2001WO-US051417.
 XX
 PR 24-OCT-2000; 2000US-0242969P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX
 XX WPI; 2002-619259/66.
 XX N-PSDB; ABT07353.
 XX
 PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX
 XX Claim 27; Page 258-261; 319pp; English.
 XX
 CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC domain of an insect ECR, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention
 XX
 XX Sequence 553 AA;
 SQ

Query Match 88.9%; Score 2731; DB 5; Length 553;

Best Local Similarity 95.3%; Pred. No. 2e-221;		Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;	
Qy	42	MKLLSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPTRAHLTEVER	101
Db	1	MKLLSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPTRAHLTEVER	60
Qy	102	LERLEQLFLIIPREDLMLKMSLQDIKALLTGLFVQDNVNVKDAVTRDLASVETDML	161
Db	61	LERLEQLFLIIPREDLMLKMSLQDIKALLTGLFVQDNVNVKDAVTRDLASVETDML	120
Qy	162	TLRQHRISATSSSESSKNGQRLTVSTRMRPECVPESTCKNKRKEAQRKDLFVS	221
Db	121	TLRQHRISATSSSESSKNGQRLTVSTRMRPECVPESTCKNKRKEAQRKDLFVS	180
Qy	222	TTTVDHMPAIIQCDDPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLV	281
Db	181	TTTVDHMPAIIQCDDPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLV	240
Qy	282	WYQGYEQPSEEDLKRVTQWQSEDESDMPFRQITMTILTQVLIQVFAKGLPGFS	341
Db	241	WYQGYEQPSEEDLKRVTQWQSEDESDMPFRQITMTILTQVLIQVFAKGLPGFS	300
Qy	342	KISQDQITLLKACSEVMMLRVARRYDAVSDFVLFANNQAYTRDNYRKAGMYVIEDLL	401
Db	301	KISQDQITLLKACSEVMMLRVARRYDAVSDFVLFANNQAYTRDNYRKAGMYVIEDLL	360
Qy	402	HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHASP	461
Db	361	HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHASP	420
Qy	462	RCAVIYAKILSVLTETLGMNSNCISLKNRKLPPFLBEIWDV-----KLAPPTD	515
Db	421	RCAVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLBEIWDV-----KLAPPTD	480
Qy	516	VSLGDELHLDGEDVAMAHADALDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQ	575
Db	481	VSLGDELHLDGEDVAMAHADALDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQ	540
Qy	576	MFTDALGIDEYGG 588	
Db	541	MFTDALGIDEYGG 553	
RESULT 12			
ADF49177			
ID	ADF49177 standard; protein; 553 AA.		
AC	ADF49177;		
XX			
DT	12-FEB-2004 (first entry)		
DE	Ecdysone receptor/VPL6 transactivation domain seq id 105.		
XX			
KW	receptor cassette; chimeric receptor polypeptide; DNA binding domain;		
KW	hinge domain; ecdysone receptor; ECR; ligand binding domain;		
KW	activation domain; transgenic seed; transgenic plant; plant line;		
KW	herbicide; pesticide; chimeric ecdysone receptor; ECR;		
KW	yeast GAL4 DNA binding domain; VPL6 transactivation domain.		
XX			
OS	Synthetic.		
OS	Manduca sexta.		
OS	Ascomycota.		
OS	Herpes simplex virus unknown type.		
XX			
PN	US2003154509-A1.		
XX			
XX	14-AUG-2003.		
XX			
PF	24-OCT-2001; 2001US-00087167.		
XX			
XX	24-OCT-2001; 2001US-00087167.		
XX			

(PASC/) PASCAL E. J.
(VALE/) VALENTINE S. A.
(BROW/) BROWN J. A.
(COCK/) COCKRELL A. S.
(JOHN/) JOHNSON B. D.
XX
Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
WPI; 2003-897756/82.
XX
New receptor cassette encoding a chimeric receptor polypeptide, useful
for regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands.
XX
Example 11; SEQ ID NO 105; 186pp; English.
XX
The invention describes a receptor cassette encoding a chimeric receptor
polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
(D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
(E) domain that is heterologous with respect to the D domain, and an
activation domain. The receptor cassette and method are useful in
regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands. The transgenic seeds and plants
can be used for the breeding of improved plant lines that, for e.g.
increase the effectiveness of conventional methods such as herbicide or
pesticide treatment. This is the amino acid sequence of an ecdysone
receptor-VPL6 transactivation domain fusion protein.
XX
Sequence 553 AA;

Query Match 88.9%; Score 2731; DB 7; Length 553;		Best Local Similarity 95.3%; Pred. No. 2e-221;	
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;			
Qy	42	MKLLSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPTRAHLTEVER	101
Db	1	MKLLSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPTRAHLTEVER	60
Qy	102	LERLEQLFLIIPREDLMLKMSLQDIKALLTGLFVQDNVNVKDAVTRDLASVETDML	161
Db	61	LERLEQLFLIIPREDLMLKMSLQDIKALLTGLFVQDNVNVKDAVTRDLASVETDML	120
Qy	162	TLRQHRISATSSSESSKNGQRLTVSTRMRPECVPESTCKNKRKEAQRKDLFVS	221
Db	121	TLRQHRISATSSSESSKNGQRLTVSTRMRPECVPESTCKNKRKEAQRKDLFVS	180
Qy	222	TTTVDHMPAIIQCDDPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLV	281
Db	181	TTTVDHMPAIIQCDDPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLV	240
Qy	282	WYQGYEQPSEEDLKRVTQWQSEDESDMPFRQITMTILTQVLIQVFAKGLPGFS	341
Db	241	WYQGYEQPSEEDLKRVTQWQSEDESDMPFRQITMTILTQVLIQVFAKGLPGFS	300
Qy	342	KISQDQITLLKACSEVMMLRVARRYDAVSDFVLFANNQAYTRDNYRKAGMYVIEDLL	401
Db	301	KISQDQITLLKACSEVMMLRVARRYDAVSDFVLFANNQAYTRDNYRKAGMYVIEDLL	360
Qy	402	HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHASP	461
Db	361	HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHASP	420
Qy	462	RCAVIYAKILSVLTETLGMNSNCISLKNRKLPPFLBEIWDV-----KLAPPTD	515
Db	421	RCAVLFGKILGVLTELTGTQNSNMCISLKNRKLPPFLBEIWDV-----KLAPPTD	480
Qy	516	VSLGDELHLDGEDVAMAHADALDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQ	575
Db	481	VSLGDELHLDGEDVAMAHADALDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQ	540
Qy	576	MFTDALGIDEYGG 588	
Db	541	MFTDALGIDEYGG 553	

```

RESULT 13
ABJ05379
ID ABJ05379 standard; protein; 620 AA.
XX
XX AC ABJ05379;
XX
XX DT 29-AUG-2003 (revised)
XX DT 07-NOV-2002 (first entry)
XX
XX DE Chimeric ecdysone receptor SEQ ID NO: 137.
XX
XX KW Plant; gene expression control; insect; hormone receptor; fertility;
XX KW ecdysone receptor.
XX
XX OS Manduca sexta.
XX OS Chimeric.
XX
XX PN WO200261102-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 24-OCT-2001; 2001WO-US051417.
XX
XX PR 24-OCT-2000; 2000US-0242969P.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX DR WPI; 2002-619259/66.
XX DR N-PSDB; ABT07377.
XX
XX
XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX PT regulating expression of target polypeptides in plants in the presence of
XX PT appropriate ligands that may be used in controlling plant fertility.
XX
XX PS Example 25; Page 304-306; 319pp; English.
XX
XX CC The present invention relates to a receptor cassette encoding a chimeric
XX CC receptor polypeptide comprising at least one DNA binding domain, a hinge
XX CC domain of an ecdysone receptor (Ecr), where the ligand binding domain is a hinge
XX CC domain of an insect Ecr, where the ligand binding domain is heterologous
XX CC with respect to the hinge domain and an activation domain. The chimeric
XX CC insect hormone receptors and receptor cassettes are useful in regulating
XX CC expression of target polypeptides in plants in the presence of
XX CC appropriate ligands that may be used in controlling plant fertility. The
XX CC method is useful for decreasing or increasing plant gene expression. The
XX CC present sequence is a protein described in the exemplification of the
XX CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX SQ Sequence 620 AA;

Query Match 83.1%; Score 2552; DB 5; Length 620;
Best Local Similarity 84.4%; Pred. No. 3.1e-206;
Matches 505; Conservative 18; Mismatches 45; Indels 30; Gaps 4;

QY 1 MQQLVDFPSPAFIRYLFAMWYCFRCRSPCCVLVLLQGSATMKLLSSIEQACDICRLKLL 60
DB 1 MQQLVDFPSPAFIRYLFAMWYCFRCRSPCCVLVLLQGSATMKLLSSIEQACDICRLKLL 60
QY 61 KCSKEKPKCAKCKLNWECRSPKTRSPFRAHLTEVESRLERLEQLFLIFPREDLDM 120
DB 61 KCSKEKPKCAKCKLNWECRSPKTRSPFRAHLTEVESRLERLEQLFLIFPREDLDM 120
QY 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLQHRISATSSSESSNK 180
DB 121 ILKMDSLQDIKALLTGLFVQDNVNDKAVTDRLASVETDMPITLQHRISATSSSESSNK 180
QY 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTTVDHHPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTTVDHHPAIMQCDPPPP 240

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DB 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTTVDHHPAIMQCDPPPP 240
QY 241 EAARIHEVVPRFLTEKLMQNRLKNVTPLSANOKSLIARLVWYODGYEQSEEDLKRVTQ 300
DB 241 EAARIHEVVPRFLTEKLMQNRLKNVTPLSANOKSLIARLVWYODGYEQSEEDLKRVTQ 300
QY 301 TWQADDEDESDMPFRQITMTILTVQLIVEPAKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TWQLEEEBEETDMPFRQITMTILTVQLIVEPAKGLPGFSKISQSDQITLLKACSEVM 360
QY 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYSMDNVHYALL 420
DB 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYSMDNVHYALL 420
QY 421 TAIVIFSDRPGLEQPOLVVEIQRYLYNTLRVYIMNQHSA SPRCAVIYAKILSVLTETL 480
DB 421 TAIVIFSDRPGLEQPOLVVEIQRYLYNTLRVYIMNQHSA SPRCAVIYAKILSVLTETL 480
QY 481 GMQNSNMCI SLKLNKRLPPFLIEIWDVKLAPPTDVSIGDEL-----HLDG 526
DB 481 GTQNSNMCI SLKLNKRLPPFLIEIWDVAEVSTTKLELATAADPGKTATTTTITSEITT 540
QY 527 EDVAMAHADAL-----DDFDLMLDGG--DSPGPGFTPHDSA-----PYGALDM 568
DB 541 ETGALESDSLAHLQLLQPGTDEAEVALGLGLSDFFSAGKAVLDDEDSFVWPAAAFDM 598

RESULT 14
ADF49209
ID ADF49209 standard; protein; 620 AA.
XX
XX AC ADF49209;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Ecdysone receptor/Dof1 transactivation domain seq id 137.
XX
XX KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
XX KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
XX KW activation domain; transgenic seed; transgenic plant; plant line;
XX KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
XX KW yeast GAL4 DNA binding domain; Dof1 transactivation domain.
XX
XX OS Synthetic.
XX OS Manduca sexta.
XX OS Ascomycota.
XX OS Zea mays.
XX
XX PN US2003154509-A1.
XX
XX PD 14-AUG-2003.
XX
XX PF 24-OCT-2001; 2001US-00087167.
XX
XX PR 24-OCT-2001; 2001US-00087167.
XX
XX PA (PASC/) PASCAL E J.
XX PA (VALE/) VALENTINE S A.
XX PA (BROW/) BROWN J A.
XX PA (COCK/) COCKRELL A S.
XX PA (JOHN/) JOHNSON B D.
XX
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX DR WPI; 2003-897756/82.
XX
XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful
XX PT for regulating the expression of target polypeptides in plants in the
XX PT presence of appropriate chemical ligands.
XX
XX PS Example 25; SEQ ID NO 137; 186pp; English.
XX
XX CC The invention describes a receptor cassette encoding a chimeric receptor

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CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-Dof1 transactivation domain fusion protein.

XX Sequence 620 AA;

Query Match 83.1%; Score 2552; DB 7; Length 620;
 Best Local Similarity 84.4%; Pred. No. 3.1e-206;
 Matches 505; Conservative 18; Mismatches 45; Indels 30; Gaps 4;

Qy 1 MQQLYVDFSPAFIRYLFAMVCFPCRCSPCLVLLQGSATMKLLSSIEQACDLCRLKL 60
 Db 1 MQQLYVDFSPAFIRYLFAMVCFPCRCSPCLVLLQGSATMKLLSSIEQACDLCRLKL 60
 Qy 61 KCSKEKPKCAKCLKNWECRSPKTRSPPLTRAHLTEVESRLERLEQLFLIFPREDLDM 120
 Db 61 KCSKEKPKCAKCLKNWECRSPKTRSPPLTRAHLTEVESRLERLEQLFLIFPREDLDM 120
 Qy 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
 Db 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
 Qy 181 GORQLTVSTRMRPECVVPESTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240
 Db 181 GORQLTVSTRMRPECVVPESTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240
 Qy 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300
 Db 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300
 Qy 301 TWQSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVM 360
 Db 301 TWQLEEEEEEETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVM 360
 Qy 361 MLRVARRYDAVSDVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALL 420
 Db 361 MLRVARRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALL 420
 Qy 421 TAIIVFSDRPGLEQPOLVEEIQRYLYLTLRVYIMNQHSAASPCAVIYAKILSVLTLERTL 480
 Db 421 TAIIVFSDRPGLEQPOLVEEIQRYLYLTLRVYIMNQHSAASPCAVIFGKILGVLTLERTL 480
 Qy 481 GMONSNMCSLKNRKLPPFLLEEIWDVVKLAPPTDVSIGDEL-----HLDG 526
 Db 481 GTQNSNMCSLKNRKLPPFLLEEIWDVAEVSSTKLELATAADPGKTATTTTTTSEITT 540
 Qy 527 EDVAHAHADAL-----DDFDLMDLGDG--DSPGGGTFPHDSA-----PYGALDM 568
 Db 541 ETGALESDSLAHLHLLQPGTDEAAVALGLSLDFPSAGKAVLDDSDSFVWPAASFD 598

RESULT 15

ABU05378
 ID ABU05378 standard; protein; 615 AA.

XX AC ABU05378;

XX DT 29-AUG-2003 (revised)

XX DT 07-NOV-2002 (first entry)

XX DE Chimeric ecdysone receptor SEQ ID NO: 135.

KW Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor.

XX OS Manduca sexta.

OS Manduca sexta.
 OS Chimeric.

PN WO200261102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

DR N-PSDB; ABT07376.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.

XX Example 25; Page 299-301; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 615 AA;

Query Match 83.1%; Score 2551.5; DB 5; Length 615;
 Best Local Similarity 89.8%; Pred. No. 3.3e-206;
 Matches 501; Conservative 11; Mismatches 35; Indels 11; Gaps 3;

Qy 1 MQQLYVDFSPAFIRYLFAMVCFPCRCSPCLVLLQGSATMKLLSSIEQACDLCRLKL 60

Db 1 MQQLYVDFSPAFIRYLFAMVCFPCRCSPCLVLLQGSATMKLLSSIEQACDLCRLKL 60

Qy 61 KCSKEKPKCAKCLKNWECRSPKTRSPPLTRAHLTEVESRLERLEQLFLIFPREDLDM 120

Db 61 KCSKEKPKCAKCLKNWECRSPKTRSPPLTRAHLTEVESRLERLEQLFLIFPREDLDM 120

Qy 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

Db 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

Qy 181 GORQLTVSTRMRPECVVPESTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Db 181 GORQLTVSTRMRPECVVPESTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Qy 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300

Db 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300

Qy 301 TWQSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVM 360

Db 301 TWQLEEEEEEETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVM 360

Qy 361 MLRVARRYDAVSDVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALL 420

Db 361 MLRVARRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHYALL 420

Qy 421 TAIIVFSDRPGLEQPOLVEEIQRYLYLTLRVYIMNQHSAASPCAVIYAKILSVLTLERTL 480

Db 421 TAIIVFSDRPGLEQPOLVEEIQRYLYLTLRVYIMNQHSAASPCAVIFGKILGVLTLERTL 480

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Qy 481 GQNSNMCISLKNRKLPPLEETIDV-----KLAPPTDVSLGDEIHLGDGVANAH 534
Db 481 GTQNSNMCISLKNRKLPPLEETIDV-----KLAPPTDVSLGDEIHLGDGVANAH 538
Qy 535 DALDDFDLMLGDDSPG 552
Db 539 ---GETATPMAGGGGGG 553
```

Search completed: April 15, 2005, 14:49:22
Job time : 81 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1025.5	33.4	878	2	A41055	ecdysone receptor
2	1018	33.1	536	2	A56590	ecdysteroid receptor
3	754	24.5	881	1	RG5Y4	regulatory protein
4	429.5	14.0	447	2	I35975	nuclear orphan receptor
5	426.5	13.9	445	2	A56043	steroid hormone receptor
6	425	13.8	446	2	I49021	retinoid X receptor
7	423	13.8	446	2	IS9354	orphan nuclear receptor
8	423	13.8	479	1	IXBE1F	alpha trans-inducible
9	423	13.8	490	1	IXBE17	alpha trans-inducible
10	406	13.2	461	2	JC4014	steroid hormone-nuclear
11	316.5	10.3	484	2	I49018	retinoid X receptor
12	307	10.0	469	2	A56918	farnesoid x-activator
13	298.5	9.7	490	1	IXBE33	alpha trans-inducible
14	298.5	9.7	490	2	JS0689	virion protein 16
15	284	9.2	448	2	A43786	retinoic acid receptor
16	283.5	9.2	448	2	B56558	retinoic acid receptor
17	283.5	9.2	459	2	A41977	retinoic acid receptor
18	283.5	9.2	464	2	A55558	retinoic acid receptor
19	281.5	9.2	448	2	S04827	retinoic acid receptor
20	281	9.1	455	2	I35152	retinoic acid receptor
21	281	9.1	462	2	S05050	retinoic acid nuclear
22	280.5	9.1	452	2	S78481	retinoic acid receptor
23	280.5	9.1	458	2	S06123	retinoic acid receptor
24	280.5	9.1	462	1	A29491	retinoic acid receptor
25	280.5	9.1	955	4	C40045	probable transcription
26	280	9.1	448	2	S05051	retinoic acid receptor
27	279.5	9.1	453	2	I50674	retinoic acid receptor
28	274.5	8.9	454	2	S06124	retinoic acid receptor
29	273.5	8.9	473	2	C36067	thyroid hormone receptor

RESULT 2

A56590
ecdysteroid receptor homolog cERH - midge (*Chironomus tentans*)
C;Species: *Chironomus tentans*
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56590
R;Imhof M.O.; Rusconi, S.; Lezzi, M.
Insect Biochem. Mol. Biol. 23, 115-124, 1993
A;Title: Cloning of a *Chironomus tentans* cDNA encoding a protein (cERH) homologous to b
A;Reference number: A56590; MUID:93250857; PMID:8485513
A;Accession: A56590
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-536 <IMH>
A;Cross-references: UNIPROT:P49882; GB:S60739; NID:g385893; PIDN:AA60500.1; PID:g385894
A;Note: Sequence extracted from NCBI backbone (NCBIN:132124, NCBI:P132127)
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: DNA binding; steroid hormone receptor; zinc finger
F;113-432/Domain: erba transforming protein homology <ERBA>

Query Match 33.1%; Score 1018; DB 2; Length 536;
Best Local Similarity 52.4%; Pred. No. 2.6e-61;
Matches 207; Conservative 65; Mismatches 79; Indels 44; Gaps 5;
Qy 138 FVQDNVNDVTDRLASVETDMLTLRQHRISATSSSESSNKGORQLTVSTRMRPCV 197
Db 138 FFRSVTKNAVYCKFGHECEMDMYMR-----KQECRLKKCLAVGMRPCV 186
Qy 198 PESTCKNRRKEAQREKDKLP-----VSTTV-----DDHMPAIM 233
Db 107 PENCAIKRKKAKQEKDKVPGVGSNTSSSLLNQSLNLSKNLEISYRELLSQLM 246
Qy 234 QCDPPPPAAIRHEVVPFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGEQSEE 293
Db 247 KCDPPP-----HPMQQLPEKLMENRAGTGPOLTANQVAVIKLYWYQDGEQSEE 299
Qy 294 DLKRVTTQWSADEDESDMPFRQITETMTILTVQILVEFAKGLPGFSKIQPDITLLK 353
Db 300 DLKRITT--ELEEEEDQHEANFRYITETITLTQVILVEFAKGLPAFIFQEDQITLLK 357
Qy 354 ACSSEVMMLRVARYDAVSDSVLFANNOAYTRDNYRKAGMAYVEDLLHFCRCMYMSMD 413
Db 358 ACSSEVMMLRVARYDHDSDSILFANNYATYKQTYQLAGMEETIDDLHFCRQYALSID 417
Qy 414 NVHYALLTAIVFSDRPGLEQPOLVEEIQRYVNTLRVYINQHSASPRCAVIYAKILSV 473
Db 418 NVEYALLTAIVFSDRPGLEKAEWVDIIQSYVTETLKVIYIVNRHGGESRCSVQFAKLGI 477
Qy 474 LTELRTLGWNSNMCISLKNRKLPPLEEIWDV 508
Db 478 LTELRTMGNKSEMCFSLKNRKLPRFLEEWDV 512

RESULT 3

RGBYG4
regulatory protein GAL4 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein P1021; protein YP248C
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A05022; S61016; S65277; S12977
R;Laughon, A.; Gesteland, R.F.
Mol. Cell. Biol. 4, 260-267, 1984
A;Title: Primary structure of the *Saccharomyces cerevisiae* GAL4 gene.
A;Reference number: A05022; MUID:84141879; PMID:6366516
A;Accession: A05022
A;Molecule type: DNA
A;Residues: 1-881 <LAU>
A;Cross-references: UNIPROT:P04386; EMBL:K01486; NID:g171557; PIDN:AAA34626.1; PID:g1715
R;Gadnavi, P.L.; Raine, A.R.C.; Alefounder, P.R.; Laue, E.D.
FEBS Lett. 276, 49-53, 1990
A;Title: Complete assignment of the (1)H NMR spectrum and secondary structure of the DNA
A;Reference number: S12977; MUID:91092433; PMID:2265711

A;Contents: annotation; zinc finger

R;Pohl, T.M.

Submitted to the EMBL Data Library, November 1995

A;Reference number: S61010

A;Accession: S61016

A;Molecule type: DNA

A;Residues: 1-881 <POH>

A;Cross-references: EMBL:Z67751; NID:g1061234; PIDN:CAA91596.1; PID:g1061241

R;Pohl, T.M.

Submitted to the Protein Sequence Database, May 1996

A;Reference number: S64899

A;Accession: S65277

A;Molecule type: DNA

A;Residues: 1-881 <POW>

A;Cross-references: EMBL:Z73604; NID:g1370510; PIDN:CAA97969.1; PID:g1370511; GSPDB:GN00

A;Experimental source: strain S288C (AB972)

C;Comment: This protein is a positive regulator for the gene expression of the galactose

C;Genetics:

A;Gene: SGD:GAL4; MIPS:YPL248C

A;Cross-references: SGD:S0006169; MIPS:YPL248C

A;Map position: 16L

C;Superfamily: regulatory protein GAL4; GAL4 zinc binuclear cluster homology

C;Keywords: DNA binding; galactose utilization; transcription regulation; zinc finger

F;6-43/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F;11-38/Region: zinc finger CCCC motif

Query Match 24.5%; Score 754; DB 1; Length 881;
Best Local Similarity 38.0%; Pred. No. 3.8e-43;
Matches 208; Conservative 58; Mismatches 129; Indels 152; Gaps 18;
Qy 42 MKLLSSIEQAACDLCRLKLCSCKEKPKCAKCLKNNECRYSPKTKRSPLTRAHLTEVESR 101
Db 1 MKLLSSIEQAACDLCRLKLCSCKEKPKCAKCLKNNECRYSPKTKRSPLTRAHLTEVESR 60
Qy 102 LERLEQLFLIFPREDLMTLKWDSLODIKALLTGLFVQDNVNDVTDRLASVETDML 161
Db 61 LERLEQLFLIFPREDLMTLKWDSLODIKALLTGLFVQDNVNDVTDRLASVETDML 120
Qy 162 TLRQHRISATSSSESSNKGORQLTVSTRMRPCVWPESCKNKRREKAEQREKDKLPVS 221
Db 121 TLRQHRISATSSSESSNKGORQLTVSI-----DSAAHNDNSTIPLD 162
Qy 222 TTTVD-----DHMPAIMQCDPP----- 238
Db 163 FMRDALHGFDSSEDDMSDGLP-FLKTDNNNGFFGDSLLCILRSIGFKPENYTSNV 221
Qy 239 ---PPEARIRHEVVPFLTEKMEQNRLKNVTPLS--ANOKSLIARLVWYQDGEQSEE 293
Db 222 NRLPTMTITDRYTLASRTTSRL--QSYLNNFHPYCPVHSPTL---MMLYNNQIEIASDK 277
Qy 294 DLKRVTTQW-----SADBEDESDMPFRQITETMTILTVQILVEFAKGLPGFS 341
Db 278 Q-----WQLFNCLIAIGAWCIEGSTDIDVFYQNAKSHLT-----S 315
Qy 342 KISQPDQITLLKACSEVMMLRVAR-----RYDAVSDSVLFANNOAYTRDNYRKAGMA 394
Db 316 KVFESSGILVLTALH---LLSRVYTWQKNTSINPHSFISIRMAISLGLNRDLPSFSDS 372
Qy 395 YVIEDLLHFCRCMYMSMDNVHYALLTAIVFSDRPGLEQPOLVEEIQRYVNTLRVYIM 454
Db 373 SILEQRRRIWMSVYSW---EIQLSLTVGRSISQNTSIFPSSVDDVOR----- 418
Qy 455 NQHSASPRCAVIY-----AKILSVLTTEL---RTLGMQNSNMCI-----SLKKNR 496
Db 419 --TTTGP---TIYHGIIETARLLQVFTKIYELDKVTVAEKSPICAKKCLMCNIEEVS 473
Qy 497 KLPPPLE 503
Db 474 QAPKFLQ 480

RESULT 4
138975

QY	251	RFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGEQSPSEEDLKRVTQTQWSADEED-	309
Db	203	Q-----LSPEQLGMIEKLVAAQQCNRRSFSDRLRVT-PWPIADPPOS	244
QY	310	-EDSDMPFRQITENTILTVQLIVFEKAGLPGFSGKISQPDQITLLKACSEVMMLRVARRY	368
Db	245	REARQORFAHPTELAIIVSQEIVDFAKQLPGFQLSREDQIALKLTSAIEVMLLETSSRY	304
QY	369	DAVSDSVLFANNQYATRDNRKAGM-AYIETDLLHFCRCWYSGMSDNVHYALLTAIVIPS	427
Db	305	NPGESITFLKDFSYNREDPAKAGLQVEFINPIFEFSRSMNELQLNDASFALLIAISIPS	364
QY	428	-DRGLQEPQVLEEIQRYLYNTLRVIMQHSAPRCAVIYAKILSVLTETLRTLGHQNSN	486
Db	365	ADRPNVODQLQVERLOHTTYVEALHAYVINSIH----PHDRLMFPRLMLKGLVSLRTLSSVHSE	421

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QY      487 MCISLKLNKRLPPFLEEWDV 508
      :|:|:|:|:|:|:|:|:|
Db      422 QVFALRLQDKKLPPLLSEIWDV 443

RESULT 6
I49021
retinoid X receptor interacting protein No.15 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49021

```

107	Conceivably	62	Mismatches	123	Indels	30	Gaps
191	NRPECVVPESTCKNKRREKAQREKOKLPVSTTTVDHMPA	191	MRPECVVPESTCKNKRREKAQREKOKLPVSTTTVDHMPA	191	MRPECVVPESTCKNKRREKAQREKOKLPVSTTTVDHMPA	191	MRPECVVPESTCKNKRREKAQREKOKLPVSTTTVDHMPA
145	MREQVLSEGIQRKRIQKQKQKQ	145	MREQVLSEGIQRKRIQKQKQKQ	145	MREQVLSEGIQRKRIQKQKQKQ	145	MREQVLSEGIQRKRIQKQKQKQ
251	RF	251	RF	251	RF	251	RF
184	AASPGTSEASQSGEGEGLTAAQELMIIQVLAALQCNKRSE	184	AASPGTSEASQSGEGEGLTAAQELMIIQVLAALQCNKRSE	184	AASPGTSEASQSGEGEGLTAAQELMIIQVLAALQCNKRSE	184	AASPGTSEASQSGEGEGLTAAQELMIIQVLAALQCNKRSE
108	RDRDS	108	RDRDS	108	RDRDS	108	RDRDS

```

485 SNMCISLKLNRKLPPLPSEIWDV 508
      |:::| | | | |
421 SEQVFAIRLQDKLPPLLSIWDV 444

```


[illegible]

A;Note: host Homo sapiens (man)

[illegible]

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Feb-1997

A:Accession: A41562
R:Greaves, R.F.; O'Hare, P.
J. Virol. 65, 6705-6713, 1991
A:Title: Sequence, function, and regulation of the Vmw65 gene of herpes simplex virus type 1
A:Reference number: A41562; MUID:92046332; PMID:1658370
A:Accession: A41562
A:Molecule type: DNA
A:Residues: 1-490 <RES>
A:Cross-references: GB:M75098
A:Superfamily: herpesvirus alpha trans-inducing protein
C:Keywords: DNA binding; trans-inducing protein; transcription

Query Match 9.7%; Score 298.5; DB 1; Length 490;
Best Local Similarity 74.4%; Pred. No. 1.2e-12;
Matches 58; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 511 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGFTPHDSAPYCALDMAD 570

Db 414 APITDVSIGDELRLDGEEDVMTPADALDDFDLEMLGDVESPSPGMT-HDPVSYGALDVDD 472

Qy 571 FEFEQMTDANGIDDEYGG 588

Db 473 FEFEQMTDANGIDDEYGG 490

RESULT 14

JS0689
virion protein 16 - human herpesvirus 2
C:Species: human herpesvirus 2
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 26-Aug-1999
A:Accession: JS0689
R:Cross, A.; Triesenberg, S.J.
Gene 103, 235-238, 1991
A:Title: Nucleotide and deduced amino acid sequences of the gene encoding virion protein 16
A:Reference number: JS0689; MUID:91365250; PMID:1653757
A:Accession: JS0689
A:Molecule type: DNA
A:Residues: 1-490 <RES>

A:Cross-references: GB:M60050; NID:9330317; PIDN:AAA45863.1; PID:9330318
A:Experimental source: strain HG52
C:Superfamily: herpesvirus alpha trans-inducing protein
C:Keywords: DNA binding; transcription regulation

Query Match 9.7%; Score 298.5; DB 2; Length 490;
Best Local Similarity 74.4%; Pred. No. 1.2e-12;
Matches 58; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 511 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGFTPHDSAPYCALDMAD 570

Db 414 APITDVSIGDELRLDGEEDVMTPADALDDFDLEMLGDVESPSPGMT-HDPVSYGALDVDD 472

Qy 571 FEFEQMTDANGIDDEYGG 588

Db 473 FEFEQMTDANGIDDEYGG 490

RESULT 15

A43786
retinoic acid receptor beta-4 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 11-Dec-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
A:Accession: A43786; S14291; A60129; S17072; S16243
R:Smith, S.M.; Eichele, G.
Development 111, 245-252, 1991
A:Title: Temporal and regional differences in the expression pattern of distinct retinoic acid receptors
A:Reference number: A43786; MUID:91199956; PMID:1849811
A:Accession: A43786
A:Molecule type: mRNA
A:Residues: 1-448 <SMI>

A:Cross-references: UNIPROT:P22448; GB:X59473; NID:963753; PIDN:CAA42077.1; PID:963754
A>Note: the authors translated the codon ACT for residue 96 as Ser, TCC for residue 167
R:Noji, S.; Nohno, T.; Koyama, E.; Muto, K.; Ohya, K.; Aoki, Y.; Tamura, K.; Ohnogi, K.

Nature 350, 83-86, 1991

A:Title: Retinoic acid induces polarizing activity but is unlikely to be a morphogen in the chicken embryo
A:Reference number: S14291; MUID:91163640; PMID:1848357
A:Accession: S14291
A:Molecule type: mRNA
A:Residues: 1-95; 'S', '97-448 <NOJ>
A:Cross-references: EMBL:X57340; NID:962976; PIDN:CAA40616.1; PID:962977
R:Rowe, A.; Richman, J.M.; Brickell, P.M.
Development 111, 1007-1016, 1991
A:Title: Retinoic acid treatment alters the distribution of retinoic acid receptor-beta in the chicken embryo
A:Reference number: A60129; MUID:91347912; PMID:1652423
A:Accession: A60129
A:Molecule type: mRNA

A:Residues: 23-24, 26-95; 'S', '97-165; 'D', '167-448 <ROW>
A:Cross-references: GB:563196; NID:9234370; PIDN:AAB19628.1; PID:9234371
R:Nohno, T.
submitted to the EMBL Data Library, January 1991
A:Reference number: S17072
A:Accession: S17072
A:Molecule type: mRNA

A:Residues: 15-95; 'S', '97-434 <NOH1>
A:Cross-references: EMBL:X57339
R:Nohno, T.; Muto, K.; Noji, S.; Saito, T.; Taniguchi, S.
Biochim. Biophys. Acta 1089, 273-275, 1991
A:Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
A:Reference number: S16243; MUID:91274365; PMID:1647216
A:Accession: S16243
A:Molecule type: mRNA

A:Residues: 15-60 <NOH2>
A:Cross-references: EMBL:X57339
C:Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; zinc finger
F:79-330/Domain: erba transforming protein homology <ERBA>
F:81-101/Region: zinc finger
F:117-141/Region: zinc finger

Query Match 9.2%; Score 284; DB 2; Length 448;
Best Local Similarity 22.8%; Pred. No. 1e-11;
Matches 119; Conservative 80; Mismatches 159; Indels 164; Gaps 19;

Qy 110 LLIFPREDLMLKMS---LQP--IKALITGLFVQDNVKNDAVTDRLASVETDMLTLR 164

Db 8 LAVSPAQMLDFYTASPSCLQKALKACFSGL-----AQTEW----- 45

Qy 165 QHRISATS-----SSEE-----SSN-----KG-- 181

Db 46 QHRHSAQSVETQSTSEELVPSPPPLPPRVKPCVQCQDKSGSYHYVTACGCKGFF 105

Qy 182 ---QRLTVSTRMRPCVVPEST-----C-----KNKRKEKAQR 213

Db 106 RRSIQKMWVYCHRDKNVCINKVTRNCQYCRLOKCEVGSKESVNDNRNKKKEPTKQ 165

Qy 214 EKOKLPVSTTTVDHMPAIMQCDDPPPEAAAIHEVVRFLTEKLMEQNRLKNVTPLSAQ 273

Db 166 ESTENYEMTAELDD-----LTKIRK-----AQTEW----- 189

Qy 274 KSILARLVWYQDGYEQSPSEEDLKRVTQTWOSADEEDSDMPFRQITMTILTQLVIVEP 333

Db 190 ETF-----PSCQLGKYT--TNSADHRVRLDLGLWDFSELATKCIKIVEF 235

Qy 334 AKGLPGFSKISQPDQITLLKACSVSEVMVLRVARYDAVSDVLFANQAVTRDNRKAGM 393

Db 236 AKLPGFTSLTIADQITLLKACGLDILILICITRYPEQDTMTFSDGLTLNRQTMHAGP 295

Qy 394 AYVIEDLLHFCRCMYGSMNDVHALLTAI-VIFSDRPLEQPOLVBEIQRYYLNTURVY 452

Db 296 GLPTDLVFTFANQLLPLEMDDTETGLLSAICLCIGDRQDLDEEPKMKVQLQEPLEALKIY 355

Qy 453 IMNQHSNPRCAVIYAKILSVLTSLRTLGNQSNMCSLKLK-NRKLPPPELEEDVVKLA 511

Db 356 IRKRPNKPH---MFPKILMKITDLRSISAKGAERVITLKVETPGSMPLIQEMLENSEG 412

Qy 512 --PPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGDS 551

Db 413 HEPLTPTSGN-----TAHSPSPSPSSVDNSSVSQSP 445

Search completed: April 15, 2005, 14:47:56
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 77 Seconds
(without alignments)
3910.423 Million cell updates/sec

Title: US-10-087-167-121

Perfect score: 3072

Sequence: 1 MQQLYVDFSPAFIRYLPWF.....ADFFEQMTDALGIDYGG 588

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1557	50.7	556	1 ECR MANSE	P49883 manduca sex
2	1552.5	50.5	518	2 Q8MYA7	Q8MYA7 chilo suppr
3	1552.5	50.5	547	2 Q8MYA6	Q8MYA6 chilo suppr
4	1525.5	49.7	541	2 Q6RVD3	Q6RVD3 plodia inte
5	1504	49.0	339	2 Q9U0R9	Q9U0R9 junonia coe
6	1470.5	47.9	576	1 ECR HELVI	Q18473 heliothis v
7	1467	47.8	513	2 Q77240	Q77240 choriostoneu
8	1467	47.8	541	2 Q77255	Q77255 choriostoneu
9	1418	46.2	346	2 Q9U3U4	Q9U3U4 bicyclus an
10	1416	46.1	606	1 ECR BOMMO	P49881 bombyx mori
11	1142	37.2	680	2 Q9U3Y4	Q9U3Y4 aedes alboop
12	1139	37.1	675	1 ECR ASDAE	P49880 aedes aegypt
13	1139	37.1	776	2 Q6VA69	Q6VA69 aedes aegypt
14	1050	34.2	757	1 ECR LUCCU	O18531 lucilia cup
15	1046	34.0	784	2 Q9GPH1	Q9GPH1 calliphora
16	1033	33.6	673	2 Q76827	Q76827 ceratitis c
17	1025.5	33.4	878	1 ECR DROME	P34021 drosophila
18	1018	33.1	536	1 ECR CHITE	P49882 chironomus
19	1003	32.6	520	2 Q7PVB2	Q7PVB2 anopheles g
20	867.5	28.1	541	2 Q97095	Q97095 locusta mig
21	864.5	28.1	491	2 O02035	O02035 tenebrio mo
22	754	24.5	881	1 GAL4 YEAST	P04386 saccharomyc
23	754	24.5	881	2 Q76MW9	Q76MW9 drosophila
24	753.5	24.5	518	2 Q76246	Q76246 uca pugilat
25	749	24.4	444	2 O44336	O44336 amblyomma a
26	749	24.4	560	2 O44337	O44337 amblyomma a
27	749	24.4	570	2 O44338	O44338 amblyomma a
28	732	23.8	336	2 Q6RIB4	Q6RIB4 carcinus ma
29	685	22.3	403	2 Q8MWR2	Q8MWR2 spodoptera
30	663	21.6	212	2 Q8MWR0	Q8MWR0 trichoplusi
31	497	16.2	182	2 Q8NGU6	Q8NGU6 sarcophaga

32	495	16.1	181	2	Q75ZW2	Q75ZW2 lucilia ser
33	463	15.1	207	2	Q9XYR8	Q9XYR8 bradyzia hy
34	433.5	14.1	402	2	Q8IWI3	Q8IWI3 homo sapien
35	433.5	14.1	447	1	NRH3 HUMAN	Q13133 homo sapien
36	428.5	13.9	445	2	Q91X41	Q91X41 mus musculu
37	427.5	13.9	445	1	NRH3 MOUSE	Q940Y9 mus musculu
38	426.5	13.9	445	1	NRH3 RAT	Q62685 ratus norv
39	425	13.8	443	2	Q8BP65	Q8BP65 mus musculu
40	425	13.8	446	1	NRH2 MOUSE	Q60644 mus musculu
41	423	13.8	446	1	NRH2 RAT	Q62755 ratus norv
42	423	13.8	479	1	ATIN_HHVL	P04486 human herpe
43	423	13.8	490	1	ATIN_HHVL	P04492 human herpe
44	418.5	13.6	409	2	Q8JHUI	Q8JHUI gallus gall
45	416.5	13.6	409	2	Q8AXU8	Q8AXU8 gallus gall

ALIGNMENTS

RESULT 1

ID	ECR MANSE	STANDARD	PRT	556 AA
AC	P49883			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor)			
DE	receptor (20E receptor)			
GN	Name=ECR; Synonyms=NR1H1;			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm)			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Sphingioidea;			
OX	Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95360028; PubMed=7633469; DOI=10.1016/0965-1748(95)00023-O;			
RA	Fujiwara H., Jindra M., Newitt R., Palli S.R., Hiruma K.,			
RA	Riddiford L.M.;			
RT	"Cloning of an ecdysone receptor homolog from Manduca sexta and the developmental profile of its mRNA in wings."			
RL	Insect Biochem. Mol. Biol. 25:845-856(1995).			
CC	-!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES).			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- TISSUE SPECIFICITY: It is found in both larval wing disks and pupal wings and in prothoracic glands. Levels increase on day 2			
CC	-!- DEVELOPMENTAL STAGE: In the wing disks reaching a maximum on day 5, and then decrease sharply on day 6. In the prothoracic glands levels increase			
CC	sharply on day 2 then remain high throughout the larval-pupal transformation and after pupal ecdysis			
CC	-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U19812; AAA86699.1; -			
DR	HSSP; P20393; IAGf.			
DR	InterPro; IPR000536; Hrmn_recept_lig.			
DR	InterPro; IPR001723; Stdhrmn_receptor.			
DR	InterPro; IPR008946; Str_ncl_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF00104; Hormone_recep; 1.			
DR	Pfam; PF00105; zf-C4; 1.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			

DR ProDom; PD000035; Znf C4steroid; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 FT DOMAIN 1 146 Modulating (Potential).
 FT DNA BIND 147 212 Nuclear receptor-type.
 FT ZN_FING 147 167 C4-type.
 FT ZN_FING 183 207 C4-type.
 FT DOMAIN 305 528 Hormone-binding (Potential).
 FT DOMAIN 75 84 Poly-Gln.
 FT DOMAIN 258 261 Poly-Pro.
 FT DOMAIN 326 332 Poly-Glu.
 SQ SEQUENCE 556 AA; 62830 MW; 9AF83AA33D551EB1 CRC64;

Query Match 50.7%; Score 1557; DB 1; Length 556;
 Best Local Similarity 91.2%; Pred. No. 2.4e-92;
 Matches 300; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRREKAEQREKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 250
 DB 212 MRPECVPESTCKNKRREKAEQREKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 271

QY 251 RFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQSADEDE 310
 DB 272 RFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQLEEEEEE 331

QY 311 DSDMPFROITETILTQVLIVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVARYDA 370
 DB 332 ETDMPFROITETILTQVLIVEFAKGLPGFSKISQSDQITLLKACSSVMMRLVARYDA 391

QY 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 430
 DB 392 ATDSVLFANNQAYTRDNYRKAGMSVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 451

QY 431 GLEQPOLVEEQRYVYLNTRVYIMNQHSAPRCVAVIYAKILSVLTETRLTGQNSMNCIS 490
 DB 452 GLEQPLVEEQRYVYLNTRVYIMNQHSAPRCVAVLFGKILGVLTELTLTGTONSMNCIS 511

QY 491 LKLNKRLPPFLEEIWDVKLAPPTDVSIG 519
 DB 512 LKLNKRLPPFLEEIWDVAEVSTTQPTPG 540

RESULT 2
 Q8MYA7
 ID Q8MYA7 PRELIMINARY; PRT; 518 AA.
 AC Q8MYA7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ecdysone receptor A isoform.
 GN Name=C8EcR-A;
 OS Chilo suppressalis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Crambinae; Chilo.
 OX NCBI_TaxID=168631;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fat body;
 RX MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
 RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
 FT "Molecular cloning, expression analysis and functional confirmation of
 RT two ecdysone receptor isoforms from the rice stem borer Chilo
 RT suppressalis.";
 RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.
 DR EMBL; AB067811; BAC11713.1; --
 DR HSSP; P34021; 1R00.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdystd receptor.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strdhmn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; Znf C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 518 AA; 58320 MW; 5E757803E248E118 CRC64;

Query Match 50.5%; Score 1552.5; DB 2; Length 518;
 Best Local Similarity 85.0%; Pred. No. 4.3e-92;
 Matches 301; Conservative 18; Mismatches 12; Indels 23; Gaps 2;

QY 191 MRPECVPESTCKNKRREKAEQREKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARI----- 245
 DB 178 MRPECVPESTCKNKRREKAEQREKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARILECLQ 237

QY 246 HEVVPFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQSA 305
 DB 238 HEVVPFLSEKLEQNRLKNVPLTANQQQLIARLVYQGYEQPSEEDLKRVTTQWQSN 297

QY 306 DEDESDMPFROITETILTQVLIVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVA 365
 DB 298 EDEEETDLFPRITETILTQVLIVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVA 357

QY 366 RRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 425
 DB 358 RRYDAASDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAVVI 417

QY 426 FSDRPGLEQPOLVEEQRYVYLNTRVYIMNQHSAPRCVAVIYAKILSVLTETRLTGQNS 485
 DB 418 FSDRPGLEQPOLVEEQRYVYLNTRVYIMNQHSAPRCVAVIYAKILSVLTETRLTGQNS 477

QY 486 NMCISLKNKRLPPFLEEIWDVKLAPPTDVSIGDELHGDGEDVAMAHADALDD 539
 DB 478 NMCISLKNKRLPPFLEEIMDV-----ADVSAAQAAPAIMD 513

RESULT 3
 Q8MYA6
 ID Q8MYA6 PRELIMINARY; PRT; 547 AA.
 AC Q8MYA6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ecdysone receptor B1 isoform.
 GN Name=C8EcR-B1;
 OS Chilo suppressalis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Crambinae; Chilo.
 OX NCBI_TaxID=168631;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fat body;
 RX MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
 RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
 RT "Molecular cloning, expression analysis and functional confirmation of
 RT two ecdysone receptor isoforms from the rice stem borer Chilo
 RT suppressalis.";
 RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AB067812; BAC11714.1; --
 DR HSP; P34021; IROO.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdysd receptor.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strdhrm_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 547 AA; 61815 MW; 33528572066256E CRC64;

Query Match 50.5%; Score 1552.5; DB 2; Length 547;
 Best Local Similarity 85.0%; Pred. No. 4.6e-92;
 Matches 301; Conservative 18; Mismatches 12; Indels 23; Gaps 2;

QY 191 MRPCVPESTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARI----- 245
 DB 207 MRPCVPEPTCAIKRKEKAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARILECLQ 266

QY 246 HGVVPRFELTEKMEQNRKKNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTTQWOSA 305
 DB 267 HGVVPRFELTEKMEQNRKKNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTTQWOSN 326

QY 306 DSEEDSDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSESVNMLRVA 365
 DB 327 DEEEDTDLPRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSESVNMLRVA 386

QY 366 RRYDAVSVLFPANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 425
 DB 387 RRYDAVSVLFPANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSLMDVHYALLTAVVI 446

QY 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSAASPRCAVIYAKILSVLTSLRTLGMONS 485
 DB 447 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSAASPRCAVLYAKILSVLTSLRTLGMONS 506

QY 486 NMCISLKNRKLPPFLEBIWVKLAPPTDVSGLDELHGDGVAMAHADALDD 539
 DB 507 NMCISLKNRKLPPFLEBIWVKLAPPTDVSGLDELHGDGVAMAHADALDD 542

RESULT 4
 Q6RVD3
 ID Q6RVD3 PRELIMINARY; PRT; 541 AA.
 AC Q6RVD3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ecdysone receptor.
 OS Plodia interpunctella (Indianmeal moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysa; Pyraloidea;
 OC Pyralidae; Phycitinae; Plodia.
 OX NCBI_TaxID=58824;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slausat D., Debernard S., Bozzolan F., Queguiner I., Porcheron P.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY489269; AAR84611.1; --
 DR HSP; P20393; 1A6Y.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdysd receptor.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strdhrm_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 541 AA; 61030 MW; 145588BE2EFA07AD CRC64;

Query Match 49.7%; Score 1525.5; DB 2; Length 541;
 Best Local Similarity 88.0%; Pred. No. 2.5e-90;
 Matches 294; Conservative 16; Mismatches 17; Indels 7; Gaps 2;

QY 191 MRPCVPESTCKNKRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARIHEVVP 250
 DB 208 MRPCVPEPTCAIKRKEKAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARIHEVVP 267

QY 251 RFLTEKMEQNRKKNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTTQWOSAEDDE 310
 DB 268 RFLTEKMEQNRKKNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTTQWOTDEDD 327

QY 311 DSDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSESVMLRVARRYDA 370
 DB 328 --DMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSESVMLRVARRYDA 385

QY 371 VDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 430
 DB 386 ATDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 445

QY 431 GLEQPOLVEEQRYLNTLRVYIMNQHSAASPRCAVIYAKILSVLTSLRTLGMONSNCIS 490
 DB 446 GLEQPOLVEEQRYLNTLRVYIMNQHSAASPRCAVVGKILSVLTSLRTLGMONSNCIS 505

QY 491 LKLNKRKLPPFLEBIWVKLAPPTDVSGLDELHL 524
 DB 506 LKLNKRKLPPFLEBIWVKLAPPTDVSGLDELHL 534

RESULT 5
 Q9UOR9
 ID Q9UOR9 PRELIMINARY; PRT; 339 AA.
 AC Q9UOR9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ecdysone receptor (Fragment).
 OS Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysa;
 OC Papilionidae; Nymphalidae; Junonia.
 OX NCBI_TaxID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=wing;
 RA Reinhardt R.K., Weber P., Koch P.B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

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CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC EMBL: AJ251809; Belongs to the nuclear hormone receptor family.
DR HSSP; P34021; 1ROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003699; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR Pfam; PF001628; Znf_C4steroid.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR SMART; SM00430; HOL1; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39363 MW; 3EC1C7AD294782EB CRC64;

Query Match 49.0%; Score 1504; DB 2; Length 339;
Best Local Similarity 89.6%; Pred. No. 3.3e-89;
Matches 283; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPPPEAAARIHEVVP 250
DB 24 MRPECVPESTCKNRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPPPEAAARIHEVVP 83

QY 251 RLTEKLMQNLKKNVPLSLANOKSLIARLVWYQGYEQPSDEDLKRVTTQWQADEDE 310
DB 84 RLTEKLMQNLKKNVPLSLANOKSLIARLVWYQGYEQPSDEDLKRVTTQWQADEDE 143

QY 311 DSDMPFROITTEMTILTVQVIFAFKGLPGFSKISQDQITLLKACSSSEVMMLRVA 370
DB 144 ESDLFPROITTEMTILTVQVIFAFKGLPGFSKISQDQITLLKACSSSEVMMLRVA 203

QY 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 430
DB 204 TTDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 263

QY 431 GLEQQLVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTETLGLMGNSNMCI 490
DB 264 GLEQQLVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTETLGLMGNSNMCI 323

QY 491 LKLNKRLPPPLEEIIW 506
DB 324 LKLNKRLPPPLEEIIW 339

RESULT 6
ECR_HELVI STANDARD; PRT; 576 AA.
AC O18473;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor) (HVECR).
GN Name=ECR; Synonyms=NRH1;
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxId=7102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRC;
RX MEDLINE=99457718; PubMed=10528411; DOI=10.1016/S0965-1748(99)00067-3;

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RA Martinez A., Scanlon D., Gross B., Perara S.C., Palli S.R.,
RT Greenland A.J., Windass J., Pongs O., Broad P., Jepson I.;
RT "Transcriptional activation of the cloned Heliothis virescens
RL (Lepidoptera) ecdysone receptor (HVECR) by muristeroneA.";
CC Insect Biochem. Mol. Biol. 29:915-930(1999).
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement. See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk.
CC -----
CC EMBL; Y09009; CAA70212.1; -.
CC PDB; 1R1K; X-ray; D=288-550.
CC InterPro; IPR000536; Hrmn_recept_lig.
CC InterPro; IPR001723; Strdhmn_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; Hormone_recep; 1.
CC Pfam; PF00105; Zf-C4; 1.
CC PRINTS; PR00398; STRDHOMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC PRODOM; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00359; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW 3D-structure; DNA-binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc-finger.
KW DOMAIN 1 162 Modulating (Potential).
FT DNA_BIND 163 228 Nuclear receptor-type.
FT ZN_FING 163 183 C4-type.
FT ZN_FING 199 223 C4-type.
FT DOMAIN 326 545 Hormone-binding (Potential).
SQ SEQUENCE 576 AA; 64638 MW; D13EF787BF263A8 CRC64;

Query Match 47.9%; Score 1470.5; DB 1; Length 576;
Best Local Similarity 88.5%; Pred. No. 1e-86;
Matches 286; Conservative 15; Mismatches 13; Indels 9; Gaps 2;

QY 191 MRPECVPESTCKNRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPPPEAAARI----- 245
DB 228 MRPECVPESTCKNRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPPPEAAARILECVQ 287

QY 246 HEVVPRELTEKLMQNLKKNVPLSLANOKSLIARLVWYQGYEQPSDEDLKRVTTQWQA 305
DB 288 HEVVPRELTEKLMQNLKKNVPLSLANOKSLIARLVWYQGYEQPSDEDLKRVTTQWQA 343

QY 306 DEDEDSMDPFRQITTEMTILTVQVIFAFKGLPGFSKISQDQITLLKACSSSEVMMLRVA 365
DB 344 DEDEDSMDPFRQITTEMTILTVQVIFAFKGLPGFSKISQDQITLLKACSSSEVMMLRVA 403

QY 366 RRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 425
DB 404 RRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 463

QY 426 FSDRPGLEQQLVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTETLGLMGNS 485
DB 464 FSDRPGLEQQLVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTETLGLMGNS 523

QY 486 NMCIISLKLKKNRKLPPPLEEIIW 508
DB 524 NMCIISLKLKKNRKLPPPLEEIIW 546

RESULT 7
O77240

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RESULT 8

ID	O77255	PRELIMINARY;	PRT;	541 AA.
AC	O77255;			
DT	01-NOV-1998	(TRENBLrel. 08, Created)		
DT	01-MAY-2000	(TRENBLrel. 13, Last sequence update)		
DT	01-MAR-2004	(TRENBLrel. 26, Last annotation update)		
DE	Ecdysteroid receptor ECR-B.			
OS	Choristoneura fumiferana (Spruce budworm).			
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
OC	Tortricoidea; Tortricidae; Tortricinae; Choristoneura.			
OX	NCBI_TaxID=71141;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=96191152; PubMed=8641050;			
RX	Kothapalli R., Palli S.R., Ladd T.R., Sohi S.S., Cress D.,			
RA	Dhadiella T.S., Tzertzinis G., Retnakaran A.;			
RA	"Cloning and developmental expression of the ecdysone receptor gene			
RT	from the spruce budworm, Choristoneura fumiferana.";			
RL	Dev. Genet. 17:319-330(1995).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Kothapalli R., Palli S.R., Ladd T., Retnakaran A.;			
RA	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	Palli R.;			
RA	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).			
CC	-1- SIMILARITY: Belongs to the nuclear hormone receptor family.			
CC	EMBL; U29531; AAC36491.2; -;			
DR	HSP; P34021; IR00.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.			
DR	GO; GO:0005496; F:steroid binding; IEA.			
DR	GO; GO:0003700; P:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR003069; Ecdystd_receptor.			
DR	InterPro; IPR000536; Hmon_recept_l1g.			
DR	InterPro; IPR001723; Stdhrmn_receptor.			
DR	InterPro; IPR008946; Str_ncl_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF001104; Hormone_recep; 1.			
DR	Pfam; PF001105; zf-C4; 1.			
DR	PRINTS; PR01283; ECDYSTEROIDR.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			
DR	ProDom; PD000035; Znf_C4steroid; 1.			
DR	SMART; SM00430; HOLI; 1.			
DR	SMART; SM00399; Znf_C4; 1.			
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.			
DR	DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;			
KW	Transcription regulation; Zinc; Zinc-finger.			
QQ	SEQUENCE 541 AA; 61153 MW; C78D28D7D2B868CD CRC64;			
SQ				

Query Match 47.8%; Score 1467; DB 2; Length 541;
Best Local Similarity 86.2%; Pred. No. 1.5e-86;
Matches 274; Conservative 27; Mismatches 17; Indels 0; Gaps

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QY 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHYALLTAIVFSDRP 430
DB 386 ASDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMALDNIHYALLTAVVIFSDRP 445
QY 431 GLEQPOLVEEQRYYLNTLRVYIMNHQASPRCAVIYAKILSVLTELRTLGQNSMNCIS 490
DB 446 GLEQPOLVEEQRYYLNTLRVYILNQLSGSARSSVIYKILSVLSELRTLGQNSMNCIS 505
QY 491 LKLKRNKLPPLFEEIWDV 508
DB 506 LKLKRNKLPPLFEEIWDV 523

RESULT 9
Q9U3U4
ID Q9U3U4 PRELIMINARY; PRT; 346 AA.
AC Q9U3U4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)
DE Ecdysteroid receptor (Fragment).
GN Name=ecr;
OS Bicyclus anynana (squinting bush brown).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Satyrinae; Elymnini; Mycalesina;
OC Bicyclus.
OX NCBI_TaxID=110368;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=wing;
RA Reinhardt R.K., Weber P., Koch P.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AJ251810; CAB63236.1; -.
DR HSSP; P34021; 1ROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strhnm_receptor.
DR InterPro; IPR008946; Str ncl_receptor.
DR InterPro; IPR001628; Znf C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zfc-C4; 1.
DR PRINTS; PRO1283; ECDYSTEROIDR.
DR PRINTS; PRO0398; STRDHORMONER.
DR SMART; SM00430; HOL1; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
FT Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 346
SQ SEQUENCE 346 AA; 40036 MW; 04323E79C2D055D2 CRC64;

Query Match 46.2%; Score 1418; DB 2; Length 346;
Best Local Similarity 84.2%; Pred. No. 1.2e-83;
Matches 272; Conservative 23; Mismatches 22; Indels 6; Gaps 2;

QY 191 MRPECVPESTCKNKRKEAQREKDKLPVSTTTVDHMPAIMQCDPPPPAAARI----- 245
DB 24 MRPECVPESTCKNKRKEAQREKDKLPVSTTTVDHMPAIMQCDPPPPAAARILECLQ 83
QY 246 HEVWPRFTEKLMQNRKLVNTPLSANOKSLIARLVVYQDGYEOPSEEDLKRVTQTWQSA 305
DB 84 HEVWPRFTEKLMQNRKLVNTPLSANOKSLIARLVVYQDGYEOPSEEDLKRVTQTWQAD 143
QY 306 DEE-DESDMPFRQITWMTILTVQIVFAKGLPGFSKISQPDQITLLKACSSYVMMLRV 364

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DB 144 TEEIGASDLPPFRQITWMTILTVQIVFAKGLPGFAKISQPDQITLLKACSSYVMMLRV 203
QY 365 ARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHYALLTAIV 424
DB 204 SRRYDMSDTSVMPFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHYALLTAVV 263
QY 425 IFSDRPGLEQPOLVEEQRYYLNTLRVYIMNHQASPRCAVIYAKILSVLTELRTLGQNSMNCIS 484
DB 264 IFSDRPGLEQPOLVEEQRYYLNTLRVYILNQLSGSARSSVIYKILSVLSELRTLGQNSMNCIS 323
QY 485 SNMCISLKLKRNKLPPLFEEIWDV 507
DB 324 SNMCISLKLKRNKLPPLFEEIWDV 346

RESULT 10
ECR_BOMMO
ID ECR_BOMMO STANDARD; PRT; 606 AA.
AC P49881;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).
GN Name=ECR; Synonyms=NR1H1;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Myosore; TISSUE=Ovary;
RX MEDLINE=95360029; PubMed=7633470; DOI=10.1016/0965-1748(95)00024-P;
RA Swevers L., Drevet J.R., Lunke M.D., Iatrou K.;
RT "The silkworm homolog of the Drosophila ecdysone receptor (B1 isoform): cloning and analysis of expression during follicular cell differentiation."
RT Insect Biochem. Mol. Biol. 25:857-866(1995).
RL [2]
RN SEQUENCE OF 61-606 FROM N.A.
RP STRAIN=Kinshu X Showa; TISSUE=Fat body;
RA Kamimura M., Tomita S., Fujiwara H.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES). May play a role in the implementation of the chorionogenic program at the end of vitellogenesis.
CC -1- SUBUNIT: Heterodimer of ECR and CFI (Potential).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49881-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49881-2; Sequence=VSP_003663;
CC -1- DEVELOPMENTAL STAGE: It is present in constant amounts in follicular cells throughout vitellogenesis but disappears transiently at the onset of chorionogenesis and reappears during the later stages of chorionogenesis.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-61 is the initiator.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC EMBL; L35266; AAA87341.1; -.
CC EMBL; L35266; AAA87340.1; -.
DR

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DR EMBL; D43943; BAA07890.1; -.
DR HSSP; P20393; IAGY.
DR InterPro; IPR000536; Hrmn recept lig.
DR InterPro; IPR001723; Strhmn receptor.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHOMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR PROSITE; PS00035; Znf_C4steroid; 1.
KW Alternative splicing; DNA-binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 1 206 Modulating (Potential).
FT DNA BIND 207 272 Nuclear receptor-type.
FT ZN FING 207 227 C4-type.
FT ZN FING 243 267 C4-type.
FT ZN FING 243 267 Hormone-binding (Potential).
FT DOMAIN 364 586 Poly-Gln.
FT DOMAIN 134 142 Poly-Pro.
FT DOMAIN 317 320 Missing (in isoform 2).
FT VARSPLIC 380 382 /FTID-VSP 003663.
FT CONFLICT 67 67 N -> D (in Ref. 2).
FT CONFLICT 81 81 S -> T (in Ref. 2).
FT CONFLICT 108 108 R -> G (in Ref. 2).
FT CONFLICT 469 470 OG -> KA (in Ref. 2).
FT CONFLICT 591 591 A -> P (in Ref. 2).
SQ SEQUENCE 606 AA; 68201 MW; 960E8B9A1E4F2202 CRC64;

Query Match 46.1%; Score 1416; DB 1; Length 606;
Best Local Similarity 82.7%; Pred. No. 3.6e-83;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;

QY 191 MRPCVVPESCKNREKEAQRKDK---LPVSTTTVDHMPATMOCDDPPPEAAIHE 247
DB 191 MRPCVVPESCKNREKEAQRKDK---LPVSTTTVDHMPATMOCDDPPPEAAIHE 247
QY 248 VVPRFLTEKLEQNRKKNVPLSANQSLIARLVWYQGYEQPSSEDLKRVTTQWSADE 307
DB 248 VVPRFLTEKLEQNRKKNVPLSANQSLIARLVWYQGYEQPSSEDLKRVTTQWSADE 307
DB 328 VVPRYSEKLEQNRKKNVPLSANQSLIARLVWYQGYEQPSSEDLKRVTTQWS-DE 386
QY 308 EDESDMPFRQITENTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSVMMMLRVAR 367
DB 308 EDESDMPFRQITENTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSVMMMLRVAR 367
DB 387 EDESDLPFRQITENTILTVQLIVEFAKGLPGFSKISQSDQITLLKACSSVMMMLRVAR 446
QY 368 YDAVSDSVLFANNQAYTRDNYRKAGMAYVEDLLHFCRCMYSMSMDNVHYALLTAIVIFS 427
DB 368 YDAVSDSVLFANNQAYTRDNYRKAGMAYVEDLLHFCRCMYSMSMDNVHYALLTAIVIFS 427
DB 447 YDAASDSVLFANNKAYTRDNYRQGMAYVEDLLHFCRCMFGMGMNDNVHYFALLTAIVIFS 506
QY 428 DRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMNSNM 487
DB 428 DRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMNSNM 487
DB 507 DRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMNSNM 566
QY 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
DB 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
DB 567 CISLKLKNRKLPPFLEEIWDVAEVATTHTPTVLPPTN 602

RESULT 11
Q9U3Y4
ID Q9U3Y4 PRELIMINARY; PRT; 680 AA.
AC Q9U3Y4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)
DE Ecdysteroid receptor.
GN Name=Ecd;
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_Taxid=7160;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20112665; PubMed=10644973;
RX DOI=10.1002/(SICI)1520-6327(200002)43:2<87::AID-ARCHS>3.0.CO;2-O;
RA Jayachandran G., Fallon A.M.;
RT "Evidence for expression of Ecr and USP components of the 20-
RT hydroxyecdysone receptor by a mosquito cell line.";
RL Arch. Insect Biochem. Physiol. 43:87-96(2000).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF210733; AAP19032.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:000496; F:steroid binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHOMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 680 AA; 74924 MW; 272C8E6AB1021C98 CRC64;

Query Match 37.2%; Score 1142; DB 2; Length 680;
Best Local Similarity 60.3%; Pred. No. 2.1e-65;
Matches 228; Conservative 61; Mismatches 67; Indels 22; Gaps 7;

QY 191 MRPCVVPESCKNREKEAQRKDKL---PVSSTTV---DHMPAIMQCDPPPEAA 243
DB 191 MRPCVVPESCKNREKEAQRKDKL---PVSSTTV---DHMPAIMQCDPPPEAA 243
QY 255 MRPCVVPENQCAIKRKEKAQKDKVQTWATVSTTNSYSEILPILMKCDPPP--- 310
DB 255 MRPCVVPENQCAIKRKEKAQKDKVQTWATVSTTNSYSEILPILMKCDPPP--- 310
QY 244 RIHEVPRFLTEKLEQNRKKNVPLSANQSLIARLVWYQGYEQPSSEDLKRVTTQW 303
DB 244 RIHEVPRFLTEKLEQNRKKNVPLSANQSLIARLVWYQGYEQPSSEDLKRVTTQW 303
DB 311 --HQAIP--LLPEKLLQENLRNIPLLTANQMAVYKLIWYQGYEQPSSEDLKRI--MIG 365
QY 304 SADEEDSDMPFRQITENTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSVMMMLR 363
DB 304 SADEEDSDMPFRQITENTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSVMMMLR 363
DB 366 SPNEEQDQHDVHFRIITEITLTVQLIVEFAKGLPAFTKIPQEDQITLLKACSSVMMMLR 425
QY 364 VARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVEDLLHFCRCMYSMSMDNVHYALLTAI 423
DB 364 VARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVEDLLHFCRCMYSMSMDNVHYALLTAI 423
DB 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMFSLTVDNVEYALLTAI 485
QY 424 VIFSDRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMQ 483
DB 424 VIFSDRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMQ 483
DB 486 VIFSDRPGLEQPOLVEEIQRYLYNTLRVYIMQHSGASPRCAVIYAKILSVLTGLTGMQ 545
QY 484 NSNMCIKLNKRLPPFLEEIWDV-----KLAPPTD 515
DB 484 NSNMCIKLNKRLPPFLEEIWDV-----KLAPPTD 515
DB 546 NSEMCFSLLKLNKRLPPFLEEIWDVQDIPP---SMQAMHSHGTPTQSSSSSSSSSSSS 602
DB 541 DLDMGLGDGDSPGPGFTPH 558
DB 603 NGSSNGNSNGPHPHPH 620

RESULT 12
Ecr_AEDAE
ID Ecr_AEDAE STANDARD; PRT; 675 AA.
AC P49880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 43 Seconds
(without alignments)
1020.783 Million cell updates/sec

Title: US-10-087-167-121
Perfect score: 3072
Sequence: 1 MQQYVDFSPAFIRYLFAM.....ADFFEQMTDALGIDEYGG 588

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1582	51.5	546	US-09-393-839-2	Sequence 2, Appli
2	1345	50.3	556	US-09-564-418-11	Sequence 11, Appli
3	1534.5	50.0	557	US-08-653-648A-12	Sequence 12, Appli
4	1461.5	47.6	575	US-08-653-648A-5	Sequence 5, Appli
5	1461.5	47.6	575	US-09-564-418-5	Sequence 5, Appli
6	1449	47.2	319	US-08-653-648A-7	Sequence 7, Appli
7	1449	47.2	319	US-09-564-418-13	Sequence 13, Appli
8	1418.5	46.2	314	US-08-653-648A-16	Sequence 16, Appli
9	1418.5	46.2	314	US-09-564-418-7	Sequence 7, Appli
10	1416	46.1	606	US-08-891-298-3	Sequence 3, Appli
11	1416	46.1	606	US-08-653-648A-11	Sequence 11, Appli
12	1416	46.1	606	US-09-564-418-10	Sequence 10, Appli
13	1139	37.1	674	US-08-653-648A-14	Sequence 14, Appli
14	1139	37.1	675	US-09-564-418-12	Sequence 12, Appli
15	1129.5	36.8	560	US-09-435-019-6	Sequence 6, Appli
16	1129.5	36.8	560	US-09-435-019-9	Sequence 9, Appli
17	1129.5	36.8	560	US-10-065-200A-6	Sequence 6, Appli
18	1129.5	36.8	560	US-10-065-200A-9	Sequence 9, Appli
19	1129.5	36.8	561	US-09-435-019-14	Sequence 14, Appli
20	1129.5	36.8	561	US-09-435-019-17	Sequence 17, Appli
21	1129.5	36.8	561	US-10-065-200A-14	Sequence 14, Appli
22	1129.5	36.8	561	US-10-065-200A-17	Sequence 17, Appli
23	1027.5	33.4	746	US-09-042-488B-5	Sequence 5, Appli
24	1025.5	33.4	550	US-08-659-188-18	Sequence 18, Appli
25	1025.5	33.4	550	US-08-653-227-18	Sequence 18, Appli
26	1025.5	33.4	550	US-08-655-241-18	Sequence 18, Appli
27	1025.5	33.4	550	US-09-398-326-18	Sequence 18, Appli

28	1025.5	33.4	550	4	US-09-853-450-18	Sequence 18, Appli
29	1025.5	33.4	746	4	US-09-042-488B-7	Sequence 7, Appli
30	1025.5	33.4	1041	4	US-09-042-488B-9	Sequence 9, Appli
31	1021.5	33.3	746	3	US-09-144-759-18	Sequence 18, Appli
32	1021.5	33.3	746	4	US-09-570-267-18	Sequence 18, Appli
33	1021.5	33.3	764	3	US-09-144-759-20	Sequence 20, Appli
34	1021.5	33.3	764	3	US-09-570-267-20	Sequence 20, Appli
35	1005	32.7	878	3	US-08-653-648A-15	Sequence 15, Appli
36	1005	32.7	878	4	US-09-564-418-8	Sequence 8, Appli
37	1003.5	32.7	226	3	US-09-133-321-2	Sequence 2, Appli
38	999	32.5	536	3	US-08-653-648A-13	Sequence 13, Appli
39	999	32.5	536	4	US-09-564-418-9	Sequence 9, Appli
40	879	28.6	231	4	US-09-324-258-20	Sequence 20, Appli
41	847.5	27.6	219	4	US-09-435-019-65	Sequence 65, Appli
42	847.5	27.6	219	4	US-09-435-019-67	Sequence 67, Appli
43	847.5	27.6	219	4	US-10-065-200A-65	Sequence 65, Appli
44	847.5	27.6	219	4	US-10-065-200A-67	Sequence 67, Appli
45	768	25.0	496	4	US-08-840-713-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1

US-09-393-839-2
; Sequence 2, Application US/09393839
; Patent No. 6504082
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garmaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/09/393,839
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-09-393-839-2

Query Match	51.5%	Score 1582;	DB 4;	Length 546;
Best Local Similarity	92.8%	Pred. No. 1.8e-135;		
Matches	308;	Conservative	7;	Mismatches 7; Indels 10; Gaps 2;
Qy	191	MRPECVPESTCKNKRREKAEQREKDLPVSTTTTVDHHPAQMCDPPPPPEAARI-----	245	
Db	206	MRPECVPESTCKNKRREKAEQREKDLPVSTTTTVDHHPAQMCDPPPPPEAARI-----	265	
Qy	246	HEVVPREFTEKLMQNRKLNKVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTOTWQA	305	
Db	266	HEVVPREFTEKLMQNRKLNKVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTOTWQA	325	
Qy	306	DEEDSDMPFRQITMTILTVQLIVEPAKGLPGFSKISQDPDITLLKACSEVNMRLVA	365	
Db	326	DEEDSDMPFRQITMTILTVQLIVEPAKGLPGFSKISQDPDITLLKACSEVNMRLVA	385	
Qy	366	RYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYMSMDNVHYALLTAIVI	425	
Db	386	RYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYMSMDNVHYALLTAIVI	445	
Qy	426	FSDRPGLEQPOLVEIQRYIYNTLRVYIMNQHSPRCVAVYAKILLSVLTRELTLGMQNS	485	
Db	446	FSDRPGLEQPOLVEIQRYIYNTLRVYIMNQHSPRCVAVYAKILLSVLTRELTLGMQNS	505	
Qy	486	NMCISLKNRKLPPFLEEIWDVKLAPPTDVS	517	
Db	506	NMCISLKNRKLPPFLEEIMDV-----ADVS	532	

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RESULT 2
US-09-564-418-11
; Sequence 11, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-564-418-11

Query Match      50.3%; Score 1545; DB 4; Length 556;
Best Local Similarity 90.9%; Pred. No. 4.e-132;
Matches 299; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

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Qy 251 RFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTTQWQSADEDE 310
Db 272 RFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTTQWQLEEEEE 331
Qy 311 DSDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVMMLRVARYDA 370
Db 332 ETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 391
Qy 371 VSDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 430
Db 392 ATDSVLFANNQAYTRDNRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 451
Qy 431 GLEQPOLVEEIQRYVLTNRVYIMNQHSPRCACAVIYAKILSVLTSLTELRTLGQNSNMCIS 490
Db 452 GLEQPLLVEEIQRYVLTNRVYILNQHSASPRCAVLFGKILGVLTSLTELRTLGQNSNMCIS 511
Qy 491 LKLKRNKLPPLFEEIWDVKLAPPTDVSIG 519
Db 512 LKLKRNKLPPLFEEIWDVAEVSTTQPTPG 540

RESULT 3
US-08-653-648A-12
; Sequence 12, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-08-653-648A-5

Query Match      47.6%; Score 1461.5; DB 3; Length 575;
Best Local Similarity 87.9%; Pred. No. 1.e-124;
Matches 284; Conservative 16; Mismatches 14; Indels 9; Gaps 2;

Qy 191 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAAARI----- 245
Db 228 MRPECVVPENQCAMKREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAAARILEVCVQ 287
Qy 246 HEVVPFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTTQWQSA 305

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Manduca sexta
US-08-653-648A-12

Query Match      50.0%; Score 1534.5; DB 3; Length 557;
Best Local Similarity 90.6%; Pred. No. 4.e-131;
Matches 299; Conservative 11; Mismatches 19; Indels 1; Gaps 1;

Qy 191 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAAARIHEVVP 250
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Db 272 RFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTTQWQLEEEEE 331
Qy 310 EDSMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSSSEVMMLRVARYD 369
Db 332 ETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYD 391
Qy 370 AVSDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDR 429
Db 392 AATDSVLFANNQAYTRDNRKAGMSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDR 451
Qy 430 PGLQPOLVEEIQRYVLTNRVYIMNQHSPRCACAVIYAKILSVLTSLTELRTLGQNSNMCI 489
Db 452 PGLQPLLVEEIQRYVLTNRVYILNQHSASPRCAVLFGKILGVLTSLTELRTLGQNSNMCI 511
Qy 490 SLKLKRNKLPPLFEEIWDVKLAPPTDVSIG 519
Db 512 SLKLKRNKLPPLFEEIWDVAEVSTTQPTPG 541

RESULT 4
US-08-653-648A-5
; Sequence 5, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-08-653-648A-5

Query Match      47.6%; Score 1461.5; DB 3; Length 575;
Best Local Similarity 87.9%; Pred. No. 1.e-124;
Matches 284; Conservative 16; Mismatches 14; Indels 9; Gaps 2;

Qy 191 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAAARI----- 245
Db 228 MRPECVVPENQCAMKREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAAARILEVCVQ 287
Qy 246 HEVVPFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTTQWQSA 305
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Db 288 HEVPRFLNEKMEQNRLKNVPLTANOKSLIARLVWYQEGYEQSEEDLKRVTQ-----S 343
Qy 306 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
Db 344 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 403
Qy 366 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 425
Db 404 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 463
Qy 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNS 485
Db 464 FSDRGLQPOLVEDIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNS 523
Qy 486 NMCISLKLKRLKLPFLBEIWDV 508
Db 524 NMCISLKLKRLKLPFLBEIWDV 546

RESULT 5

US-09-564-418-5
; Sequence 5, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-5

Query Match 47.6%; Score 1461.5; DB 4; Length 575;
Best Local Similarity 87.9%; Pred. No. 1.9e-124;
Matches 284; Conservative 16; Mismatches 14; Indels 9; Gaps 2;
Qy 191 MRPCVPESTCKNRKEAQRKDKLPVSTTTVDHMPIMQCDPPPPPEAARI----- 245
Db 228 MRPCVWPENQCAMRKEKKAQRKDKLPVSTTTVDHMPPIMQCDPPPPPEAARILECVQ 287
Qy 246 HEVPRFLTEKLMQNRLKNVPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQTWSA 305
Db 288 HEVPRFLNEKMEQNRLKNVPLTANOKSLIARLVWYQEGYEQSEEDLKRVTQ-----S 343
Qy 306 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
Db 344 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 403
Qy 366 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 425
Db 404 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 463
Qy 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNS 485
Db 464 FSDRGLQPOLVEDIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNS 523
Qy 486 NMCISLKLKRLKLPFLBEIWDV 508
Db 524 NMCISLKLKRLKLPFLBEIWDV 546

RESULT 6

US-08-653-648A-7
; Sequence 7, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-7

Query Match 47.2%; Score 1449; DB 3; Length 319;
Best Local Similarity 87.9%; Pred. No. 1.1e-123;
Matches 284; Conservative 15; Mismatches 14; Indels 10; Gaps 3;
Qy 192 RPECVPESTCKNRKEAQRKDKLPVSTTTVDHMPIMQCDPPPPPEAARI-----H 246
Db 1 RPECVWPENQCAMRKEKKAQRKDKLPVSTTTVDHMPPIMQCDPPPPPEAARILECVQH 60
Qy 247 EVPRFLTEKLMQNRLKNVPLSANOKSLIARLVWYQDGYEQSEEDLKRVTQTWSAD 306
Db 61 EVPRFLNEKLMQNRLKNVPLTANOKSLIARLVWYQEGYEQSEEDLKRVTQ-----SD 116
Qy 307 EEDESDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 366
Db 117 EEDESDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 176
Qy 367 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 426
Db 177 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 236
Qy 427 SDRFGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNSN 486
Db 237 SDRFGLQPOLVEIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNSN 296
Qy 487 MCISLKLKRLKLPFLBEIWDV 508
Db 297 MCISLKLKRLKLPFLBEIWDV 319

RESULT 7

US-09-564-418-13
; Sequence 13, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0

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; SEQ ID NO 13
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-13

Query Match      47.2%; Score 1449; DB 4; Length 319;
Best Local Similarity 87.9%; Pred. No. 1.1e-123; Mismatches 14; Indels 10; Gaps 3;
Matches 284; Conservative 15;

Qy 192 RPECVVPSTCKNKRREKAQREKDKLPVSTTTVDHMPAIMQCDPPPEAARI-----H 246
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTVDHMPPIMQCDPPPEAARILECVQH 60

Qy 247 EVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVWQDGYEQPSEEDLKRVTQWOSAD 306
Db 61 EVVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQPSEEDLKRVTQ----SD 116

Qy 307 BEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVAR 366
Db 117 EDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQSQITLLKACSEVMMLRVAR 176

Qy 367 RYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIF 426
Db 177 RYDAATOSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIF 236

Qy 427 SDRGLEQPOLVEEIQRYLYNLTRVYIMNQHSPRCAYIVAKILSVLTTELTLGMQNSN 486
Db 237 SDRGLEQPOLVEEIQRYLYNLTRVYILNQNRSRSPCCPVIVAKILGILTELTLGMQNSN 296

Qy 487 MCISLKLKRLKLPPLLEEI-WDV 508
Db 297 MCISLKLKRLKLPPLLEEIDWDV 319

RESULT 8
US-08-653-648A-16
; Sequence 16; Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-16

Query Match      46.2%; Score 1418.5; DB 3; Length 314;
Best Local Similarity 86.5%; Pred. No. 6.4e-121;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 192 RPECVVPSTCKNKRREKAQREKDKLPVSTTTVDHMPAIMQCDPPPEAARIHEVVR 251
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTVDHMPPIMQCDPPPEAARIHEVVR 60

Qy 252 FLTEKMEQNRLKNVTPLSANQKSLIARLVWQDGYEQPSEEDLKRVTQWQSADEDED 311
Db 61 FLNEKLMERTLRNVPPLTANQKSLIARLVWYQEGYEQPSEEDLKRVTQ----SDEEEE 116

Qy 312 SDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVARVDV 371
Db 117 SDMPFRQITMTILTVQLIVEFAKGLPAFAKISQSQITLLKACSEVMMLRVARVDAA 176

Qy 372 SDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRPG 431
Db 177 TDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRPG 236

Qy 432 LEQPOLVEEIQRYLYNLTRVYIMNQHSPRCAYIVAKILSVLTTELTLGMQNSNMCI 491
Db 237 LEUTLVEEIQRYLYNLTRVYILNQNRSRSPCCPVIVAKILGILTELTLGMQNSNMCI 296

Qy 492 KLKRLKLPPLLEEI-WDV 508
Db 297 KLKRLKLPPLLEEIDWDV 314

US-09-564-418-7
; Sequence 7; Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-09-564-418-7

Query Match      46.2%; Score 1418.5; DB 4; Length 314;
Best Local Similarity 86.5%; Pred. No. 6.4e-121;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 192 RPECVVPSTCKNKRREKAQREKDKLPVSTTTVDHMPAIMQCDPPPEAARIHEVVR 251
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTVDHMPPIMQCDPPPEAARIHEVVR 60

Qy 252 FLTEKMEQNRLKNVTPLSANQKSLIARLVWQDGYEQPSEEDLKRVTQWQSADEDED 311
Db 61 FLNEKLMERTLRNVPPLTANQKSLIARLVWYQEGYEQPSEEDLKRVTQ----SDEEEE 116

Qy 312 SDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVARVDV 371
Db 117 SDMPFRQITMTILTVQLIVEFAKGLPAFAKISQSQITLLKACSEVMMLRVARVDAA 176

Qy 372 SDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRPG 431
Db 177 TDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRPG 236

Qy 432 LEQPOLVEEIQRYLYNLTRVYIMNQHSPRCAYIVAKILSVLTTELTLGMQNSNMCI 491
Db 237 LEUTLVEEIQRYLYNLTRVYILNQNRSRSPCCPVIVAKILGILTELTLGMQNSNMCI 296

Qy 492 KLKRLKLPPLLEEI-WDV 508
Db 297 KLKRLKLPPLLEEIDWDV 314

RESULT 10
US-08-891-298-3
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; Sequence 3, Application US/08891298
; Patent No. 6300488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; APPLICANT: Suhr, Steven T.
; TITLE OF INVENTION: Modified Lipidoperan Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-891-298-3

Query Match 46.1%; Score 1416; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 2.9e-120;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;
QY 191 MRPCVPESTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDDPPPPAARIHE 247
DB 272 MRPCVVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVDHMPIMQCDPPPPAARIHE 327
QY 248 VVPFELTEKLMQENRKNVTPLSANQKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADE 307
DB 328 VVPYRLSEKLMQENRQKNIPPLSANQKSLIARLVYQEGYEQPSDEDLKRVTQTWQSD-DE 386
QY 308 EDESDMPFRQITMTILTTLVQIVEFAKGLPGFSGKISQPDQITLLKACSSVMMMLRVARR 367
DB 387 EDESDLPFRQITMTILTTLVQIVEFAKGLPGFSGKISQSDQITLLKASSSEVMMMLRVARR 446
QY 368 YDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFS 427
DB 447 YDAASDSVLFANNKAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHFALLTAIVIFS 506
QY 428 DRPGLQEPOLVEEIQRYVYLTIRVYIMNOHSASPRCAVIYAKILSVLTETLGTQNSNM 487
DB 507 DRPGLQEPOLVEEIQRYVYLTIRVYIINQNSASRCACAVIYGRILSVLTETLGTQNSNM 566
QY 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
DB 567 CISLKLKNRKLPPFLEEIWDVAEVATHTPTVLPPTN 602

RESULT 11
US-08-653-648A-11
; Sequence 11, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepsen, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-08-653-648A-11

Query Match 46.1%; Score 1416; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 2.9e-120;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;
QY 191 MRPCVPESTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDDPPPPAARIHE 247
DB 272 MRPCVVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVDHMPIMQCDPPPPAARIHE 327
QY 248 VVPFELTEKLMQENRKNVTPLSANQKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADE 307
DB 328 VVPYRLSEKLMQENRQKNIPPLSANQKSLIARLVYQEGYEQPSDEDLKRVTQTWQSD-DE 386
QY 308 EDESDMPFRQITMTILTTLVQIVEFAKGLPGFSGKISQPDQITLLKACSSVMMMLRVARR 367
DB 387 EDESDLPFRQITMTILTTLVQIVEFAKGLPGFSGKISQSDQITLLKASSSEVMMMLRVARR 446
QY 368 YDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFS 427
DB 447 YDAASDSVLFANNKAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHFALLTAIVIFS 506
QY 428 DRPGLQEPOLVEEIQRYVYLTIRVYIMNOHSASPRCAVIYAKILSVLTETLGTQNSNM 487
DB 507 DRPGLQEPOLVEEIQRYVYLTIRVYIINQNSASRCACAVIYGRILSVLTETLGTQNSNM 566
QY 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
DB 567 CISLKLKNRKLPPFLEEIWDVAEVARRHPTVLPPTN 602

RESULT 12
US-09-564-418-10
; Sequence 10, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418

RESULT 15
 US-09-435-019-6
 ; Sequence 6, Application US/09435019
 ; Patent No. 6489140
 ; GENERAL INFORMATION:
 ; APPLICANT: Wisniewski, Nancy
 ; APPLICANT: Bechter, Anna M.
 ; APPLICANT: Jarvis, Eric
 ; TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPINACLE NUCLEIC ACID
 ; TITLE OF INVENTION: MOLECULES, PROTEINS AND USES THEREOF
 ; FILE REFERENCE: FC-4
 ; CURRENT APPLICATION NUMBER: US/09/435,019
 ; CURRENT FILING DATE: 1999-11-05
 ; EARLIER APPLICATION NUMBER: 60/107,559
 ; EARLIER FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Ctenocephalides felis
 US-09-435-019-6

Query Match	36.8%;	Score 1129.5;	DB 4;	Length 560;
Best Local Similarity	62.6%;	Pred. No. 3.3e-94;		
Matches 221;	Conservative 52;	Mismatches 51;	Indels 29;	Gaps 5;
Qy	191	MRPECVVPESTCKNKRREKAQREKDKLPVSTTT-----VDHMPAIMQCD	236	
Db	207	MRPECVVPEQCAWKREKKAQEKDGPISGTGKSAAPLANSALLQKPDILPAVWKCD	266	
Qy	237	PPPEAARIHEVVPFLTEKLMENRRLKNVTPLSANOKSLIARLVVYQDGVEQSEEDLK	296	
Db	267	PLPPEATKV-----KPLSDKILAENIRNVPPPLTANQYVIARLVVYQDGVEQSEEDLR	321	
Qy	297	RVVTQWQSADEEBEDSDMPFRQITTEMILTIVQLLVEFAKGLPGFSKISQPDQITLLKACS	356	
Db	322	RIMISTPA-----EDEALEFRHTEITILTVQLLVEFAKGLPAFTKIPQEDQITLLKACS	376	
Qy	357	SEVWMRLVARRYDAVSDSVLFANNAQVTRDNYRKAGMAYVIEDLLHFCRCWYSMSMDNVH	416	
Db	377	SEVWMRLMARRYDAVSDSILFANNRSYTRDSYKNAGMADTIEDLLHFCRCQMTWTVDNVE	436	
Qy	417	YALLTAIVIESDRPGLPQQLVEEIQRYLYLNTLRVYIMNHSASPRCAVIYAKILSVLTE	476	
Db	437	YALLTAIVIESDRPGLSQADLVEQIQSYVIKTKCYILNRHSGDPKCGILFAKLLSILTE	496	
Qy	477	LRLTGMQNSNWCISLKLKNRKLPPFLBEIWDV-KLAPPTDVSLGDEIHLHGCD	528	
Db	497	LRLTGMQNSMCFALKLNKRLPFLBEIWDVTDNVPPTI-----DSMHVSYSEN	545	

Search completed: April 15, 2005, 14:50:11
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 137 Seconds
(without alignments)
1426.525 Million cell updates/sec

Title: US-10-087-167-121

Perfect score: 3072

Sequence: 1 MQQLYVDFSPAFIRYLFAW.....ADFFEQMTDALGIDYGG 588

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3072	100.0	588	14	US-10-087-167-121
2	3002.5	97.7	593	14	Sequence 121, App
3	2968.5	96.6	591	14	Sequence 119, App
4	2965	96.5	588	14	Sequence 115, App
5	2895.5	94.3	599	14	Sequence 123, App
6	2731	88.9	553	14	Sequence 127, App
7	2552	83.1	620	14	US-10-087-167-105
8	2551.5	83.1	615	14	US-10-087-167-137
9	2494.5	81.2	599	14	Sequence 135, App
10	2493	81.2	602	14	Sequence 148, App
11	2312	75.3	475	14	US-10-087-167-143
12	2082	67.8	499	14	Sequence 129, App
13	2012.5	65.5	504	14	US-10-087-167-68
					Sequence 76, Appl

14	1978.5	64.4	502	14	US-10-087-167-66
15	1975	64.3	499	14	US-10-087-167-70
16	1975	64.3	505	14	US-10-087-167-94
17	1909	62.1	507	14	US-10-087-167-78
18	1905.5	62.0	510	14	US-10-087-167-80
19	1741	56.7	501	14	US-10-087-167-64
20	1716.5	55.9	500	14	US-10-087-167-92
21	1691	55.0	521	14	US-10-087-167-90
22	1670	54.4	513	14	US-10-087-167-74
23	1666.5	54.2	516	14	US-10-087-167-72
24	1638.5	53.3	496	14	US-10-087-167-86
25	1638	53.3	487	14	US-10-087-167-84
26	1582	51.5	546	14	US-10-295-370-2
27	1582	51.5	546	14	US-10-292-356-2
28	1582	51.5	546	14	US-10-292-324-2
29	1557	50.7	556	14	US-10-083-842A-7
30	1557	50.7	556	14	US-10-087-167-2
31	1545	50.3	556	15	US-10-606-060A-11
32	1467	47.8	401	15	US-10-468-199-70
33	1467	47.8	412	9	US-09-965-703-11
34	1467	47.8	412	9	US-09-965-703-12
35	1467	47.8	412	15	US-10-239-134-11
36	1467	47.8	412	15	US-10-239-134-12
37	1467	47.8	440	9	US-09-965-703-71
38	1467	47.8	440	15	US-10-239-134-63
39	1467	47.8	513	9	US-09-965-703-59
40	1467	47.8	513	15	US-10-239-134-50
41	1461.5	47.6	575	15	US-10-606-060A-5
42	1457	47.4	320	9	US-09-965-703-15
43	1457	47.4	320	15	US-10-239-134-15
44	1457	47.4	320	15	US-10-468-199-7
45	1457	47.4	334	9	US-09-965-703-13

ALIGNMENTS

RESULT 1
US-10-087-167-121
; Sequence 121, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 121
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-121

Query Match 100.0%; Score 3072; DB 14; Length 588;
Best Local Similarity 100.0%; Pred. No. 5.5e-248;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQQLYVDFSPAFIRYLFAWYCFRCSPCCVLLQGSATMKLLSSIEQACDLCRLKKL	60
Db	1	MQQLYVDFSPAFIRYLFAWYCFRCSPCCVLLQGSATMKLLSSIEQACDLCRLKKL	60
Qy	61	KCSKEKPKCAKCKKNWECRYSPKTKGSPKTRAHLTVEESLRLEQLFLIFPREDLDM	120
Db	61	KCSKEKPKCAKCKKNWECRYSPKTKGSPKTRAHLTVEESLRLEQLFLIFPREDLDM	120

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QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
QY 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
Db 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
QY 241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
Db 241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
QY 301 TWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
Db 301 TWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
QY 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420
Db 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420
QY 421 TAIIVFSDRPGLEQPOLVEEIQRYLYNLTRVYIMNQHSAASPRCAVIYAKILSVLTELTL 480
Db 421 TAIIVFSDRPGLEQPOLVEEIQRYLYNLTRVYIMNQHSAASPRCAVIYAKILSVLTELTL 480
QY 481 GQNSNMCIISLKNRKLPPLEIEIWDVKLAPPTDVSGLGDELHLDGEDVAMAHADLDDF 540
Db 481 GQNSNMCIISLKNRKLPPLEIEIWDVKLAPPTDVSGLGDELHLDGEDVAMAHADLDDF 540
QY 541 DLDMLGDSGPGGFTPHDSAPYGALDNADFEFQMFMTDALGIDEYGG 588
Db 541 DLDMLGDSGPGGFTPHDSAPYGALDNADFEFQMFMTDALGIDEYGG 588
RESULT 2
US-10-087-167-125
; Sequence 125, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-125
Query Match 97.7%; Score 3002.5; DB 14; Length 593;
Best Local Similarity 97.0%; Pred. No. 3.6e-242;
Matches 575; Conservative 7; Mismatches 6; Indels 5; Gaps 1;
QY 1 MOQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKLL 60
Db 1 MOQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKLL 60
QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLDM 120
Db 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLDM 120
QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
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QY 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
Db 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
QY 241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
Db 241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
QY 296 KRVOTQWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 355
Db 301 KRVOTQWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 360
QY 356 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNV 415
Db 361 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNV 420
QY 416 HYALLTAIIVFSDRPGLEQPOLVEEIQRYLYNLTRVYIMNQHSAASPRCAVIYAKILSVLT 475
Db 421 HYALLTAIIVFSDRPGLEQPOLVEEIQRYLYNLTRVYIMNQHSAASPRCAVIYAKILSVLT 480
QY 476 ELRTILGQNSNMCIISLKNRKLPPLEIEIWDVKLAPPTDVSGLGDELHLDGEDVAMAHAD 535
Db 481 ELRTILGQNSNMCIISLKNRKLPPLEIEIWDVKLAPPTDVSGLGDELHLDGEDVAMAHAD 540
QY 536 ALDDFDLMDLGDGSPGGFTPHDSAPYGALDNADFEFQMFMTDALGIDEYGG 588
Db 541 ALDDFDLMDLGDGSPGGFTPHDSAPYGALDNADFEFQMFMTDALGIDEYGG 593
RESULT 3
US-10-087-167-119
; Sequence 119, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/242,969
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-119
Query Match 96.6%; Score 2968.5; DB 14; Length 591;
Best Local Similarity 95.9%; Pred. No. 2.5e-239;
Matches 568; Conservative 13; Mismatches 6; Indels 5; Gaps 2;
QY 1 MOQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKLL 60
Db 1 MOQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKLL 60
QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLDM 120
Db 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLDM 120
QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
QY 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
Db 181 GORQLTVSTRMRPECVVPSTCKNKRREKEAQEKDPLVSTTTTVDHMPAIMQCDDPPPP 240
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Qy 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDLKRVTQ 300
Db 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDLKRVTQ 300
Qy 301 TWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQPODITLLKACSSVM 360
Db 301 TWQS-DEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQPODITLLKACSSVM 359
Qy 361 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Db 360 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 419
Qy 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYLNTLRVYINNOHSASPRCAVIYAKILSVLTETL 480
Db 420 TAIIVFSRDRPGLQEPQVVEEIQRYLYLNTLRVYINNOHSASPRCAVIYAKILSVLTETL 479
Qy 481 GMQNSNMCIISLKNRKLPPLEETWV- - - - -KLAPPTDVSIGDELHLDGEDVAMAHADA 536
Db 480 GMQNSNMCIISLKNRKLPPLEETWV- - - - -KLAPPTDVSIGDELHLDGEDVAMAHADA 539
Qy 537 LDDFDLMLGDSGSPGPGFTPHDSAPYCALDMADFEFQMTDALGIDEYGG 588
Db 540 LDDFDLMLGDSGSPGPGFTPHDSAPYCALDMADFEFQMTDALGIDEYGG 591

RESULT 4

US-10-087-167-123
; Sequence 123, Application US/10087167
; Publication No. US20030154509A1

GENERAL INFORMATION:

; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-123

Query Match 96.5%; Score 2965; DB 14; Length 588;
Best Local Similarity 96.3%; Pred. No. 4,9e-239;
Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MQQLYVDFSPAFIRYLFAMWCFRCSPCCVLVLLQGSATMKLLSSIEQACDICRLK 60
Db 1 MQQLYVDFSPAFIRYLFAMWCFRCSPCCVLVLLQGSATMKLLSSIEQACDICRLK 60
Qy 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPTRAHLTEVESLERLEQLFLIFREDLDM 120
Db 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPTRAHLTEVESLERLEQLFLIFREDLDM 120
Qy 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Qy 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240
Db 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240
Qy 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDLKRVTQ 300
Db 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDLKRVTQ 300

Qy 301 TWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQPODITLLKACSSVM 360
Db 301 TWQLESEEBETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKASSSEVM 360
Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Db 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Qy 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYLNTLRVYINNOHSASPRCAVIYAKILSVLTETL 480
Db 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYLNTLRVYINNOHSASPRCAVIYAKILSVLTETL 480
Qy 481 GMQNSNMCIISLKNRKLPPLEETWV- - - - -KLAPPTDVSIGDELHLDGEDVAMAHADA 540
Db 481 GTQNSNMCIISLKNRKLPPLEETWV- - - - -KLAPPTDVSIGDELHLDGEDVAMAHADA 540
Qy 541 DLDMLGDSGSPGPGFTPHDSAPYCALDMADFEFQMTDALGIDEYGG 588
Db 541 DLDMLGDSGSPGPGFTPHDSAPYCALDMADFEFQMTDALGIDEYGG 588

RESULT 5

US-10-087-167-127

; Sequence 127, Application US/10087167
; Publication No. US20030154509A1

GENERAL INFORMATION:

; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-127

Query Match 94.3%; Score 2895.5; DB 14; Length 599;
Best Local Similarity 92.7%; Pred. No. 3.3e-233;
Matches 555; Conservative 17; Mismatches 16; Indels 11; Gaps 2;
Qy 1 MQQLYVDFSPAFIRYLFAMWCFRCSPCCVLVLLQGSATMKLLSSIEQACDICRLK 60
Db 1 MQQLYVDFSPAFIRYLFAMWCFRCSPCCVLVLLQGSATMKLLSSIEQACDICRLK 60
Qy 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPTRAHLTEVESLERLEQLFLIFREDLDM 120
Db 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPTRAHLTEVESLERLEQLFLIFREDLDM 120
Qy 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
Qy 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240
Db 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPP 240
Qy 241 EAARIHEVVPFLTEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDL 295
Db 241 EAARILECLQHEVVPFLSEKLMQNRKLVNTPLSANQKSLIARLVVYQDGYEQPSEEDL 300
Qy 296 KRVTQWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQPODITLLKAC 355
Db 301 KRVTQWQLESEEBETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKAS 360

QY 421 TAIVFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOHSASPRCAVYAKILSVLTELRTL 480
DB 421 TAIVFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOHSASPRCAVYAKILSVLTELRTL 480
QY 481 GQNSNMCSLSKLNKRLPPFLLEEIWDVYKLAAPPTDVSIGDEL-----HLDG 526
DB 481 GQNSNMCSLSKLNKRLPPFLLEEIWDVYKLAAPPTDVSIGDEL-----HLDG 526
QY 527 EDVAMAHADAL-----DDFDLMDLGDG--DSFGPGFTPHDSA-----PYGALDM 568
DB 541 ETGALEDSLSLAHLQLQCTEDAERVALGGLGSLDFPSAGKAVLDDDEDSFVMPAAAFDM 598
RESULT 8
US-10-087-167-135
; Sequence 135, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 135
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-135
Query Match 83.1%; Score 2551.5; DB 14; Length 615;
Best Local Similarity 89.8%; Pred. No. 2.1e-204;
Matches 501; Conservative 11; Mismatches 35; Indels 11; Gaps 3;

QY 1 MQQLVDFPSPAFIRYLPFWYCFRCRCPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLVDFPSPAFIRYLPFWYCFRCRCPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
QY 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
DB 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
QY 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
DB 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
QY 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
QY 241 EAARLHVVPRLTEKMEQNLKNVTPLSANQKSLIARLVYQGYEQPSEEDLKRVTQ 300
DB 241 EAARLHVVPRLTEKMEQNLKNVTPLSANQKSLIARLVYQGYEQPSEEDLKRVTQ 300
QY 301 TWQSADEDESDMPFRQITENTILTVLIVEFAKGLPGFSKISQSDQITLLKACSSVM 360
DB 301 TWQSADEDESDMPFRQITENTILTVLIVEFAKGLPGFSKISQSDQITLLKACSSVM 360
QY 361 MLRVARRYDAVSDSVLFANNOYATRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
DB 361 MLRVARRYDAVSDSVLFANNOYATRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
QY 421 TAIVFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOHSASPRCAVYAKILSVLTELRTL 480
DB 421 TAIVFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOHSASPRCAVYAKILSVLTELRTL 480

QY 481 GQNSNMCSLSKLNKRLPPFLLEEIWDV-----KLAPPTDVSIGDELHLDGEDVAMAH 534
DB 481 GQNSNMCSLSKLNKRLPPFLLEEIWDVAEVSTTKL--PKAVRCTGGGLFFPHRDITPAHA 538
QY 535 DALDDFDLMDLGDGDSPG 552
DB 539 ---GETATPMAGGGGGG 553
RESULT 9
US-10-087-167-148
; Sequence 148, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 148
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-148
Query Match 81.2%; Score 2494.5; DB 14; Length 599;
Best Local Similarity 82.6%; Pred. No. 1.2e-199;
Matches 488; Conservative 10; Mismatches 10; Indels 83; Gaps 1;

QY 1 MQQLVDFPSPAFIRYLPFWYCFRCRCPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLVDFPSPAFIRYLPFWYCFRCRCPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
QY 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
DB 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIFPPREDLDM 120
QY 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
DB 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
QY 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 200
DB 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
QY 201 -----TCNKRKEAQRKDK 217
DB 241 DGDSPPGFTPHDSA PYGALDMADPEFQPMFTDALGIDEGYGNCTCKNKRKEAQRKDK 300
QY 218 LPVSTTTVDHMPAIMQCDPPPEAARLHVVPRLTEKMEQNLKNVTPLSANQKSLI 277
DB 301 LPVSTTTVDHMPAIMQCDPPPEAARLHVVPRLTEKMEQNLKNVTPLSANQKSLI 360
QY 278 ARLVYQGYEQPSEEDLKRVTQWQSADEDESDMPFRQITENTILTVLIVEFAKGL 337
DB 361 ARLVYQGYEQPSEEDLKRVTQWQSADEDESDMPFRQITENTILTVLIVEFAKGL 420
QY 338 PGFSKISQSDQITLLKACSSVMMLRVARRYDAVSDSVLFANNOYATRDNYRKAGMAYVI 397
DB 421 PGFSKISQSDQITLLKACSSVMMLRVARRYDAVSDSVLFANNOYATRDNYRKAGMAYVI 480
QY 398 EDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOH 457
DB 481 EDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVYINTLRVYIMNOH 540


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; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 68
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-68

Query Match      67.8%; Score 2082; DB 14; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.9e-165;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 250
DB 102 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARILECIQ 161

QY 246 HEVVPRLFTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQSA 305
DB 162 HEVVPRLFTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQSA 221

QY 306 DEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
DB 222 DEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 281

QY 366 RRYDAVSDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 425
DB 282 RRYDAVSDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 341

QY 426 FSDRPGLEQPOLVBEIQRYIYNTLRVYIMNQHSPRCVIAKYLSVLTGTMQNS 485
DB 342 FSDRPGLEQPOLVBEIQRYIYNTLRVYIMNQHSPRCVIAKYLSVLTGTMQNS 401

QY 486 NMCISLKLKRNKLPFLFEEIWDVKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLML 545
DB 402 NMCISLKLKRNKLPFLFEEIWDVKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLML 461

QY 546 GDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588
DB 462 GDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 504

RESULT 14
US-10-087-167-66
; Sequence 66, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 66
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-66

Query Match      64.4%; Score 1978.5; DB 14; Length 502;
Best Local Similarity 94.0%; Pred. No. 1.3e-156;
Matches 378; Conservative 13; Mismatches 6; Indels 5; Gaps 2;

QY 191 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 250
DB 102 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 161

QY 251 RFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADEDE 310
DB 162 RFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADEDE 220

QY 311 DSDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 370
DB 221 DSDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 280

QY 371 VSDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 430
DB 281 ATDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 340

; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-76

Query Match      65.5%; Score 2012.5; DB 14; Length 504;
Best Local Similarity 95.5%; Pred. No. 1.9e-159;
Matches 385; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

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Qy 431 GLEQPLVEEIQRYYLNTLRVYIMNQHSASPRCAVIYAKILSVLTSLTGLGMQNSNCIS 490
Db 341 GLEQPLAVEEIQRYYLNTLRVYILNQNSASPRCPVWFAKILGILTELTLGMQNSNCIS 400
Qy 491 LKLNKRLPPFLEEIWV-----KLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLG 546
Db 401 LKLNKRLPPFLEEIWVESRGLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLG 460
Qy 547 DGDSPGCGFTPHDSAPYCALDMADFEFQMFTDALGIDEYGG 588
Db 461 DGDSPGCGFTPHDSAPYCALDMADFEFQMFTDALGIDEYGG 502
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RESULT 15

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US-10-087-167-70
; Sequence 70, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-70
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Query Match 64.3%; Score 1975; DB 14; Length 499;
Best Local Similarity 94.5%; Pred. No. 2.6e-156;
Matches 376; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 191 MRPECVWPSTCKNKRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPEAAARIHEVVP 250
Db 102 MRPECVWPSTCKNKRKEKAQREKDLPVSTTTVDHMPAIMQCDPPPEAAARIHEVVP 161
Qy 251 RPLTEKLMQNRLKNVTPLSANQKSLIARLWYQDGYEQPSEEDLKRVTQTWQSADDEE 310
Db 162 RPLTEKLMQNRLKNVTPLSANQKSLIARLWYQDGYEQPSEEDLKRVTQTWQLEEEEEE 221
Qy 311 DSDMPFQITMTILTTLVQLIVEFAKLPFGFSKISQPDQITLLKACSEVMMLRVARRYDA 370
Db 222 ETDMFPQITMTILTTLVQLIVEFAKLPFGFSKISQSDQITLLKASSEVMMLRVARRYDA 281
Qy 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 430
Db 282 ATDSVLFANNQAYTRDNYRKAGMSYVIGDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 341
Qy 431 GLEQPLVEEIQRYYLNTLRVYIMNQHSASPRCAVIYAKILSVLTSLTGLGMQNSNCIS 490
Db 342 GLEQPLAVEEIQRYYLNTLRVYILNQNSASPRCAVLFGKILGVLTELTLGTQNSNCIS 401
Qy 491 LKLNKRLPPFLEEIWVKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLGDGDS 550
Db 402 LKLNKRLPPFLEEIWVKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLGDGDS 461
Qy 551 FPGGFTPHDSAPYCALDMADFEFQMFTDALGIDEYGG 588
Db 462 FPGGFTPHDSAPYCALDMADFEFQMFTDALGIDEYGG 499
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Search completed: April 15, 2005, 14:54:00
Job time : 139 secs